Interrupted gene

An **interrupted gene** (also called a [split gene](https://en.wikipedia.org/wiki/Split_gene_theory)) is a gene that contains expressed regions of DNA called [exons](https://en.wikipedia.org/wiki/Exon), split with unexpressed regions called [introns](https://en.wikipedia.org/wiki/Intron) (also called intervening regions). Exons provide instructions for coding proteins, which create [mRNA](https://en.wikipedia.org/wiki/MRNA) necessary for the synthesis of [proteins](https://en.wikipedia.org/wiki/Protein). Introns are removed by recognition of the donor site (5' end) and the splice acceptor site (3' end).[[1]](https://en.wikipedia.org/wiki/Interrupted_gene#cite_note-:0-1) The architecture of the interrupted gene allows for the process of [alternative splicing](https://en.wikipedia.org/wiki/Alternative_splicing), where various mRNA products can be produced from a single gene.[[2]](https://en.wikipedia.org/wiki/Interrupted_gene#cite_note-:1-2) The function of introns are still not fully understood and are called [noncoding or junk DNA](https://en.wikipedia.org/wiki/Noncoding_DNA).

Discovery

Interrupted genes were independently discovered by [Richard J. Roberts](https://en.wikipedia.org/wiki/Richard_J._Roberts) and [Phillip A. Sharp](https://en.wikipedia.org/wiki/Phillip_Allen_Sharp) in 1977, for which they shared the 1993 Nobel Prize in Physiology or Medicine.[[3]](https://en.wikipedia.org/wiki/Interrupted_gene#cite_note-3) Their discovery implied the existence of then-unknown machinery for [splicing](https://en.wikipedia.org/wiki/RNA_splicing) out introns and assembling genes; namely, the [spliceosome](https://en.wikipedia.org/wiki/Spliceosome). Unlike prokaryotic genomes, eukaryotic genomes were largely complex and inconsistent. It was soon accepted that 94% of human genes are interrupted, and 50% of hereditary diseases are involved in splicing intron errors out of interrupted genes.[[2]](https://en.wikipedia.org/wiki/Interrupted_gene#cite_note-:1-2) The best known example of a disease caused by a splicing error is [Beta-thalassemia](https://en.wikipedia.org/wiki/Beta-thalassemia), in which extra intronic material is erroneously spliced into the gene for making [hemoglobin](https://en.wikipedia.org/wiki/Hemoglobin).

Prokaryotes

Unlike eukaryotes, [prokaryotes](https://en.wikipedia.org/wiki/Prokaryote) have a less complex genome. The structure of prokaryotic genomes contain fewer to none regions of introns and have longer continuous lines of exons, or uninterrupted regions.[[1]](https://en.wikipedia.org/wiki/Interrupted_gene#cite_note-:0-1) In other words, they contain more regions of DNA that are expressed. The idea that genome density decreases as the complexity of the organism increases hold true. This is due to the fact that eukaryotes have a much stronger presence of introns than prokaryotes. For example, prokaryotes contain about 1000 genes/Mb while humans contain about 6 genes/Mb.[[4]](https://en.wikipedia.org/wiki/Interrupted_gene#cite_note-4) Another example are lower [eukaryotes](https://en.wikipedia.org/wiki/Eukaryote), such as [yeast](https://en.wikipedia.org/wiki/Yeast), that have many uninterrupted regions. However, this does not mean that these sections are fully uninterrupted, as [tRNA](https://en.wikipedia.org/wiki/TRNA) synthesis requires excision of a nucleotide sequence, followed by [ligation](https://en.wikipedia.org/wiki/RNA_ligase_%28ATP%29).

Most bacteria have some interruption of some genes. Interrupted genes are universal in eukaryotes; yeasts may display single interruptions of a minority of genes, while in higher organisms most genes are interrupted. Some eukaryotes may contain multiple interruptions with introns that can be longer than exons. Introns are well-conserved across evolutionary history, suggesting their structure has some importance for the organism. They are longer in advanced organisms (higher plants and animals). Longer growth and development requires longer sequences of gene activation and down-regulation. Details of the role of introns in the regulation of gene accessibility and transcription have yet to be worked out.

References

* 1. ^ [Jump up to:***a***](https://en.wikipedia.org/wiki/Interrupted_gene#cite_ref-:0_1-0) [***b***](https://en.wikipedia.org/wiki/Interrupted_gene#cite_ref-:0_1-1) *Sharp PA (June 2005). "The discovery of split genes and RNA splicing". Trends in Biochemical Sciences.****30****(6): 279–81.*[*doi*](https://en.wikipedia.org/wiki/Doi_%28identifier%29)*:*[*10.1016/j.tibs.2005.04.002*](https://doi.org/10.1016/j.tibs.2005.04.002)*.*[*PMID*](https://en.wikipedia.org/wiki/PMID_%28identifier%29)[*15950867*](https://pubmed.ncbi.nlm.nih.gov/15950867)*.*
	2. ^ [Jump up to:***a***](https://en.wikipedia.org/wiki/Interrupted_gene#cite_ref-:1_2-0) [***b***](https://en.wikipedia.org/wiki/Interrupted_gene#cite_ref-:1_2-1) *Ward AJ, Cooper TA (January 2010).*[*"The pathobiology of splicing"*](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2855871)*. The Journal of Pathology.****220****(2): 152–63.*[*doi*](https://en.wikipedia.org/wiki/Doi_%28identifier%29)*:*[*10.1002/path.2649*](https://doi.org/10.1002/path.2649)*.*[*PMC*](https://en.wikipedia.org/wiki/PMC_%28identifier%29)[*2855871*](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2855871)*.*[*PMID*](https://en.wikipedia.org/wiki/PMID_%28identifier%29)[*19918805*](https://pubmed.ncbi.nlm.nih.gov/19918805)*.*
	3. [**^**](https://en.wikipedia.org/wiki/Interrupted_gene#cite_ref-3) [*"The Nobel Prize in Physiology or Medicine 1993"*](https://www.nobelprize.org/prizes/medicine/1993/press-release/)*. NobelPrize.org. Retrieved 2020-03-26.*
	4. [**^**](https://en.wikipedia.org/wiki/Interrupted_gene#cite_ref-4) *Watson JD (2014). Molecular biology of the gene. Pearson.*[*ISBN*](https://en.wikipedia.org/wiki/ISBN_%28identifier%29)[*978-0-321-85149-9*](https://en.wikipedia.org/wiki/Special%3ABookSources/978-0-321-85149-9)*.*[*OCLC*](https://en.wikipedia.org/wiki/OCLC_%28identifier%29)[*839779760*](https://www.worldcat.org/oclc/839779760)*.*

# Housekeeping gene

**Definition**

Any of the [genes](https://www.biologyonline.com/dictionary/genes) that are constitutively expressed at a relatively [constant](https://www.biologyonline.com/dictionary/constant) level across many or all known conditions.
**Supplement**
Housekeeping genes are those [genes](https://www.biologyonline.com/dictionary/genes) that are always expressed because they code for [proteins](https://www.biologyonline.com/dictionary/proteins) that are constantly required by the [cell](https://www.biologyonline.com/dictionary/cell), hence, they are essential to a cell and always present under any conditions. It is assumed that their [expression](https://www.biologyonline.com/dictionary/expression) is unaffected by experimental [conditions](https://www.biologyonline.com/dictionary/conditions). The proteins they code are generally involved in the basic functions necessary for the sustenance or maintenance of the [cell](https://www.biologyonline.com/dictionary/cell). Examples of housekeeping genes include [actin](https://www.biologyonline.com/dictionary/actin), GAPDH and [ubiquitin](https://www.biologyonline.com/dictionary/ubiquitin).

# Luxury gene

**Definition**

A [gene](https://www.biologyonline.com/dictionary/gene) that codes for specialized cell products and is expressed abundantly.
**Supplement**
Luxury genes are [tissue](https://www.biologyonline.com/dictionary/tissue)-specific or [organ](https://www.biologyonline.com/dictionary/organ)-specific, which means they are not expressed in all cells. They are not constantly expressed, only when their [function](https://www.biologyonline.com/dictionary/function) is needed. Examples of luxury genes are [plasmids](https://www.biologyonline.com/dictionary/plasmids) of [bacteria](https://www.biologyonline.com/dictionary/bacteria) and [genes](https://www.biologyonline.com/dictionary/genes) coding for [heat-shock protein](https://www.biologyonline.com/dictionary/heat-shock-protein)s.