



EMGEN Newsletter

Vol. 5, Issue 5

IN THIS ISSUE:

1. Training, P 2
2. Trends, P 6
3. News, P 10
4. Journal Alert, P 11
5. Book Alert, P 12
6. Announcement, P 13
7. Cover pictures description, P 14

Eastern Mediterranean Health Genomics and Biotechnology Network (EMGEN) was created in 2004 with collaboration of representatives of selected centers of excellence in (health related) molecular biology, biotechnology & genomics in the Eastern Mediterranean region by recommendations and efforts of WHO/EMRO. Sponsored by Biotechnology Development Council of Iran.

Address:

Biotechnology building, #69, Pasteur Ave., Pasteur Institute of Iran
Tehran, Iran, 13164

Tel: +98-21-66954324

Fax: +98-21-66465132

E-mail: emhgbn@gmail.com, emgen@pasteur.ac.ir

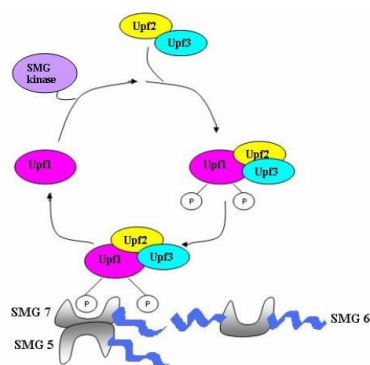
Websites: www.emgen.net
www.emhgbn.net

Prepared by: Maryam Ghoreishi

Page design: Mahdi Aalikhani

Assistant editor: Mahdi Aalikhani

Editor: Dr. Soroush Sardari



Training



PLASMIDS ARE ESPECIALLY IMPORTANT IN MEDICINE

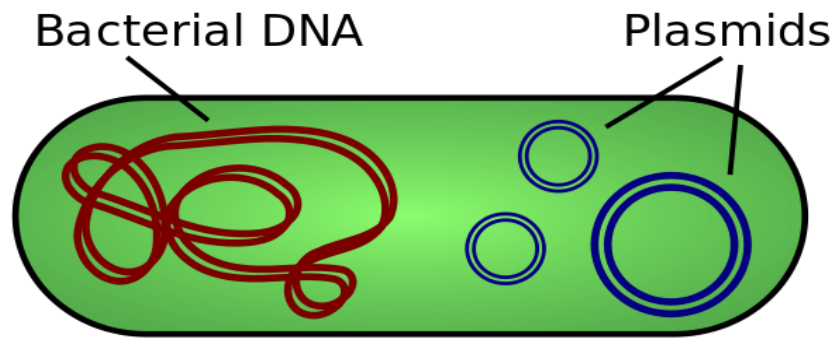


Figure 1: Chromosomal DNA and plasmid.

Plasmids are double-stranded and usually spherical DNA sequences that are able to independently duplicating in a host cell. A bacterial plasmid is a species of nonessential extra-chromosomal deoxyribonucleic acid (DNA) that replicates autonomously as a stable component of the cell's genome; nevertheless, plasmids are occasionally extant in eukaryotic organisms and archaea.

Plasmid issues original investigation on genetic elements in all kingdoms of life with importance on maintenance, transition and evolution of extra-chromosomal elements.

Whereas, the chromosomes are immense and hold all the essential information for living, plasmids generally are precise small and comprise only additional information.

Molecular properties of plasmids

1. Plasmids are believed replicons, a part of DNA able to duplicating autonomously inside a suitable host. Two forms of plasmid integration into a host bacteria are:
 - a. Non-integrating plasmids replicate.
 - b. Integrate into the host chromosome.



Training

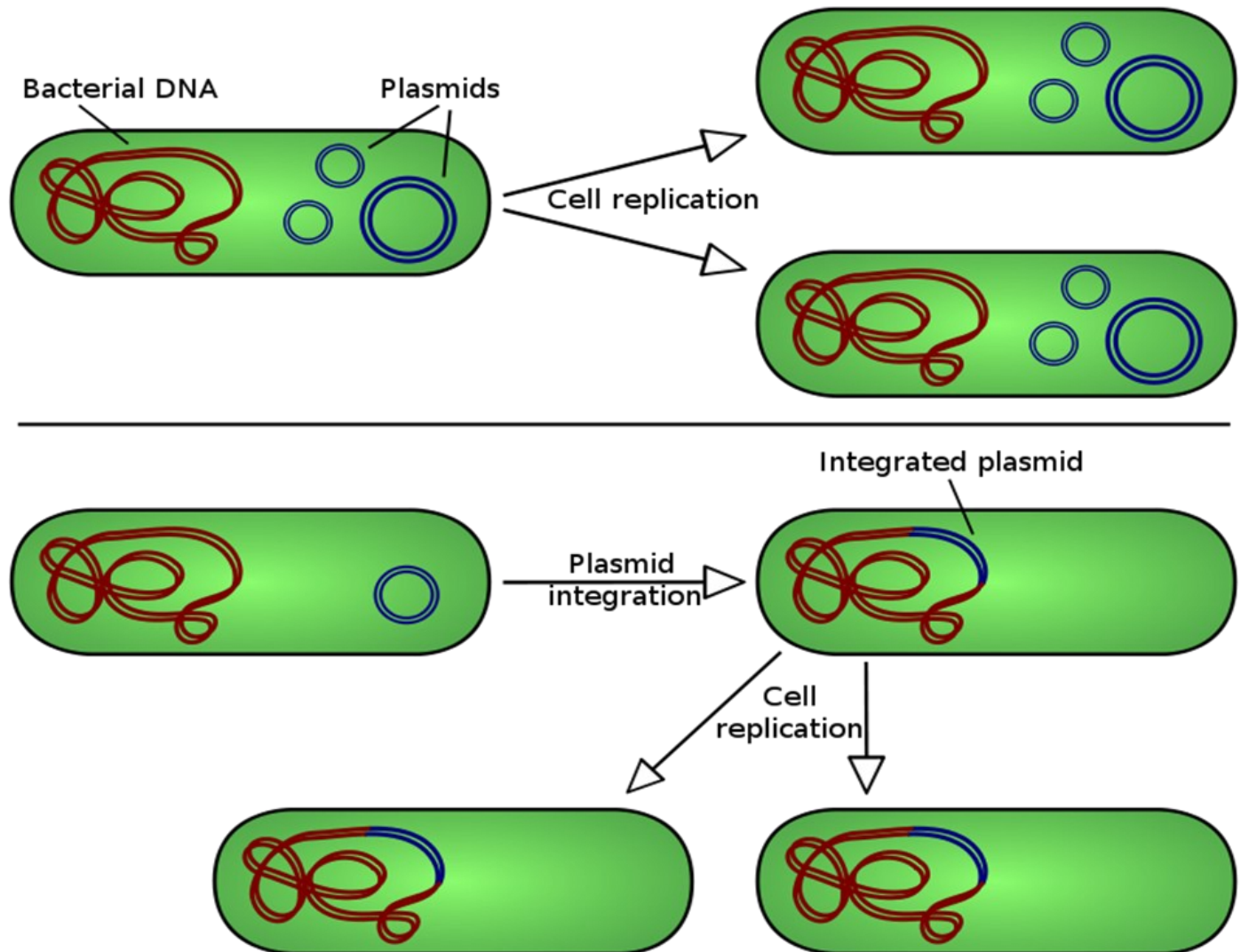


Figure 2: At the top of picture, illustrated non-integrating plasmid, whereas at the bottom example, plasmid infiltrated inside the host chromosome.

2. Plasmids are "naked" DNA and do not translate genes essential to enclose the genetic material for removal to a new host.
3. Plasmids are not generally categorized as life, like viruses.
4. Plasmids can be diffused from one bacterium to another (even of another species) via three main mechanisms: transformation, transduction, and conjugation.



Training



5. The extent of the plasmid diverges from 1 to over 200 kbp.
6. The number of duplicate plasmids in a single cell can vary anywhere from one to thousands in some situations.

Attributes and specifications

Plasmids nearly evermore have minimum one gene. Some of the genes transported by the plasmid are helpful for the host cells, for example:

1. Antibiotic resistance: Normally, plasmids often transfer genes that may help the existence of the organism; for example, antibiotic resistance. The prevalence of multiple antimicrobial resistance has been amended by selective pressure from human medicine.
2. Virulence determinants: The two common classes of toxicogenic plasmids are large, low-copy-number plasmids, and small, high-copy-number plasmids.
3. Colicins and bacteriocins: ColE1 is a plasmid detected in bacteria. Its name adapted to the fact that it transports a gene for colicin E1. It is considered as a vector candidate.

A plasmid can be grouped in several of these practical groups.

Table 1: The proteins coded by plasmid can behave as toxins in equivalent conditions.

The bacteria of content Plasmid	Disease	Protein product
<i>Yersinia enterocolitica</i>	Gastroenteritis	Yops (Yersinia outer proteins)
<i>Clostridium tetani</i>	Tetanus	Toxin
<i>Escherichia coli</i>	Gastroenteritis	Enterotoxins
<i>Escherichia coli</i>	Gastroenteritis	Adhesion



Training



Recognition and classification of plasmids are important in medicine for the reason that genes for clinically significant characters, for instance drug resistance and virulence factors, are generally present in plasmids. The identification of the type of resistance (R) plasmid or virulence plasmid existent in a pathogen can be involved in tracing the cause and extent of an infection, and it may also attend in creating a diagnosis.

Bacterial strains of medical importance regularly hold plasmids which extract them pathogenic and multiresistant to antibiotics. Hence, it is of concern to medicinal microbiologists to recognize these plasmids. The accessibility of the replicon typing method makes such analysis achievable. Colony hybridization with the replicon probes facilitates the identification of a large number of strains and introduces an indication of the replicon types existing in a throng of pathogenic strains.

Replicon typing of plasmid DNA detached by agarose gel electrophoresis allows one to identify the replicon types approved by each plasmid. For association, such typing may also be implemented with probes resulting from virulence and from drug resistance genes. It is important that most plasmids of medical prominence, such as plasmids with genes for toxin production, colonization factors, invasiveness, etc., are diagnosed and organized as plasmid. For such plasmids, the usage of replicon typing for recognition is undoubtedly beneficial.

Replicon typing is created on the opportunity of specify sequence relationships between plasmid replicons by nucleic acid hybridization methods. The usage of plasmids as a performance in molecular biology is retained by bioinformatics software. These programs identify the DNA sequence of plasmid vectors, relief to envisage cut sites of restriction enzymes, and to design manipulations. Plasmid may also be applied for gene convey into human cells as capacity remedy in gene therapy.

References:

1. Couturier M., Bex F., Bergquist P.L. and Maas W.K. (1988). Identification and Classification of Bacterial Plasmids. *Journal of Microbiology Reviews*, 3(52): 375-395.
2. Dale J.W. and Park S.F. (2010). Molecular genetics of bacteria. 5th edition, *Wiley-Blackwell*.
3. <http://en.wikipedia.org/wiki/Plasmid>
4. <http://en.wikipedia.org/wiki/ColE1>
5. <http://en.wikipedia.org/wiki/Colicin>



YEAST SPECIES PROVIDE PERFECT MODELS FOR PRINCIPAL BIOLOGICAL RESEARCH

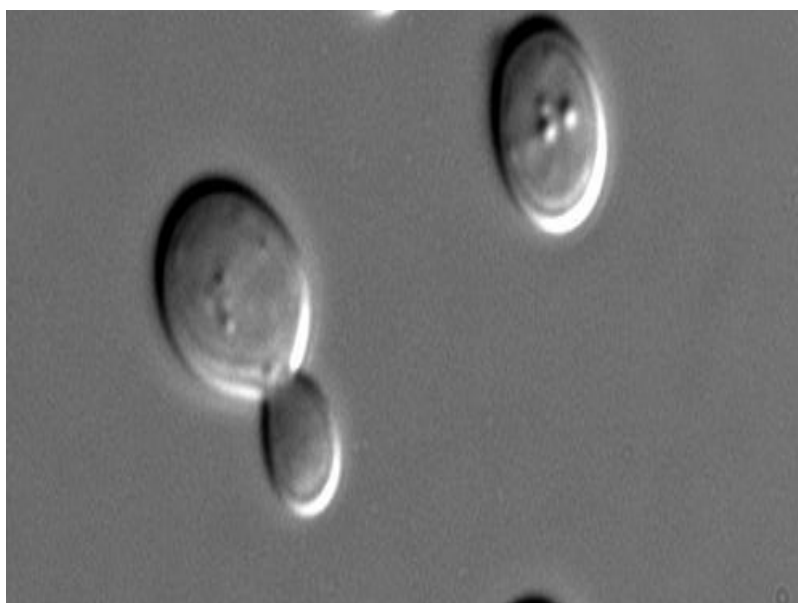


Figure 1: This picture shows that cells divide mitotically by forming a bud.

The yeast *Saccharomyces cerevisiae* is now known as a typical system demonstrating, a simple eukaryote whose genome was entirely sequenced and simply manipulated. Yeast has only a little greater genetic complexity than bacteria, and had many of the technical benefits that allowed rapid evolution in the molecular genetics of prokaryotes.

The yeasts *S. pombe* and *S. cerevisiae* are the typical organism of modern cell biology. These two organisms provide advanced genetic and molecular tools, as well as genome-level schemes to survey gene regulation and cellular responses. Several studies have shown that the yeast confer beneficial effects against various microorganisms for example:

1. *S. cerevisiae* is a simple eukaryotic cell, attending as a model for all eukaryotes, comprising humans.
2. A large amount of *Saccharomyces cerevisiae* is commercially available and can deliver a cheap source for biochemical researches.

- 3- Yeast cells will grow on a minimal medium comprising dextrose (glucose) as a carbon source and salts that source nitrogen, phosphorus, and trace metals.
- 4- Physiologically (yeast can exist stably in either haploid or diploid states).
- 5- Rapid growth (approx. 90 min).
- 6- Yeast can be grown in either liquid medium or on the surface of a solid agar plate.
- 7- The genome of yeast comprises 16 linear chromosomes, extending from nearabout 200 to 2200 kb.
- 8- For training the essential cellular actions suchlike the DNA replication, cell cycle, recombination, cell division, and metabolism.
- 9- The isolation of numerous nutritional auxotrophs mutant separation.
- 10- The facility of replica plating.
- 11- Yeast is particularly accessible to gene cloning.
- 12- Synthetic genetic array analysis.
- 13- Yeast two-hybrid.
- 14- Tetrad analysis.
- 15- Mutant separation.
- 16- Plasmids can be introduced into yeast cells either as replicating molecules or by integration into the genome (in conflict to other organisms, integrative recombination of transforming DNA in yeast proceeds exclusively via homologous recombination).
- 17- Being nonpathogenic (yeast can be handled with little precautions).

Numerous proteins momentous in human biology were first figured out by studying their homologues in yeast; these proteins include signaling proteins, cell cycle proteins, and protein-processing enzymes. *S. cerevisiae* was pronounced to be the first eukaryote to have its genome, containing of 12 million base pairs, completely sequenced as part of the Genome Plan.

On various circumstances, baker's yeast (*Saccharomyces cerevisiae*) has been mentioned to as the *Escherichia coli* of the eukaryotic world. Yeast has been extensively determined genetically and a full physical chart is now accessible.

Human Diseases

The efficient characterization of imperfect human proteins in yeast can expose abnormal enzyme functions that may not be specious from analyzes in humans or from review of the protein sequence. A brilliant sample for this is hMSH2. These weaknesses, which occur to lead to tumor construction, were unexpected by direct study of humans. Another advantage of studying human disease gene function in yeast is the probability of identifying and treating the insufficiencies responsible for the illnesses. Many missense mutations cause reduced empathy for substrate or cofactor that consequence in a metabolic imperfection as a result of inadequate invention.

It is satisfied that yeast has performed as a model system that consents implication of individual gene functions, of gene and protein interfaces, and of network constructions through several kinds of investigations ranging from individual assesses to high-throughput genome-scale experiments. We have underlined how yeast has tend to our accepting of fundamental biology in other eukaryotes and of human disease. We have every object to anticipate that these aids will carry on and even develop in significance since the technology, specifically for DNA sequencing, is ongoing to enhance promptly. *Saccharomyces* has administered an essential function in the pharmaceutical fields. Yeast has a quantity of benefits for processes that involve production on a massive scale.

Considerable is identifying the transmission of the traditional transporters of information, DNA and RNA, throughout mitosis and meiosis, but scarcely is known about the heritage of macromolecules and organelles; for example, lipids and polysaccharides, and the innumerable slight molecules that settle the cells of living organisms.

Conclusion

Hence, yeast come to be one of the key organisms for genomic investigation, comprising widespread use of DNA microarrays for examining the transcriptome as well as genome-wide analysis of gene functions by gene disruption, of 2-D protein maps, of serial analysis of gene expression (SAGE), of enzymatic activities, of protein localization, of protein-protein interactions by using two-hybrid analysis, and of functional analysis synthetic lethality.

Numerous yeast species have been genetically engineered to professionally produce a number of drugs, a technique called metabolic engineering. *S. cerevisiae* is no trouble to genetically engineer; its physiology, metabolism and genetics are renowned, and it is agreeable for usage in exacting industrial conditions.

A wide variety of chemicals in various categories can be manufactured by modified yeast, including polyketides, alkaloids, isoprenoids, and phenolics. Approximately 20% of biopharmaceuticals are manufactured in *S. cerevisiae*, such as vaccines for hepatitis, insulin, and human serum albumin.

References:

1. Bergman L.W. (2001). Growth and Maintenance of Yeast, in Two-Hybrid Systems: Methods and Protocols, *Humana Press: Totowa*, 177: 9-14.
2. Sherman F. (2002). Getting Started with Yeast. *Methods Enzymol.*, 350: 3-41.
3. Botstein D. and Fink G. R. (2011). Yeast: An experimental organism for 21st century biology, *Journal of Genetics*, 189(3): 695–704.
4. <http://en.wikipedia.org/wiki/Yeast>

SLIME MOLD GIVES INSIGHT INTO INTELLIGENCE OF NEURONLESS ORGANISMS

Nearly all the vita has no brain and a large number of beings miss neurons totally. Plants, bacteria and fungi all have to confront with the identical difficulties as humans to make the finest selections in a wrapped and variable world or confront with death without the assistance of an ordinary nervous system in various situations.

A team of academics newly studied this obstacle in an unicellular slime mold, *Physarum polycephalum*, a creature that can grow to several square meters in size. This huge cell, which naturally lives in shadowy, cool and humid spaces of temperate jungles, spreads out to hunt its environment like an amoeba, elongating oozy tendrils along the forest ground in search of its quarry of fungi, bacteria and spoiling vegetable substances.

In this study, the scientists studied the decision-making skill of slime mold via an experiment classically applied in mankind and further brained creatures: the two-armed bandit problem, called for the slot machine. In a two-armed bandit problem, the issue has two arms to pull, each of them carries a definite, randomly determined prize.

One of the arms is most probably to carry a higher reward totally, so the trial for contributors is to choose at what point to stop discovering both decisions and choose to completely apply just one choice in order to take full advantage of their final result. In this way, it has been a classical application for testing the decision-making capabilities of humans and other creatures, but it has never earlier been used on a creature lacking a brain. The slime mold's decision-making process can be statistically defined as an orientation to operate environments in relation to their reward practiced through past selection. The procedure is intermediary in computational difficulty between simple, resilient heuristics and calculation-rigorous ideal performance procedures, yet it has very good comparative efficiency.

"Working with *Physarum* repetitively tests our predetermined ideas of the smallest biological hardware that is essential for complex behavior," says Simon Garnier, an associate professor of biology at NJIT and the chief researcher of the investigation.

Reference: <https://www.sciencedaily.com/releases/2016/06/160608112930.htm>

Journal Alert



GENOME BIOLOGY

ISSN: 1474-760X

Genome Biology covers all areas of biology and biomedicine studied from a genomic and post-genomic perspective.

Impact Factor: 10.8

Genome
Biology

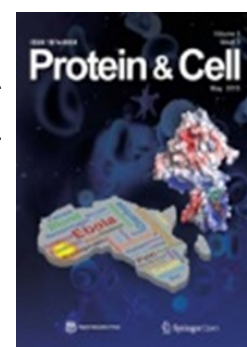


PROTEIN & CELL

ISSN: 1674-800X

Protein & Cell publishes original research articles, reviews, and commentaries concerning the latest developments in multidisciplinary areas in biology and biomedicine, with an emphasis on protein.

Impact Factor: 3.247



BMC MEDICAL GENETICS

ISSN: 1471-2350

BMC Medical Genetics is an open access journal publishing original peer-reviewed research articles in the effects of genetic variation in individuals, families and among populations in relation to human.

Impact Factor: 1.44

BMC
Medical Genetics



Book Alert



CELLULAR AGEING AND REPLICATIVE SENESCENCE

Publisher: Springer international publishing

Authors: Rattan, S. and Hayflick, L.

Publication date: 2016

ISBN: 331926237



CONSUMER HEALTH INFORMATICS

Publisher: Springer international publishing

Author: Wetter, Thomas

Publication date: 2016

ISBN: 3319195891



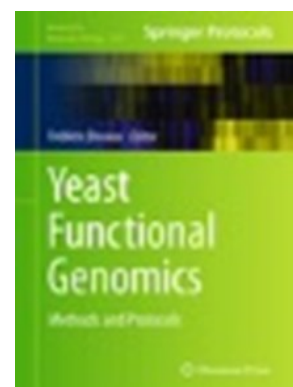
YEAST FUNCTIONAL GENOMICS

Publisher: Springer international publishing

Author: Devaux, Frederic

Publication date: 2016

ISBN: 9781493930784



Announcements



Stem Cell Congress 2016

Aug 04-05, 2016

Manchester, UK

<http://www.omicsonline.org/international-scientific-conferences/>

Cancer Genomics 2016

Aug 08-09, 2016

Las Vegas, USA

<http://www.omicsonline.org/international-scientific-conferences/>

Genomics Medicine 2016

Aug 11-12, 2016

Birmingham, UK

<http://www.omicsonline.org/international-scientific-conferences/>



ERYTHROPOIETIN

Erythropoietin or EPO, is a glycoprotein hormone that adjusts erythropoiesis, or red blood cell construction. It is a cytokine for erythrocyte (red blood cell) originators in the bone marrow. EPO has a molecular heaviness of 34 kDa in human. Correspondingly known as hematopoietin or hemopoietin, it is brought about by interstitial fibroblasts in the kidney in fuse relationship with peritubular capillary and nearest complicated tubule. It is as well generated in perisinusoidal cells in the liver. While liver secretion is the majority in the fetal and perinatal period, renal construction is predominant throughout adulthood. As well as erythropoiesis, erythropoietin correspondingly has other identified biological purposes. For instance, it acts in a significant function in the brain's reply to neuronal damage. EPO is as well complicated in the wound remedial procedure. Exogenous erythropoietin is created by recombinant DNA technology in cell culture. More than a few diverse pharmaceutical representatives are accessible with a variability of glycosylation patterns, and are in a group named erythropoiesis-stimulating causes (ESA). The exact particulars for considered usage differ between the package supplements, but ESAs have been charity in the care of anemia in chronic kidney illness, anemia from cancer chemotherapy, and anemia in myelodysplasia. Exogenous erythropoietin has been exerted illegally as a performance-enhancing drug; it can frequently be identified in blood, because of small variances from the endogenous protein, such as in features of post translational modification.

Reference: <http://en.wikipedia.org/wiki/Erythropoietin>

HUMAN GROWTH HORMONE

Earlier to the advantage of recombinant DNA technology to convert bacteria to generate human growth hormone (HGH), the hormone was produced by distillation from the pituitary glands of cadavers, as animal growth hormones have no beneficial utility in humans. Nowadays, human growth hormone is produced by inserting DNA coding for human growth hormone into a plasmid that was set in *Escherichia coli* bacteria. The gene that was implanted into the plasmid was produced by reverse transcription of the mRNA found in pituitary glands to completing DNA. HaeIII, a kind of restriction enzyme which performances at restriction sites "in the 3' noncoding region" and at the 23rd codon in corresponding DNA for human growth hormone, was

Cover Pictures



applied to generate a DNA fragment of 551 base pairs which consist of coding sequences for amino acids 24-191 of HGH. The procedure of totally synthetic procedures of DNA generation to generate a gene that would be translated to human growth hormone in *E. coli* can be very difficult because of the important length of the amino acid sequence in human growth hormone. Nevertheless, if the cDNA reverse transcribed from the mRNA for human growth hormone were implanted in a straight line into the plasmid implanted into the *Escherichia coli*, the bacteria would translate parts of the gene that are not translated in humans, by this means creating a "pre-hormone inclosing an extra 26 amino acids" which might be challenging to eradicate.

Reference: http://en.wikipedia.org/wiki/growth_hormone

mRNA SURVEILLANCE

mRNA surveillance mechanisms are trail applied by organisms to confirm reliability and excellence of messenger RNA (mRNA) molecules. There are an amount of investigation mechanisms present within cells. These apparatus purpose at different steps of the mRNA biogenesis trail to identify and degrade transcripts that have not correctly been treated. The translation of messenger RNA transcripts into proteins is an essential section of the central dogma of molecular biology. mRNA molecules are, nevertheless, likely to a host of reliability inaccuracies which can cause errors in translation of mRNA addicted to superiority proteins.

The picture shows that, UPF1 is a preserved helicase which is phosphorylated in the procedure of NMD (nonsense-mediated decay). This phosphorylation is catalyzed by SMG1 kinase. Dephosphorylation of UPF1 is catalyzed by SMG5, SMG6 and SMG7 proteins. RNA surveillance mechanisms are system cells use to comfort the value and reliability of the mRNA molecules. It generally attained complete marking atypical mRNA molecule for deprivation by a number of endogenous nucleases. mRNA surveillance has been recognized in bacteria and yeast. In eukaryotes, these appliances are identified to utility in not only the nucleus but also cytoplasm.

Reference: http://en.wikipedia.org/wiki/MRNA_surveillance

