

GLOSSARY

A: Abbreviated symbol for the base adenine.

Allele: One of several alternate forms of a gene which occupies a specific locus on a chromosome.

Allele: One of the two gene pairs situated at the same location (locus) on a chromosome; one allele is inherited from the mother and the other from the father.

Allelic exclusion: The expression in a particular lymphocyte of one specific allele which codes for the expressed immunoglobulin.

Alu family: A set of dispersed, related sequences in the human genome. Each is approximately 300 bp long and can be cleaved at each end by an Alu restriction endonuclease.

Amber codon: The nucleotide triplet UAG, a "nonsense" codon that causes termination of protein synthesis.

Amplification: The production of added copies of a chromosomal sequence.

Annealing: The pairing of complementary single strands of nucleic acid.

Anticodon: A trinucleotide sequence on a tRNA molecule which is complementary to the codon representing its amino acid, enabling the tRNA to recognize the codon on the mRNA via complementary base pairing.

Antiparallel: Refers to the strands of duplex nucleic acid which are organized in opposite orientation, with the 5' end of one strand aligned with the 3' end of the other strand.

Base pair: A partnership of A with T or of C with G in a double stranded DNA. Often abbreviated "bp."

Biallelic damage: Damage to both maternal and paternal copies of a gene.

Bioinformatics: The computational biological process designed to handle and interpret the streams of DNA data entering various computer data bases in association with the effort to sequence the human genome

Blunt-end: Refers to two strands of DNA whose ends are of identical length, with complete base pairing. See staggered cuts or skickey ends.

bp: Abbreviation for "base pairs." Often used as a measure for the distance along DNA.

C: Abbreviation for the base cytosine.

CAAT box: A conserved sequence, located approximately 75 bp upstream of the

startpoint of most eukaryotic transcription units. It is recognized by a large group of transcription factors.

Cap: The structure at the 5' end of eukaryotic mRNA, which is added after transcription by linking the terminal phosphate of 5' GTP to the terminal base of the mRNA.

cDNA clone: A double stranded DNA sequence which represents an RNA, carried in a cloning vector.

cDNA: Abbreviation for "complementary DNA," a single stranded DNA molecule which is complementary to an RNA. It is synthesized in vitro from the RNA by reverse transcription.

CGAP: Cancer Genome Anatomy Project; objective is to identify all human cancer genes. There is also a mouse CGAP.

Chromatin: The complex of DNA and protein in the nucleus of the cell.

Chromosome walking: The process by which clones carrying overlapping sequences of DNA are sequentially isolated, allowing large regions of the chromosome to be spanned.

Cis-acting locus: A property which affects the activity only of DNA sequences on its own molecule of DNA, usually implying that the locus is in the DNA sequence itself and does not code for protein.

Cistron: A segment of DNA or RNA that encodes a single polypeptide chain.

Clonal: pertaining to a clone; a line of cells decendent from a single cell.

Clone: A large number of cells or molecules identical to a single ancestral cell or molecule.

Cloning vector: A plasmid or a phage which is used to carry inserted foreign DNA.

Closed reading frame: Refers to a reading frame of a nucleotide sequence which contains termination codons which would prevent translation into protein.

Coding strand: A strand of DNA which has the same sequence as mRNA. Often called the positive strand. The complementary or negative strand is referred to as the template strand.

Codon: A triplet of nucleotides which represents an amino acid or a termination (nonsense) signal.

Concatemer: A series of unit genomes which are repeated in tandem.

Consensus sequence: An idealized sequence in which each position represents the base most often found when many actual sequences are compared.

Constitutive genes: Genes which are expressed all the time, without added regulatory processes. Also called housekeeping genes.

Cotransfection: The simultaneous transfection of two markers.

Cruciform: A structure produced at inverted repeats of DNA when the repeated sequence pairs with its complement on the same strand.

Degeneracy: Refers to situations where there is lack of an effect of the third base of the codon on the amino acid that is represented.

Deletion: The removal of a sequence of DNA with the regions on either side being joined together.

Denaturation: The conversion of DNA from double stranded to single stranded state.

Direct repeats: Identical or related sequences which are present in two or more copies in the same orientation in the same molecule of DNA. The repeats do not have to be adjacent.

DNA: abbreviation for deoxyribonucleic acid; the basic building block of genetic material in all organisms except RNA viruses.

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DNase: An enzyme that attacks bonds in DNA.

DNA polymerase: An enzyme that synthesizes a daughter strand of DNA in either replication or repair.

DNA replicase: An enzyme that synthesizes DNA and is specifically required for replication.

Domain: A discrete structural entity within a chromosome where supercoiling is independent of other domains. May also refer to an extensive region including an expressed gene with heightened sensitivity to degradation by DNAase.

Downstream: Sequences proceeding farther in the direction of expression, i.e. toward the 3' end of the nucleic acid.

Elongation factors: Proteins which associate with ribosomes in a cyclic fashion for the sequential addition of each amino acid to the polypeptide chain.

End labeling: The addition of a radioactive or fluorescent labeled group to one end (either 5' or 3') of a nucleic acid.

Endonuclease: An enzyme which cleaves bonds within a nucleic acid chain. It may be specific for RNA, DNA, single stranded DNA, or double stranded DNA.

Enhancer: An element which is cis-acting, which increases the utilization of some eukaryotic promoters, and which can function in either orientation and in any location (downstream or upstream) relative to the promoter.

Epigenetic: Changes which influence the phenotype without changing the genotype.

EST: Expressed sequence tag. Short coding sequences (~150-300 nucleotides) representing portions of expressed genes. A current effort is underway to catalog thousands of EST's and identify the genes from which they originate.

Eukaryote: An organism whose genes are located in chromosomes inside a nucleus.

Exon: A segment of an interrupted gene that is represented in the mature RNA product.

Exonuclease: An enzyme which cleaves nucleotides one at a time from the end of a polynucleotide chain. The enzyme may be specific for either DNA, RNA, or the 3' or 5' end.

Expression vector: A cloning vector which is designed so that a coding sequence inserted at a particular site will be transcribed and translated into protein.

Filter hybridization: The incubation of a denatured nucleic acid (usually DNA) preparation immobilized on a filter with a solution of radioactively or fluorescently labeled RNA or DNA.

Fingerprint: A pattern within DNA where there is a pattern of polymorphic restriction fragments that differ between individual genomes.

Five Prime (5'): Refers to the 5' carbon position of ribose or deoxyribose to which phosphate groups may be attached; signifying one end of a polynucleotide chain.

Footprinting: A technique to identify the site on DNA which is bound by a protein by virtue of the protection of phosphodiester bonds in this region against attack by nucleases.

Frameshift mutation: A mutation which arises by deletions or insertions which are not a multiple of 3 bp. This results in a change in the reading frame in which triplets are translated into protein.

G: Abbreviation of the base guanine.

Gap: The absence of one or more nucleotides in one of the strands of duplex DNA.

Gene cluster: A group of adjacent genes which are identical or related.

Gene dosage: The number of copies of a particular gene in the genome.

Gene family: A set of genes whose exons are related, usually derived by duplication and variation from an ancestral gene.

Gene: A segment of DNA involved in producing a polypeptide chain or a specific RNA molecule. It is sometimes called a cistron. A gene may include regions preceding and following the coding regions (leader, trailer) as well as introns between individual exons.

Gene: the basic biological unit of heredity which is located on a chromosome.

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Genetic code: The correspondence between triplets in DNA or RNA and the amino acids in protein.

Genome: the total complement of genes present in the set of chromosomes characteristic of a given organism.

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Genomic clone: A clone which contains sequences of the genome carried by a cloning vector.

Genotoxic: toxic to DNA; an agent or process that interacts with cellular DNA either directly or after metabolic transformation; mutagens are genotoxic agents.

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Genotype: The genetic constitution of an organism.

Growth factors: agents that contribute to and stimulate tissue growth.

GT-AG rule: The presence of specific dinucleotides at the first two and the last two positions of introns of nuclear genes.

Hairpin: A double helical region formed by base pairing between adjacent, inverted, complementary sequences in a single strand of nucleic acid.

Haploid: Refers to the set of chromosomes which contains one copy of each autosome and one sex chromosome.

Hemizygote: A diploid individual that has lost one of the two copies of a particular gene (e.g., because a chromosome or part of a chromosome has been lost), resulting in only a single copy of that gene. A transgenic animal may be hemizygous for a particular transgene if that animal has only one copy of the transgene.

Heterochromatin: Regions of the genome which are permanently in a highly condensed condition and are not genetically expressed.

Heteroduplex DNA: DNA which is generated by base pairing between complementary single strands derived from the different parental duplex molecules. Also called hybrid DNA.

Heterozygote: An individual with different alleles at a particular locus .

Heterozygous: having different alleles at a specific position on a chromosome.

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Histones: Conserved DNA binding proteins of eukaryotes which form the nucleosome, the basic subunit of chromatin.

Hogness box: Also called the TATA box. A conserved A-T rich septamer which is approximately 25 bp upstream of the startpoint of nuclear genes and which is thought to be involved in the correct positioning of RNA polymerase II for initiation of transcription.

Homeo box: The conserved sequence which is a part of the coding region of Drosophila melanogaster homeotic genes. It is also found in amphibian and mammalian genes expressed in early embryonic development.

Homeotic genes: Genes which are defined by mutations that convert one body part into another in Drosophila melanogaster.

Homologous: Chromosomes which carry the same genetic loci. A diploid cell therefore has two copies of each homologue, one from each parent.

Homozygote: An individual with the same allele at a particular locus on the homologous chromosomes.

Homozygous: having identical alleles at a specific position on a chromosome.

Hotspot: A site at which the frequency of mutation or recombination is much increased.

Housekeeping genes: Genes theoretically expressed in all cells because they provide for basic functions needed for sustenance of all cell types. (See constitutive).

Hybridization: The pairing of complementary RNA or DNA strands to give a double stranded nucleic acid.

Hyperchromatocity: The increase in optical density that occurs when DNA is denatured.

Hypersensitive site: A short region of chromatin which is detected by its extreme sensitivity to cleavage by DNase I or other nucleases. It probably comprises an area from which nucleosomes are excluded.

Imprinting: Describes a change in a gene that occurs during passage through the sperm or egg and results in the paternal and maternal alleles having different properties of expression, particularly important in early embryogenesis and appearing to play a role in some cancers. may be caused by methylation of DNA.

In situ hybridization: The technique of hybridization applied to cells to provide the precise localization of a specific nucleic acid sequence.

Inducer: A molecule that triggers gene transcription by binding to a regulatory protein.

Induction: The switching on of transcription as a result of interaction of an inducer with a regulatory protein, resulting in increased gene expression.

Initiation factors: Proteins which associate with the small subunit of the ribosome specifically at the stage of initiation of protein synthesis.

Insertion: The presence of additional base pairs of DNA.

Intercistronic region: The distance between the termination codon of one gene and the initiation codon of the next gene.

Intervening sequence: **See intron.

Intron: A segment of DNA which is transcribed, but is later removed from within the transcript by splicing together the sequences (exons) on either side of it. Also called intervening sequence.

Inverted repeat: Two copies of the same sequence of DNA which are repeated in opposite orientation to each other on the same molecule. If the inverted repeats are adjacent to each other, a palindrome is formed.

Karyotype: The entire chromosomal complement of a cell visualized during mitosis.

kb: Abbreviation for 1000 base pairs of DNA or 1000 bases of RNA.

Kinase: An enzyme that adds a gamma phosphate from ATP to the 5' end of a polynucleotide chain.

Knockout: An experiment in which a defective gene replaces a normal gene in the genome of an organism.

Leader: The nontranslated sequence at the 5' end of mRNA which precedes the initiating methionine.

Library: A set of cloned fragments which together represent either an entire genome or a representative sample of a particular subset of expressed genes.

Ligation: The formation of a phosphodiester bond to link two bases.

Linkage: The tendency of genes to be inherited together as a result of their location on the same chromosome.

Linker fragment: A short synthetic duplex oligonucleotide which contains the target site for a restriction enzyme, which may be added to ends of a DNA fragment during reconstructions of recombinant DNA.

Locus: The position on a chromosome at which the gene for a particular trait is located.

LTR: Abbreviation of "long terminal repeat," a sequence directly repeated at both ends of a retroviral DNA.

Luxury genes: Genes coding for specialized functions and generally produced in large amounts in particular cell types.

Map distance: A measurement of the distance between points on a chromosome, measured as centiMorgans (cM), as determined by the percent recombination between two loci.

Marker: A fragment of known size used to calibrate an electrophoretic gel.

Melting temperature: The midpoint of the temperature range over which DNA is denatured, often abbreviated as T_m .

Melting: The denaturation of DNA.

Microsatellites (short tandem repeats): Dinucleotide (and sometimes trinucleotide) repeats (e.g., CA:GT) scattered throughout the genome. The number of repeats at any given locus varies between individuals and, thus, may be used as a genetic marker. A microsatellite instability assay has been used as a generic measure of genetic damage.

Modification: Changes made to the nucleotides after their initial incorporation into the polynucleotide chain.

Modified base: A base other than the usual T, C, A, G, or U which results from postsynthetic changes in the nucleic acid.

mRNA: Abbreviation of messenger RNA.

Mutation: A change in the sequence of genomic DNA.

Mutation: a structural alteration in DNA that is hereditary and may give rise to an altered phenotype.

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Negative strand: Sometimes used to refer to that strand of duplex DNA which is the template to direct the synthesis of RNA that is complementary to it; the negative strand is complementary to the coding strand.

Nick translation: A technique used to introduce labeled nucleotides into DNA in vitro, made possible by the ability of *E. coli* DNA polymerase I to use a nick as a starting point from which one strand of a duplex DNA is degraded and then replaced by the resynthesis of new material containing the label.

Nick: The absence of a phosphodiester bond between two adjacent nucleotides on one strand of a duplex DNA.

Nonsense codon: Any one of three triplets (UAG, UAA, UGA) that cause termination of protein synthesis. Also called amber (UAG), ochre (UAA), umber (UGA).

Nonsense mutation: A change in the DNA that causes a nonsense codon to replace a codon representing an amino acid.

Northern blotting: A technique for transferring RNA from an agarose gel to a filter on which it can be hybridized to complementary DNA.

Nucleosome: The basic structural subunit of chromatin, consisting of approximately 200 bp of DNA and an octamer of histone proteins.

Nucleotide: a biochemical component of DNA that consists of a purine or pyrimidine base, a ribose or deoxyribose sugar, and a phosphate group; a basic building block of DNA.

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Ochre codon: The triplet UAA, one of three nonsense codons that causes termination of protein synthesis.

Oligonucleotide: A short stretch of DNA (or RNA) consisting of just a few nucleotides.

Oligo-dT: A short chain of DNA whose bases are all thymine.

Oncogene activation: the process whereby a protooncogene is altered such that it stimulates enhanced cellular growth; several different mechanisms can lead to such activation.

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Oncogene: a 'so-called' cancer gene because alterations in its structure or expression are typically associated with neoplasms; an activated form of a protooncogene.

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Oncogenes: Genes whose products have the ability to transform eukaryotic cells so that they grow like tumor cells. They are carried by retroviruses.

Open reading frame: Refers to a series of triplets coding for amino acids resulting in a sequence which is potentially translatable into protein.

Operator: The site on DNA at which a repressor protein binds to prevent transcription from initiating at the adjacent promoter.

Operon: A unit of bacterial gene expression and regulation, often containing a series of related structural genes and DNA control elements recognized by regulatory proteins. The cluster of genes is often transcribed together to give a single molecule of mRNA.

Origin (ori): The sequence of DNA at which replication is initiated.

Palindrome: A sequence of DNA that is the same when one strand is read left to right, or the other strand is read right to left, consisting of adjacent inverted repeats.

PCR: Polymerase chain reaction

Periodicity: Refers to the number of bp per turn of the double helix.

Phenotype: The characteristics (outward appearance) of an organism which result from the interaction of the genetic constitution and the environment.

Phenotype: the physical appearance, biochemical makeup, and physiological behavior of an individual.

Phosphatase: An enzyme that removes the 5' phosphate from a polynucleotide chain.

Plasmid: An autonomous self-replicating extrachromosomal circular DNA.

Ploidy: The number of copies of the chromosome set which is present in a cell: e.g., haploid has one copy, diploid has two copies, and polyploid has more than two copies, etc.

Point mutation: A change involving a single base pair.

PolyA tail: A string of adenines on the 3' end of mRNA in eukaryotes.

Polyadenylation: The addition of a sequence of polyadenylic acid (multiple A's) to the 3' end of a eukaryotic RNA after transcription.

Polymerase chain reaction: The enzymatic synthesis and amplification of specific DNA sequences. Referred to as PCR.

Polymorphism: The simultaneous occurrence in the population of genomes showing allelic variations.

Polysome: A polyribosome, with a mRNA associated with a series of ribosomes engaged in translation.

Positive strand: Sometimes used to refer to the coding strand of duplex DNA, having the same sequence as the mRNA.

Primary transcript: The original and unmodified RNA product corresponding to a transcription unit. In eukaryotic cells, it contains the introns.

Primer: A short sequence which is paired with one strand of DNA to provide a free 3' OH end at which a DNA polymerase starts synthesis of a deoxyribonucleotide chain. A short sequence of nucleic acid that binds to the template strand and allows synthesis of a new chain of DNA to commence. RNA primers are used in vivo and DNA primers are used in the PCR reaction.

Probe: A nucleic acid which is labeled (usually radioactively or with a fluorescent dye) and can hybridize to another nucleic acid on the basis of complementarity.

Promoter: A region of DNA involved in binding of RNA polymerase to initiate transcription.

Proto-oncogenes: The normal counterparts in the eukaryotic genome to the oncogenes carried by retroviruses, usually given names of the form c-onc; normal cellular structural genes that, when activated by mutations, amplifications, rearrangements, or viral transduction, functions as oncogenes and are associated with neoplasia; regulate normal processes related to cell growth and differentiation.

Pseudogene: An inactive but stable component of the genome which is derived by mutation of an ancestral active gene.

Purine: Fused five and six member rings. The bases adenine (A) and guanine (G) are purines.

Pyrimidine: Six member rings. The bases thymine (T), uracil (U), and cytosine (C) are pyrimidines.

Reading frame: **One of three possible ways of reading a nucleotide sequence as a series of triplets.

Reassociation: The pairing of complementary single strands of DNA to form a double helix.

Recognition site: Specific base sequence where a restriction enzyme binds.

Regulatory gene: A gene which encodes an RNA or protein product whose function is to control the expression of other genes.

Renaturation: The reassociation of denatured complementary single strands of a DNA double helix. May also be used to describe the recovery of structure of a denatured protein.

Repression: Inhibition of transcription or translation by the binding of a repressor protein to a specific site on DNA or RNA.

Restriction enzyme: An enzyme (endonuclease) which recognizes a specific short sequence of DNA and cleaves the DNA either at that site or at some defined distance from it.

Restriction fragment length polymorphism: Refers to a change in the length of a restriction fragment due to an inherited difference in sites for restriction enzymes. Abbreviated form is RFLP.

Restriction fragment: Refers to a fragment of DNA which has been cleaved from a larger piece of DNA by the action of a specific restriction enzyme.

Restriction map: A linear array of sites on DNA cleaved by various restriction enzymes.

Retrovirus: An RNA virus that propagates via conversion into duplex DNA.

Reverse transcription: The synthesis of DNA on a template of RNA, accomplished by reverse transcriptase enzyme.

Reverse translation: A technique for isolating genes or cDNAs by their ability to hybridize with a short oligonucleotide sequence which is prepared by predicting the nucleic acid sequence from the known protein sequence.

RFLP: Restriction fragment length polymorphism

RNase: An enzyme which attacks bonds in RNA.

rRNA: Abbreviation of ribosomal RNA.

S1 nuclease: An enzyme that specifically degrades single stranded sequences of DNA.

Saturation hybridization: A hybridization experiment in which a large excess of one component is present, causing all complementary sequences in the other component to enter a duplex form.

Selection: The use of particular conditions, e.g. antibiotic resistance, to allow survival only of cells with a particular phenotype.

Shotgun experiment: The cloning of an entire genome or set of DNA fragments in the form of randomly generated fragments.

Shuttle vector: A vector, often a plasmid, which is constructed to have origins for replication for two hosts, so that it can be used to carry a foreign sequence in either prokaryotes or eukaryotes.

Silent mutation: A change in the DNA which does not change the product of the gene.

snRNA: Small nuclear RNA species which are in the nucleus and which may be involved in splicing or other RNA processing reactions.

Snurps: Small nuclear ribonucleoproteins; snRNAs associated with proteins.

Somatic cells: Cells of an organism which are not those of the germ line.

Somatic mutation: A mutation occurring in a somatic cell, affecting only the descendants of that particular cell, and therefore not inherited by the individual.

Southern blotting: The procedure by which denatured DNA is transferred from an agarose gel to a filter on which it can be hybridized with a complementary nucleic acid.

Splicing junctions: The sequences immediately surrounding the exon-intron boundaries, which often show conserved features.

Splicing: The removal of introns and the joining of exons in RNA.

Spontaneous mutation: A mutation which occurs in the absence of any known added reagent to increase the mutation rate.

ssDNA: Single stranded DNA.

Staggered cuts: The cuts which are made in duplex DNA when two strands are cleaved (usually by a restriction enzyme) at different points near each other. The result is a duplex DNA with either an overhang of 5' or 3' sequences on each strand, called sticky ends.

Stem: The base paired segment of a hairpin.

Sticky ends: Complementary single strands of DNA that protrude from opposite ends of a duplex molecule, often generated by staggered cuts in duplex DNA.

Stop codon: Codon that signals the end of a protein. Also called nonsense codon.

Structural gene: A gene which codes for any RNA or protein product other than a regulator.

STS: A sequence tag site that is used in the human genome project to construct overlapping maps of gene fragments.

Subcloning: The process in which a fragment of a gene that has already been cloned is recloned into a vector.

Suppression: The occurrence of changes that eliminate the effects of a mutation, without reversing the original change in the DNA.

Suppressor: A compensating mutation that restores the original meaning of a gene. It may be extragenic, undoing a mutant tRNA which reads the mutated codon in the sense of the original codon, or it may be intragenic, restoring the original reading frame after a frameshift mutation.

T: Abbreviation for the base thymine.

Tandem repeats: Multiple copies of the same sequence which lie in a series.

TATA box: Also called a Hogness box. A conserved A-T rich septamer found approximately 25 bp before the startpoint of most eukaryotic nuclear genes and thought to be involved in positioning the RNA polymerase II for correct initiation of transcription.

Termination codon: Also called a nonsense codon. One of three triplet sequences, UAG, UAA, or UGA that cause termination of protein synthesis.

Thymine dimer: A chemically cross-linked pair of adjacent thymine residues in DNA, the result of damage induced by ultraviolet radiation.

T_m: Abbreviation for melting temperature.

Trailer: The nontranslated sequence at the 3' end of an mRNA following the termination codon.

Trans: Refers to the presence of two sites on two different molecules of DNA.

Transcription: The synthesis of RNA on a DNA template.

Transduction: The transfer of a bacterial gene from one bacterium to another by a phage.

Transfection: The acquisition of new genetic material by incorporation of added DNA into eukaryotic cells.

Transformation: In bacteria, the acquisition of new genetic markers by incorporation of added DNA, usually by a plasmid. In eukaryotic cells, refers to the conversion to a state of unrestrained growth in culture, resembling the tumorigenic condition.

Transgenic mouse: A mouse in which a foreign gene has been introduced into the germline, with propagation of the added genetic material to the progeny.

Transition: A mutation in which one pyrimidine is substituted by the other, or in which one purine is substituted for the other.

Translation: The synthesis of protein on the mRNA template.

Transition: A mutation in which one pyrimidine is substitute for another pyrimidine or one purine is substitute for another purine.

Translocation: A rearrangement in which one part of a chromosome is detached by breakage and then becomes attached to another chromosome.

Transversion: A mutation in which a purine is replaced by a pyrimidine, or vice versa.

tRNA: Abbreviation of transfer RNA.

Tumor suppressor gene: a gene that normally functions to suppress uncontrolled tissue growth by inhibiting the activity of oncogenes; sometimes called an ‘ anti-oncogene.

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U: Abbreviation of the base uracil.

Umber codon: The nucleotide triplet UGA, a nonsense codon that causes termination of protein synthesis.

Upstream: Sequences proceeding in the opposite direction from expression (in the 5' direction) or located on the 5' side of a particular point.

Wobble hypothesis: A hypothesis which accounts for the ability of a tRNA to recognize more than one codon by unusual pairing with the third base of a codon.

YAC: Abbreviation for a yeast artificial chromosome, which is a fragment of a chromosome from one species with regions of yeast chromosomes that permit the

chromosome to be perpetuated in yeast. YACs are used in the human genome project to clone large segments of genes from human or other species.

Zoo blot: Use of Southern blotting to test the ability of a DNA probe from one species to hybridize with the DNA of a variety of other species.