

2. Acetyl coenzyme A (CoA) acyltransferase (Act) (accession number KT600799)

expasy - Yahoo S x SWISS-MODEL x Untitled Project x SWISS-MODEL x Expasy - Translat x Expasy ProtPara x Rhodococcus er x +

ncbi.nlm.nih.gov/nuccore/KT600799.1?report=fasta

Nucleotide Nucleotide Advanced Search Help

FASTA Send to: Change region shown Customize view

Rhodococcus erythropolis strain MI2 acetyl-CoA acyltransferase gene, complete cds

GenBank: KT600799.1
[GenBank](#) [Graphics](#)

>KT600799.1 Rhodococcus erythropolis strain MI2 acetyl-CoA acyltransferase gene, complete cds

```
ATGGGGACAATCATGACCACACCCGAACCGATCGTCATCGTCGACGGGGCCAGGACCCCGTCGGTAGCT
TCGGCGCGCTCTTCAAGGACGTACCCGACACAGAGCTGGGTGCCGACGAGCCAAAGCCGCGCTGAGCCG
CGCCGGCGTTGCACCCGAAGACATCGACGAGGTCGTATGGGCTGCATCGGCCAGGTGCGGCCAGAGCGCC
TACAACGCACGCCGCTGGGATCGCCGCCGACTGCCGAGAACGTTCCCGCTACACCGTCAACCGCC
TCTGTGGCAGCGGCTGCAAGCCGCTGTGGTCTGCGGCATGACAGATGCGCTGGGGCGCAGCTGCCATCAC
CCTCGCCGGCGGCGACGAGAGCATGTCCCGCATGCCGTTCTACGATTTCCGCCGCCGCTCGGGCTACAAG
CTCGGCGATCGACGCTCGTCGACGGCACCGTCGCCATGCTCACCGACCCGTTCAAGAAAGGCCATATGG
GCCGACCCGCCGAAGCCGTCGCCCGCAAGTACGGCGTCAGCCGCGAGCAGCAGGACGAGTTGCCGCTCGA
ATCTCAGCGCCGCGCTGCTACTGACGAGCAAGGCGAGCATTGCGCGAGGAGATCACTCCGCTCGAGACC
GGTGGTCGGCGCTCCGTACCGTCACCCGAAGACGAGCACCCAAAGCCCGGAACCACTGTGCAAAACCTCG
CCAAGCTGCGCCCTGCATTGGAAGGGCGGATCCGTACCGCCGGTAACGCGTCGGGATCAACGACGG
CGCCGGCGCACTGTCCTCGCTACAGGAACCGAGGCGAGCAAGCGCGGCTCACCGGACTGGTCAAGCTC
GAAACCGTCACGACGGCAGCCATGGAGCCCGGCTGATGGGCTACGCTCCGCTGCTCGCTCTCGAAAGC
TTTTTGGCAAAACAGGATTGAAACCGTCCGACATCGGCACCGCGAGGTCAACGAGGCCCTTGGCTTCGCA
GGCCATCGCCGTATCCGTGACAGTGGCTGGATCCGGAGAAGACCAACCGTACGGCGGAGCAATCGCC
CTCGGACACCCGGTGGCGCTACCGGAGCCATCCTCAGCTGCGCGCGGACGCGACATGGTCCGTGCGG
ACCTCGAATTCGGCATCGTCACCATGTGCATCGGCGGCGGTGAGGCACTCGCTGCCCTGCTGAAGCGGT
CTGA
```

Analyze this sequence
Run BLAST
Pick Primers

Related information
Protein
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- Rhodococcus erythropolis strain MI2 acetyl-CoA acyltransferase gene, complete Nucleotide
- Rhodococcus erythropolis strain MI2 RNA sigma factor, hypothetical protein, N: Nucleotide
- Parainfluenza Virus - StatPearls

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Translate tool

Translate is a tool which allows the translation of a nucleotide (DNA/RNA) sequence to a protein sequence.

DNA or RNA sequence

```
KT600799.1 Rhodococcus erythropolis strain MI2  
acetyl-CoA acyltransferase gene, complete cds  
ATGGGGACAATCATGACCACACCCGAACCGATC  
GTCATCGTCGACGGGGCCAGGACCCCGTCGG  
TAGCT  
TCGGCGGCGTCTTCAAGGACGTACCCGCACAC  
GAGCTGGGTGCCGACGAGCAAGGCCGCGC  
TGAGCCG  
CGCCGGCGTTGCACCCGAAGACATCGACGAGG  
TCGTCATGGGCTGCATCGGCCAGGTCGGCCCA
```

Output format

- ☐ Verbose: Met, Stop, spaces between residues
☒ Compact: M, -, no spaces
☐ Includes nucleotide sequence
☐ Includes nucleotide sequence, no spaces

DNA strands

- ☒ forward ☒ reverse

Genetic codes - [See NCBI's genetic codes](#)

Standard

reset

TRANSLATE!

```
cgccggcgctctcaaggacgtaccgcacacgagctgggtgccga  
gcagccaaggccgctgagccgcgcggcggtgcacccaagac  
atcgacgaggtgctcatgggctgcatcgccaggctcgccagacg  
ctacaacgcacgcgcgctgggcatgcgcgggactgccgaga  
acgtccgcctacacgcacacgcctctgtggcagcggtcgcag  
gccgtgtgtctgcggcgatgcagatgcgtggggcgacgtgccat  
caccctcgccggcggcgacgagagcatgtcccgatgccgttctacg
```

- ☐ Includes nucleotide sequence
☐ Includes nucleotide sequence, no spaces

DNA strands

- ☒ forward ☒ reverse

Genetic codes - [See NCBI's genetic codes](#)

Standard

reset

TRANSLATE!

Results of translation

- Open reading frames are highlighted in red
- Select your initiator on one of the following frames to retrieve your amino acid sequence

Download all the translated frames

5'3' Frame 1

```
XXXXXXXXXXXXXXXXXXXXMGTIMTPEPIVVDGARTPVGSFGGVFKDVP  
AHELGAAAAAALSRAGVAPEDIDEVVMGCI  
GQVGPDAYNARRVGIAAGLPENVPAYTVNRLCGSGLQAVWSAAMQMRW  
GAAAITLAGGDESMRSMPFYDFAARSGYKLGDRSLVDGT  
VAMLTDPFSAHMGRTAEAVARKYGVSRQQDEFIVESQRRRAATDAKAA  
FAEEITPVETGGRRSVIVTEDEHPKPGTTVETLAKLR  
PAFEEGGSVTAGNASGINDGAGALVLATGTEAAKRGITGLVLTLETVT  
TAAMEPGLMGYAPVLALEKLFQATGLKPSDIGTAEVNEAF  
ASQAIAVIRDSGLDPEKTNPFYGAIALGHPVGATGAILTLRAARDMV  
RRDLEFGIVTMCIGGGQALAAALKRV-
```

5'3' Frame 2

expasy - Yahoo Search xSWISS-MODEL - SIB xUntitled Project | Mo xSWISS-MODEL Inter xExpasy - Translate to xExpasy ProtParam too x

web.expasy.org/cgi-bin/protparam/protparam?VIRT30430

ExpasyProtParamHomeContact

ProtParam

User-provided sequence:

102030405060

XXXPPXXXXX XXXXXXXXXX XXXXGTIMT TPEPIVIDG ARTPVGSFGG VFKDVPAPHEL

708090100110120

GAAAAKAALS RAGVAPEDID EVVMGICIGQV GPDAYNARRV GIAAGLPENV PAYTVNRLCG

130140150160170180

SGLQAVWSAA MQMRWGAAAI TLAGGDESMS RMPFYDFAAR SGYKLGDRSL VDGTVAMLTQ

190200210220230240

PFSKAHMGRT AEAVARKYGV SREQQDEFV ESQRRATDA AKAFAEEIT PVETGGRRSV

250260270280290300

TVTEDEHPKP GTTVETLAKL RPAFEEGGSV TAGNASGIND GAGALVLATG TEAAKRLTG

310320330340350360

LVTLETVTTA AMEPGLMGYA PVLALEKLFA QTGLKPSDIG TAEVNEAFAS QAIIVIRDSG

370380390400410420

LDPEKTNPYG GAIALGHPVG ATGAILTLRA ARDMVRRDLE FGIVTHCIGG GQALAALLKR

V

References and documentation are available.

Number of amino acids: 421

Molecular weight: undefined

Theoretical pI: Sequence contains several non-standard amino acids

Type here to search

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expasy - Yah xSWISS-MOD xUntitled Proj xSWISS-MOD xExpasy - Tran xExpasy ProtP xexpasy - Yah xExpasy - Tran x

swissmodel.expasy.org/interactive

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SWISS-MODEL

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Start a New Modelling Project

Target Sequence(s):

(Format must be FASTA, Clustal, plain string, or a valid UniProtKB AC)

Target

Target

Target

Target

100200300397

Add Hetero Target

Reset

Project Title:

Optional

Search For Templates

Build Model

By using the SWISS-MODEL server, you agree to comply with the following terms of use and to cite the corresponding articles.

Supported Inputs

Sequence(s)

Target-Template Alignment

User Template

DeepView Project

You are currently not logged in - to take advantage of the workspace, please log in or create an account.

(There is no requirement to create an account to use any part of SWISS-MODEL, however you will gain the benefit of seeing a list of your previous modelling projects here.)

Modelling Projects in Session

Untitled Project

397 residues. 50 templates were found. 2 models have been built.

Created: today
(Expires: Next week)

Untitled Project

Created: today

Type here to search

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