Appendix B: **AP Biology Equations** and Formulas

Statistical Analysis and Probability

Standard Error

 $SE_{\overline{X}} = \frac{S}{\sqrt{n}}$

$$\overline{X} = \frac{1}{n} \sum_{i=1}^{n} X_i$$

Standard Deviation

Chi-Square

$$S = \sqrt{\frac{\sum (x_i - \bar{x})^2}{n - 1}}$$

$$\chi^2 = \sum \frac{(o-e)^2}{e}$$

16.81

18.48

20.09

o = observed individuals with observed genotype

e = expected individuals with observed genotype Degrees of freedom equals the number of distinct

s = sample standard deviation (i.e., the sample based estimate of the standard deviation of the population)

 $\overline{x} = \text{mean}$

n =size of the sample

possible outcomes minus one.

Chi-Square Table Degrees of Freedom 5 9,49 15.51

Metric Prefixes

Laws of Probability

0.01 6,64 9,32

If A and B are mutually exclusive, then P(A or B) = P(A) + P(B)

11,34 13.28 15.09

If A and B are independent, then $P(A \text{ and } B) = P(A) \times P(B)$

Hardy-Weinberg Equations

 $p^2 + 2pq + q^2 = 1$

p =frequency of the dominant allele

in a population

q = frequency of the recessive allele

in a population

<u>Factor</u>	Prefix	Symbol
$\frac{10^{9}}{10^{9}}$	giga	G
10^{6}	mega	M
10^{3}	kilo	k
10 ⁻²	centi	С
10 ³ 10 ⁻² 10 ⁻³ 10 ⁻⁶ 10 ⁻⁹ 10 ⁻¹²	milli	m
10 ⁻⁶	micro	μ
10 ⁻⁹	nano	n
10-12	pico	p

Mode = value that occurs most frequently in a data set

Median = middle value that separates the greater and lesser halves of a data set

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n =size of the sample

o = observed individuals with observed genotype

s = sample standard deviation (i.e., the sample based estimate of the standard deviation of the population)

e = expected individuals with observed genotype

Degrees of freedom equals the number of distinct possible outcomes minus one.

Chi-Square Table

	Degrees of Freedom							
P	1	2	3	4	5	6	7	8
0.05	3.84	5.99	7.82	9.49	11.07	12.59	14.07	15.51
0.01	6,64	9.32	11.34	13,28	15,09	16,81	18,48	20,09

Laws of Probability

If A and B are mutually exclusive, then P(A or B) = P(A) + P(B)If A and B are independent, then $P(A \text{ and } B) = P(A) \times P(B)$

Hardy-Weinberg Equations

 $p^2 + 2pq + q^2 = 1$

p = frequency of the dominant allele

in a population

q = frequency of the recessive allele in a population

Mode = value that occurs most frequently in a data set

Median = middle value that separates the greater and lesser halves of a data set

Mean = sum of all data points divided by number of data points

Range = value obtained by subtracting the smallest observation (sample minimum) from the greatest (sample maximum)

<u>Factor</u>	Prefix	Symbol
Factor 10 ⁹	giga	G
10 ⁶	mega	M
10 ³	kilo	k
10 ⁻²	centi	c
10 ³ 10 ⁻² 10 ⁻³ 10 ⁻⁶ 10 ⁻⁹ 10 ⁻¹²	milli	m
10-6	micro	μ
10-9	nano	n
10 ⁻¹²	pico	p