

Promoter finder

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Introduction

Using this NCBI API program, you can retrieve a promoter region of your gene of interest.

WARNING! This script uses the coordinates of the gene of interest to define the area to be extracted. However, it is not possible to select a specific transcript. Please always check the extracted region (see below).

Gene ID

<https://www.ncbi.nlm.nih.gov/gene/>

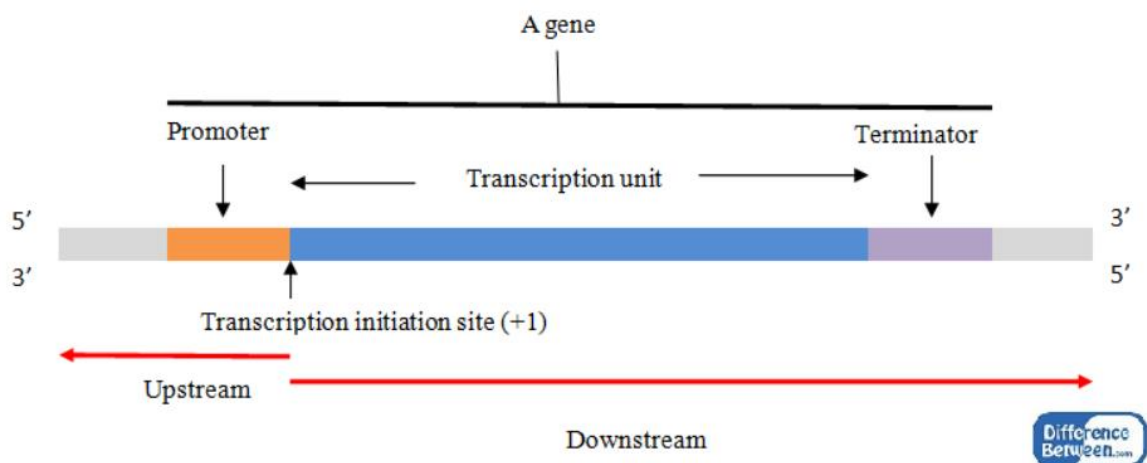
The screenshot shows the NCBI Gene database interface. At the top, there's a search bar with 'Gene' selected. Below the search bar, the gene 'NOS2 nitric oxide synthase 2 [Homo sapiens (human)]' is displayed. The gene ID '4843' is highlighted in a red box. The page includes a 'Summary' section with details about the gene's official symbol, full name, primary source, and various annotations. On the right side, there's a 'Table of contents' with links to different sections like Summary, Genomic context, Expression, Bibliography, Phenotypes, Variation, HIV-1 interactions, Pathways from PubChem, Interactions, General gene information, Markers, Related pseudogene(s), Homology, Gene Ontology, General protein information, NCBI Reference Sequences (RefSeq), Related sequences, and Additional links.

Species

Only human, mouse and rat are allowed (yet)

The screenshot shows the NIH National Library of Medicine Gene database interface. The top navigation bar includes the NIH logo and a search bar. The main content area displays the gene entry for NOS2 (nitric oxide synthase 2) in Homo sapiens (human). The entry includes the gene ID (4843), the official symbol (NOS2), and the official full name (nitric oxide synthase 2). It also lists the primary source (HGNC:HGNC:7873) and the RefSeq status (REVIEWED). The organism is Homo sapiens, and the lineage is Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Catarrhini; Hominidae; Homo. The summary section provides a detailed description of the gene, stating that it encodes a nitric oxide synthase which is expressed in liver and is inducible by a combination of lipopolysaccharide and certain cytokines. It also mentions that three related pseudogenes are located within the Smith-Magenis syndrome region on chromosome 17. The expression section indicates that the gene is biasedly expressed in small intestine (RPKM 10.3), appendix (RPKM 7.9) and 5 other tissues. The orthologs section lists mouse and rat. A table of contents on the right side of the page lists various sections including Summary, Genomic context, Expression, Bibliography, Phenotypes, Variation, HIV-1 interactions, Pathways from PubChem, Interactions, General gene information, Markers, Related pseudogene(s), Homology, Gene Ontology, General protein information, NCBI Reference Sequences (RefSeq), Related sequences, and Additional links.

Upstream/downstream



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The script analyzes the gene to find out whether it's on the sense or anti-sense strand.

Simply enter the number of base pairs upstream and downstream of the transcription initiation site.

The transcription initiation site is retrieved via the API. It is in the gene's FASTA and the GeneBank.

WARNING! The API does not allow you to select a specific transcript. Check the coordinates of the transcription initiation site. It may be different from the desired transcript. Adjust the upstream/downstream window accordingly.

NC_XXXXXX.XX is the chromosome accession number. The chromosome corresponds to the last 2 digits before the "."



National Library of Medicine
National Center for Biotechnology Information

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FASTA

Homo sapiens chromosome 17, GRCh38.p14 Primary Assembly

NCBI Reference Sequence NC_000017.11

[GenBank](#)
[Graphics](#)

>NC_000017.11:c27800529-27756766 Homo sapiens chromosome 17, GRCh38.p14 Primary Assembly

ATAACTTTTGAGCGAGTCGAAACCTCGGCTCCGGCCGACAGAACTCAGCCTCATTCTGCTTTAAAAATCTCTCGCCACCTTTGATGAGGGGACTGGGAGTCTAGACAGCTCCGAAGTCTCAAGGCACAGGTCTCTTCCTGGTTGACTGTCTTACCCGGGAGGACAGTCAGCCAGCTGCAAGGTGAGTTGCCCTCATTTTGGGGAAGCGGCTTTTGGAGAGGGTTTGTCTTCTCTCTTTGGAAGGCTCAGAAATTTGTGGGAATTTCTGCCTACAGAGAGAAGGTGTTGGAAAGTCTAGTAAAAAATGCCGACATGAGGTTGGTCATTGTGAACATGGCATCTTGGTCAGATTTCTTTTCTGCAAAATATTAGCTGTGGTTTATCATGACAAGGAAAAAATCTCTGAAAGTCTCAAAATGGGAGTTTGTATCTGCTAAGAATTTTTTAAACAGAGATTATCTATCAGTCCCTATAACATGTAACTCCCCCAAACTCTGTAAGATGGATATATTAAACCATTTTATGGATGAATAAATGAGTTTCAGTTAAATAACTTGATCCAGGACACATAACTGGTAGAGCTAGGATCCAGGATTGAAACCAAGTCTATGGGGGCTATAAGTTCTTTTCTTTCTTCCCTCTTCTCTCTCTTCTCTCTCTGTCCTTTCTCTCCCTTCCCTCCCTTCCCTTCTCTTCTTTCTTTTCTTTTGGAAACAGCTTGACTGCCAGCCTCAAGCAATCTCTGCTCAGCCTCCGAGTAGCTGGGACTACAGGCACAAGACACATGCTGCTGCTGGCTGAATTTTCAATTTTTTGTAGTCAAGGTCTCCCTATGTGTGCCAGGCTGAACCTGAACTCTGGACTCAGGCAGATCTCTGCCCTGGTCTCCGAAATGCTGGATTACAGGCGTGAGCCATGCACCTTGGCTTAAATTTCTTACATGGCTATATTCACTACACTGTCTTCAAGACAGATTTTTTGGCTCTTTGATCTCTCTCTGTCTGTGTTCAAGAGAGATGATCTCAGATTTGAGGGATGAGTGCATTTTTCACAAATATTTCTCTCCACATATAAAGAGAGGCAAGTAATAATGCTGAGTTAGAACACAACTGCAAACTTTTAAAGAAAGGTGAGTACAGC

Change region shown

☐ Whole sequence
☒ Selected region

from: 27756766 to: 27800529

Customize view

Display options
☒ Show reverse complement
☐ Show gap features

Analyze this sequence

[Run BLAST](#)

[Pick Primers](#)

The transcription initiation site is as previously indicated. It's an aid to help you locate the gene directly on the map.

