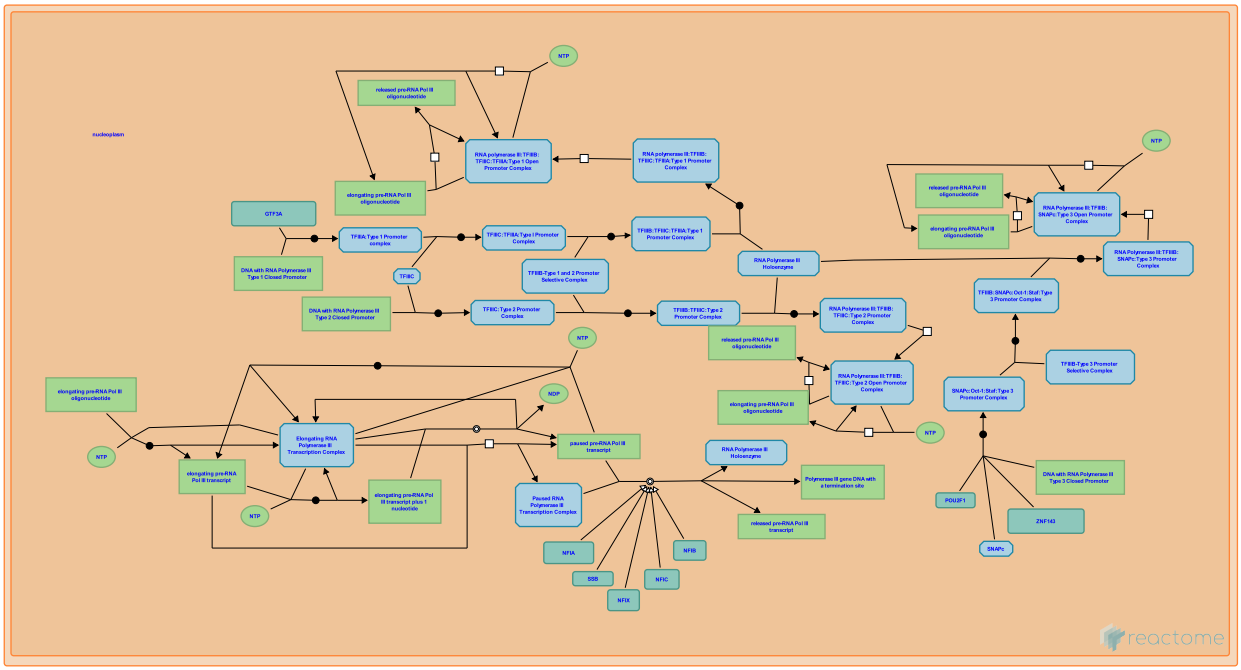
# RNA Polymerase III Transcription



Geiduschek, EP., Gillespie, ME., Hernandez, N., Joshi-Tope, G., Kassavetis, GA.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.



This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

05/05/2024

# Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.
The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

## Literature references

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

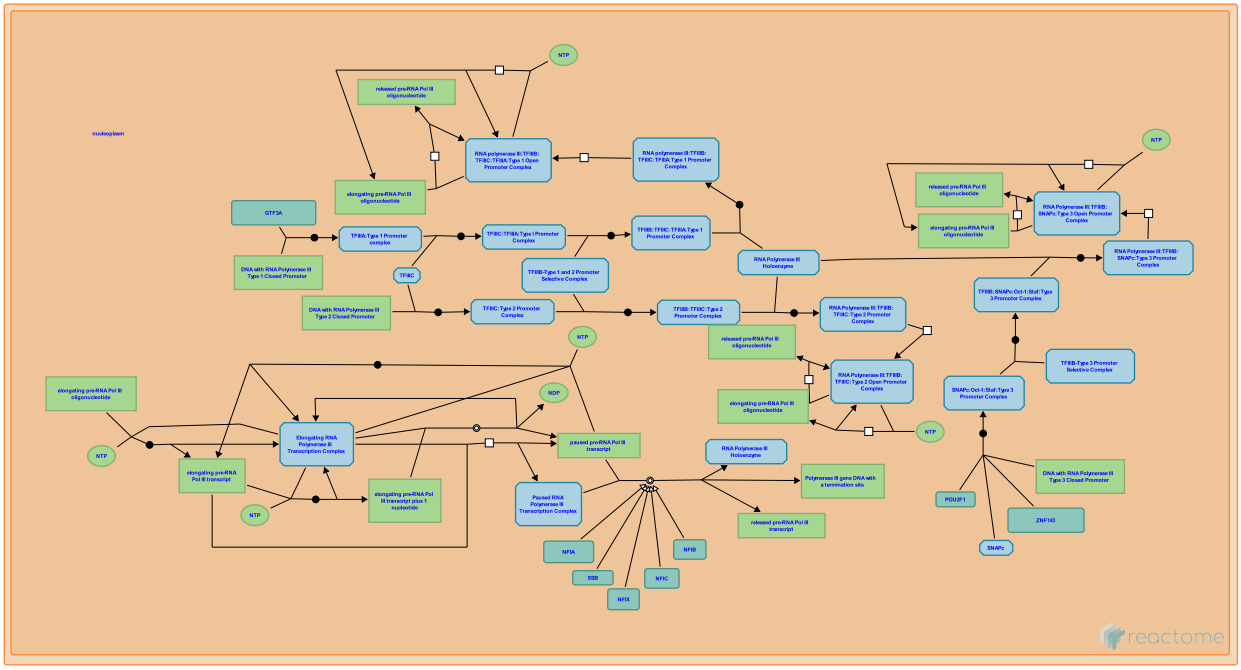
Reactome database release: 88

This document contains 5 pathways (see Table of Contents)

## RNA Polymerase III Transcription ↗

**Stable identifier:** R-HSA-74158

**Compartments:** nucleoplasm




RNA polymerase III is one of three types of nuclear RNA polymerases present in eucaryotic cells. About 10% of the total transcription in dividing cells can be attributed to its activity. It synthesizes an eclectic collection of catalytic or structural RNA molecules, some of which are involved in protein synthesis, pre-mRNA splicing, tRNA processing, and the control of RNA polymerase II elongation, whereas some others have still unknown functions. Like other RNA polymerases, RNA polymerase III cannot recognize its target promoters directly. Instead it is recruited to specific promoter sequences through the help of transcription factors. There are three basic types of RNA polymerase III promoters, called types 1, 2, and 3(Geiduschek and Kassavetis, 1992). Although in vivo, RNA polymerase III may be recruited to these promoters as part of a large complex (holo RNA polymerase III) containing the polymerase and its initiation factors (Wang et al., 1997), in vitro the reaction can be divided into several steps. First, the promoter elements are recognized by DNA binding factors, which then recruit a factor known as TFIIIB. TFIIIB itself then directly contacts RNA polymerase III. In human cells but not in *S. cerevisiae*, there are at least two versions of TFIIIB. One contains TBP, Bdp1, and Brf1 (Brf1-TFIIIB), and the other TBP, Bdp1, and Brf2 (Brf2-TFIIIB) (Schramm et al., 2000; Teichmann et al., 2000).

## Literature references


Yamamoto, KR., McKnight, SL. (1992). RNA polymerase III Transcription Complexes, Transcriptional Regulation. *Cold Spring Harbor Laboratory Press*, 247-280.

Luo, T., Wang, Z., Roeder, RG. (1997). Identification of an autonomously initiating RNA polymerase III holoenzyme containing a novel factor that is selectively inactivated during protein synthesis inhibition. *Genes Dev, 11*, 2371-82. ↗

Wang, Z., Teichmann, M., Roeder, RG. (2000). A stable complex of a novel transcription factor IIB- related factor, human TFIIIB50, and associated proteins mediate selective transcription by RNA polymerase III of genes with upstream promoter elements. *Proc Natl Acad Sci U S A, 97*, 14200-5. ↗

Sun, Y., Schramm, L., Pendergrast, PS., Hernandez, N. (2000). Different human TFIIIB activities direct RNA polymerase III transcription from TATA-containing and TATA-less promoters. *Genes Dev, 14*, 2650-63. ↗


## Editions

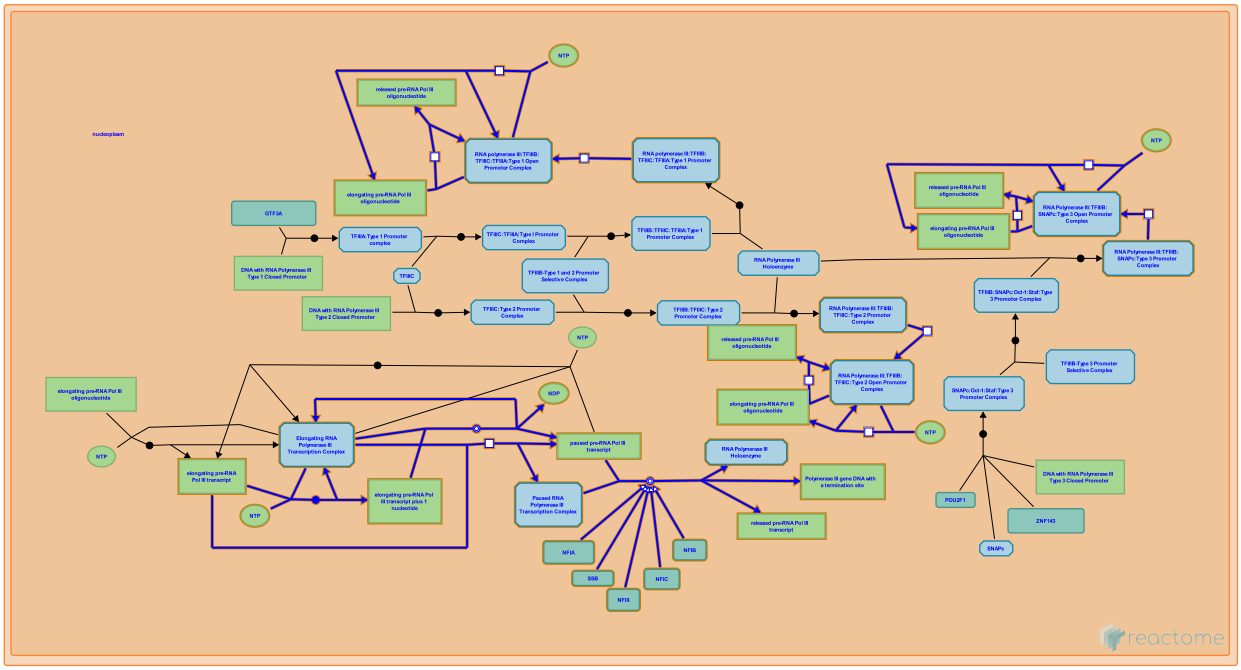
| | | |
|---|---|---|
| 2003-09-11 | Authored | Hernandez, N. |
| 2024-03-06 | Edited | Joshi-Tope, G. |

## RNA Polymerase III Abortive And Retractive Initiation ↗

**Location:** RNA Polymerase III Transcription

**Stable identifier:** R-HSA-749476

**Compartments:** nucleolus




Abortive initiation, the repetitive formation of short oligonucleotides, is a ubiquitous feature of transcriptional initiation. This Pathway contains events inferred from events in Saccharomyces cerevisiae.

## Editions

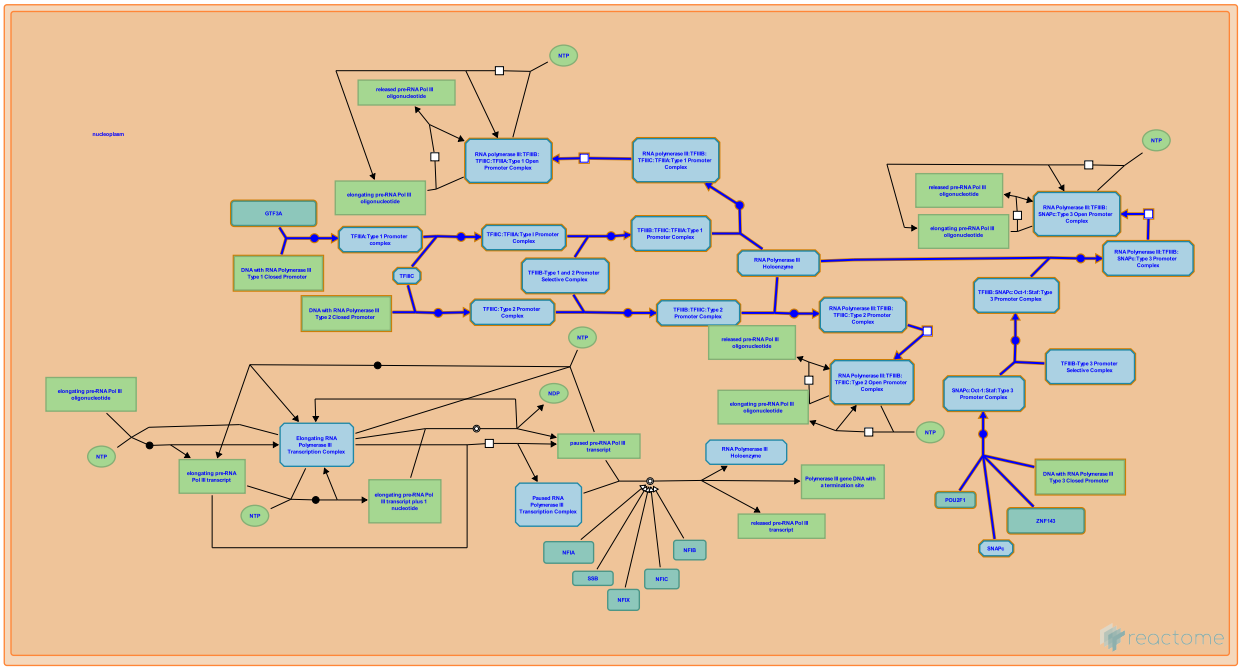
| | | |
|---|---|---|
| 2004-03-29 | Authored | Geiduschek, EP. |
| 2024-03-06 | Edited | Gillespie, ME. |

## RNA Polymerase III Transcription Initiation ↗

**Location:** RNA Polymerase III Transcription

**Stable identifier:** R-HSA-76046

**Compartments:** nucleoplasm




There are three basic types of RNA polymerase III promoters. The three types of RNA polymerase III promoters are known as type 1, type 2, and type 3 promoters. Type 1 promoters are found in the 5S genes and consist of a gene-internal element called the internal control region (ICR), that is subdivided into A block, intermediate element, and C block (Bogenhagen, 1985; Sakonju et al., 1980). Type 2 promoters are found in tRNA genes, Adenovirus 2 VAI gene, and other genes (Galli et al., 1981; Sharp et al., 1981). These promoters consists of two gene-internal elements called the A and the B boxes. Type 3 promoters consist of a distal sequence element (DSE) that serves as an enhancer, a proximal sequence element (PSE), and a TATA box (Baer et al., 1989; Lobo and Hernandez, 1989).

Some promoters combine elements from type 2 and 3 promoters. For example, the S. cerevisiae U6 promoter, also shown in the figure, contains the TATA box typical of type 3 promoters and the A and B boxes typical of type 2 promoters. Moreover, in S. pombe, nearly all tRNA and 5S genes contain a TATA box in addition to gene-internal elements, and the TATA box is required for transcription.

## Literature references


Lobo, SM., Hernandez, N. (1989). A 7 bp mutation converts a human RNA polymerase II snRNA promoter into an RNA polymerase III promoter. *Cell, 58*, 55-67. ↗

Nilsen, TW., Altman, S., Baer, M., Costigan, C. (1990). Structure and transcription of a human gene for H1 RNA, the RNA component of human RNase P. *Nucleic Acids Res, 18*, 97-103. ↗

Sharp, S., Farrell, P., Soll, D., DeFranco, D., Dingermann, T. (1981). Internal control regions for transcription of eukaryotic tRNA genes. *Proc Natl Acad Sci U S A, 78*, 6657-61. ↗

Birnstiel, ML., Hofstetter, H., Galli, G. (1981). Two conserved sequence blocks within eukaryotic tRNA genes are major promoter elements. *Nature, 294*, 626-31. ↗

Brown, DD. (1980). A control region in the center of the 5S RNA gene directs specific initiation of transcription: I. The 5' border of the region. *Cell, 19*, 13-25. ↗

## Editions

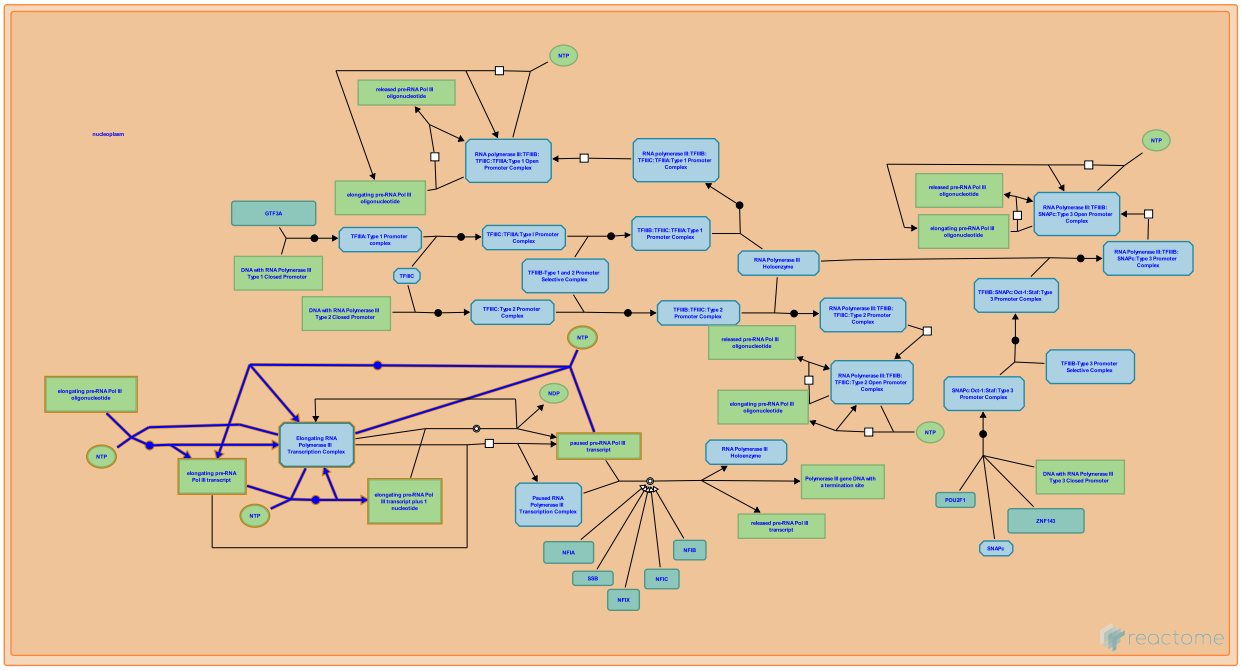
| | | |
|---|---|---|
| 2003-09-11 | Authored | Hernandez, N. |
| 2024-03-06 | Edited | Joshi-Tope, G. |

## RNA Polymerase III Chain Elongation ↗

**Location:** RNA Polymerase III Transcription

**Stable identifier:** R-HSA-73780

**Compartments:** nucleoplasm




Pol III initiation complexes open the promoter spontaneously similar to the mechanism employed in archaeal and bacterial transcription.

## Editions

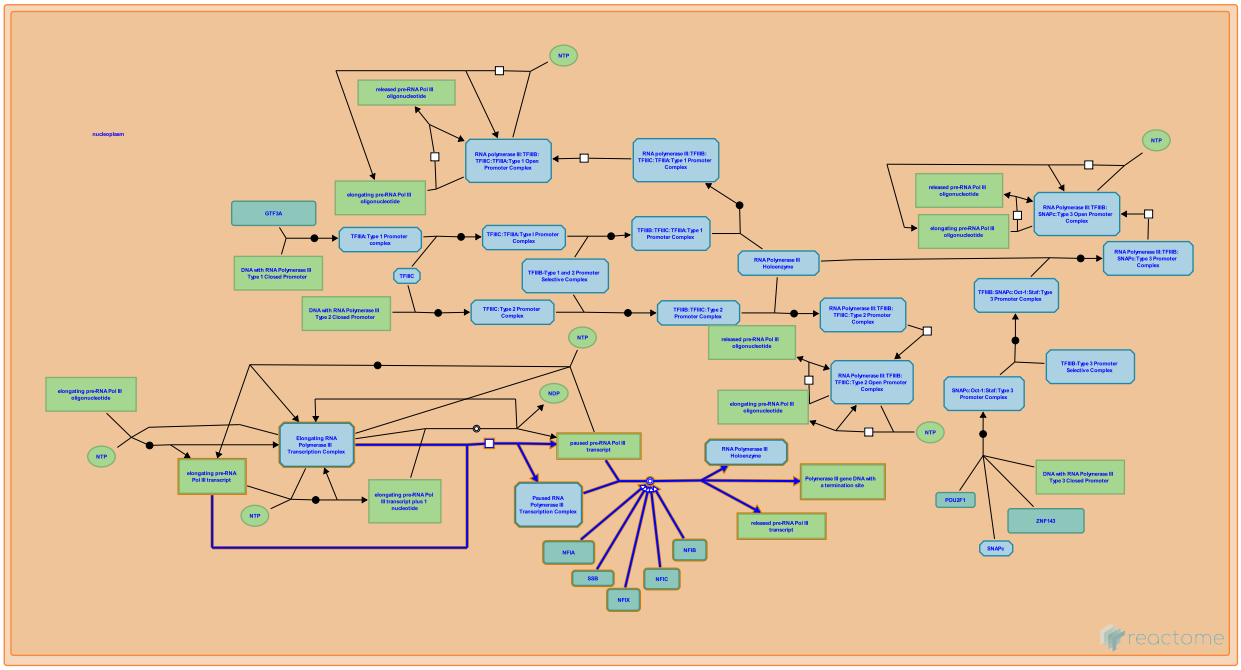
| | | |
|---|---|---|
| 2004-02-27 | Authored | Kassavetis, GA., Geiduschek, EP. |
| 2024-03-06 | Edited | Gillespie, ME. |

## RNA Polymerase III Transcription Termination ↗

**Location:** RNA Polymerase III Transcription

**Stable identifier:** R-HSA-73980

**Compartments:** nucleoplasm




At the end of the cycle, the elongation complex (EC) must be destabilized to release its transcript and DNA. Analogous to initiation, cis-signals and protein factors are required to mediate EC destabilization and release of the transcript from the grip of the RNA polymerase (RNAP). RNAP III achieves efficient termination despite the apparent simplicity of its cis-acting DNA terminator element, a stretch of five or more T residues on the non-template (NT) strand, which directs termination within this site without need for additional cis-elements or trans-acting factors.

## Literature references


Maraia, RJ., Arimbasseri, AG. (2015). Mechanism of Transcription Termination by RNA Polymerase III Utilizes a Non-template Strand Sequence-Specific Signal Element. *Mol. Cell, 58*, 1124-32. ↗


## Editions

| | | |
|---|---|---|
| 2004-02-27 | Authored | Kassavetis, GA., Geiduschek, EP. |
| 2024-03-06 | Edited | Joshi-Tope, G. |

# Table of Contents