https://www.ncbi.nlm.nih.gov/pmc/articles/PMC524190/

- "This switching on and off of each gene is executed by an assembly of transcription factors forming a transcription initiation complex (TIC)."
- "The methods that solve this problem are based on a comparative (differential) approach. A test (target) sample, containing active genes is compared with a control sample in which the genes have not been activated. Using this approach, the active genes are singled out among the multitude of inactive genes. However, the comparisons may reveal the opposite of activation, i.e., downregulation of genes."
- "Non-activated genes in the control tissue do not produce any corresponding mRNAs."
- "There are essentially two approaches for finding activated genes: (i) an individual identification, or (ii) an identification of expression profiles after hybridization to a set of known gene fragments (probes) attached to chips in microarrays."
- Electrophoresis

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC95378/

- "A gene is predicted highly expressed (PHX) if its codon frequencies are close to those of the ribosomal proteins, major translation/transcription processing factor, and chaperone/degradation standards but strongly deviant from the average gene codon frequencies."
- "Also PHX genes generally include those encoding enzymes of essential energy metabolism pathways of glycolysis, pyruvate oxidation, and respiration (aerobic and anaerobic), genes of fatty acid biosynthesis, and the principal genes of amino acid and nucleotide biosyntheses."
- "The spatial distribution of PHX genes within each genome reveals clusters and significantly long regions without PHX genes."
- "The minimal doubling time for these four bacteria in cultures is significantly less than 1 h. Fast growth implies many ribosomes, and these four bacteria have large numbers of rRNA operons per genome."
    - Ribosomes are what translate the mRNA and turn it in to amino acids which join together through peptide bonds and create proteins
- Under Methods section, there are formulas they used and they concluded that:
    - "A gene is predicted highly expressed (PHX) if the following two conditions are satisfied: at least two of the three expression values $ERP(g)$, $ECH(g)$, and $ETF(g)$ exceed 1.05, and the general expression level $E(g)$ is ≥1.00."
- "The majority of protein synthesis factors are PHX over all prokaryotic genomes."
- Microarrays
    - "The current microarray methodology is restricted to discriminating transcription levels and not levels of translation or protein abundances"
    - "Also, DNA chip hybridizations are generally unable to detect unambiguously low-abundance gene transcripts."
- "Experimental evaluations of protein abundances under different cellular conditions can be assayed by 2D gel electrophoresis (reviewed in reference 46) supplemented by mass spectrometry (51), by antibody associations, and by biochemical tests."

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC33975/

- "The genes that are still undiscovered are expressed at low levels or are specifically expressed only in certain cell types, developmental stages, or growth conditions."
- Microarrays
    - "cDNA tags for thousands of expressed genes are arrayed on a glass or membrane support. When incubated with labeled first-strand cDNA produced from cellular RNA, each tag hybridizes to its cognate mRNA and allows relative quantitation of the expression levels."

https://www.nature.com/scitable/topicpage/gene-expression-is-analyzed-by-tracking-rna-6525038/

- "researchers often use laboratory techniques such as a **Northern blot** or **serial analysis of gene expression** (**SAGE**). Both of these techniques make it possible to identify which genes are turned on and which are turned off within cells. Subsequently, this information can be used to help determine what circumstances trigger expression of various genes."
    - Measure levels of mRNA
    - Northern blot: expose cells to protease, which breaks down cell membrane and exposes genetic material. Next, mRNA is separated. Next, gel electrophoresis is utilized. Then, it is transferred to a filter. Next, the mRNA is incubated with a single-strand of RNA or DNA that is labeled with a radioactive molecule, which will bind to the original mRNA. Lastly, once the filter is against x-ray film, the radioactivity in the RNA or DNA will expose the intensity of bands, which shows how much the gene was expressed.

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3235009/

- "Highly expressed genes are associated with slower evolutionary rates in yeast and mammals"

https://www.annualreviews.org/doi/10.1146/annurev-genet-110711-155517?url_ver=Z39.88-2003&rfr_id=ori%3Arid%3Acrossref.org&rfr_dat=cr_pub++0pubmed

- "eusocial honey bee (*Apis mellifera*)"
- "These experiments demonstrate that brain gene expression is closely linked with behavior, that changes in brain gene expression mediate changes in behavior, and that the association between specific genes and behavior exists over multiple timescales, from physiological to evolutionary."
- "changes in the expression of specific genes in the brain affect behavior"
- "First, differences in behavior are closely linked with changes in the expression of many genes in the brain. Second, changes in brain gene expression are caused by both hereditary and environmental factors, and both result in changes in behavior. Third, there are parallels in the effects of some genes over physiological, developmental, and evolutionary timescales."
- "Early bee microarray studies demonstrating extensive differences in whole-brain gene expression as a function of behavioral state (35, 46, 130) suggested that brain gene expression profiles can provide reasonable reflections of behaviorally related

transcriptomic activity, thus facilitating the BeeSpace analyses, which were mostly done at the whole-brain level."

- "Gene expression in the brain provides the first measure of the interaction between the genome and the environment—the first phenotype"
- "Whitfield et al. (130) showed that young and old foragers shared similar brain profiles distinct from those of young and old nurses, thereby demonstrating that behavior, and not age, was the major driver in patterns of brain gene expression. The nurse and forager neurogenomic states were so different that an unsupervised clustering algorithm was able to predict the behavioral state of individual workers with 95% accuracy given their brain profiles (130)."
- "It was also confirmed by treating bees with substances (pheromones, hormones, and intracellular signaling molecules) known to either speed up or slow down behavioral maturation, which induced brain gene expression profiles that were either more forager-like or nurse-like, respectively (129)."
- "The neurogenomic state associated with aggression was also enriched for molecular functions involved in oxidative phosphorylation: Aggressive bees have relatively lower brain expression of oxidative phosphorylation genes (4)."
- Since there are different "jobs" for bees, the researchers compared the different jobs to see which genes were expressed in the brain.
- "Naeger et al. (78) found 624 genes that varied in expression between the morning and afternoon, hinting at an influence of circadian rhythm on brain gene expression. … These two studies suggest that, similar to mammals, changes in the expression of clock genes and their targets in the brains of foragers are related to their circadian food anticipatory behavior (78)."

https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-020-06911-5

https://europepmc.org/article/MED/26737772