Resource Summary Report

Generated by NIF on May 25, 2025

Coding Potential Calculator

RRID:SCR_002764
Type: Tool

Proper Citation

Coding Potential Calculator (RRID:SCR_002764)

Resource Information

URL: http://cpc.cbi.pku.edu.cn/

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Description: A Support Vector Machine-based classifier to assesses the protein-coding potential of a transcript based on six biologically meaningful sequence features. CPC can discriminate coding from noncoding transcripts with high accuracy and speed. In addition to predicting the coding potential of the input transcripts, the CPC web server also graphically displays detailed sequence features and additional annotations of the transcript that may facilitate users' further investigation. The coding potential calculator tool reads FASTA data format as input.

Abbreviations: CPC

Resource Type: production service resource, data analysis service, analysis service resource, service resource, software resource

Defining Citation: PMID:17631615

Keywords: fasta, transcript, protein coding, coding potential, bio.tools

Funding:

Availability: Acknowledgement requested

Resource Name: Coding Potential Calculator

Resource ID: SCR_002764

Alternate IDs: biotools:cpc, rid_000106

Alternate URLs: https://bio.tools/cpc

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250525T030719+0000

Ratings and Alerts

No rating or validation information has been found for Coding Potential Calculator.

No alerts have been found for Coding Potential Calculator.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 193 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Zhang H, et al. (2024) The haplotype-resolved genome assembly of autotetraploid rhubarb Rheum officinale provides insights into its genome evolution and massive accumulation of anthraquinones. Plant communications, 5(1), 100677.

Tian H, et al. (2024) Current understanding of functional peptides encoded by lncRNA in cancer. Cancer cell international, 24(1), 252.

Huang X, et al. (2024) The long noncoding RNA loc107053557 acts as a gga-miR-3530-5p sponge to suppress the replication of vvIBDV through regulating STAT1 expression. Virulence, 15(1), 2333237.

Zhao K, et al. (2024) LncRNA ZNF674-AS1 drives cell growth and inhibits cisplatin-induced pyroptosis via up-regulating CA9 in neuroblastoma. Cell death & disease, 15(1), 5.

Zhang W, et al. (2024) Signaling pathways and regulatory networks in quail skeletal muscle development: insights from whole transcriptome sequencing. Poultry science, 103(5), 103603.

Xiao L, et al. (2024) Whole-transcriptome sequencing revealed the ceRNA regulatory network during the proliferation and differentiation of goose myoblast. Poultry science, 103(11), 104173.

Faulkes CG, et al. (2024) Naked mole-rats have distinctive cardiometabolic and genetic adaptations to their underground low-oxygen lifestyles. Nature communications, 15(1), 2204.

Xiong W, et al. (2024) The mitochondrial long non-coding RNA lncMtloop regulates mitochondrial transcription and suppresses Alzheimer's disease. The EMBO journal, 43(23), 6001.

Gorji AE, et al. (2024) Identification and analysis of differentially expressed lncRNAs and their ceRNA networks in DMD/mdx primary myoblasts. Scientific reports, 14(1), 23691.

Fan L, et al. (2024) Long Noncoding RNA EMX2-AS Facilitates Osteoblast Differentiation and Bone Formation by Inhibiting EMX2 Protein Translation and Activating Wnt/?-Catenin Pathway. Stem cells international, 2024, 4397807.

Xiong H, et al. (2024) Whole transcriptome analysis revealed the regulatory network and related pathways of non-coding RNA regulating ovarian atrophy in broody hens. Frontiers in veterinary science, 11, 1399776.

Shen J, et al. (2024) N6-methyladenosine (m6A)-circHECA from secondary hair follicle of cashmere goats: identification, regulatory network and expression regulated potentially by methylation of its host gene promoter. Animal bioscience, 37(12), 2066.

Zhang C, et al. (2023) Conjoint Analysis of Genome-Wide lncRNA and mRNA Expression during the Salicylic Acid Response in Populus × euramericana. Plants (Basel, Switzerland), 12(6).

Li Y, et al. (2023) Long noncoding RNA DIAPH2-AS1 promotes neural invasion of gastric cancer via stabilizing NSUN2 to enhance the m5C modification of NTN1. Cell death & disease, 14(4), 260.

Li D, et al. (2023) LINC01393, a Novel Long Non-Coding RNA, Promotes the Cell Proliferation, Migration and Invasion through MiR-128-3p/NUSAP1 Axis in Glioblastoma. International journal of molecular sciences, 24(6).

Zhang F, et al. (2023) FAR591 promotes the pathogenesis and progression of SONFH by regulating Fos expression to mediate the apoptosis of bone microvascular endothelial cells. Bone research, 11(1), 27.

Huo Y, et al. (2023) Combined Transcriptome and Proteome Analysis Provides Insights into Petaloidy in Pomegranate. Plants (Basel, Switzerland), 12(13).

Qin M, et al. (2023) IGFL2-AS1-induced suppression of HIF-1? degradation promotes cell proliferation and invasion in colorectal cancer by upregulating CA9. Cancer medicine, 12(7), 8415.

Loganathan T, et al. (2023) Non-coding RNAs in human health and disease: potential function as biomarkers and therapeutic targets. Functional & integrative genomics, 23(1), 33.

Munkhzul C, et al. (2023) The microRNA-mediated gene regulatory network in the hippocampus and hypothalamus of the aging mouse. PloS one, 18(11), e0291943.