

# 1. Nox ( accession number KT600797)

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ncbi.nlm.nih.gov/nuccore/KT600797.1?report=fasta

An official website of the United States government [Here's how you know](#)

**NIH** National Library of Medicine  
National Center for Biotechnology Information

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Recent activity

**Rhodococcus erythropolis strain MI2 RNA sigma factor, hypothetical protein, NoxR, Nox, TrxB, and TrxA genes, complete cds**

GenBank: KT600797.1

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>KT600797.1 Rhodococcus erythropolis strain MI2 RNA sigma factor, hypothetical protein, NoxR, Nox, TrxB, and TrxA genes, complete cds

```
GTGGTCAATGCCTGCTTGACCGGATCCGACGCAACAAATCGCGGCGCGTCTCTCTGTCTCCGAGA
ATGCGGAGGAACCCGATGATCACCAGGATTACGCGCGCGGCGTGGACAGGAGCCTGACCGTCGAACAAGC
GCTGGCATCGCTGCCCTGAGCAGCGCGTCCGCTCGTCCGCTCGATGTCGAGGGGATCCGGTGGCC
GAGGCCCGCGAGAGGTTGGGCGTGCCGTAGGGACCGTGAAGAGTCGCTGCGCCCGCGCACGCAAGCGCC
TCGCCGCCAGTTGGAGGACTTTCGCGAAGCGGGAAACATTCTGTAACCGCGCGCTCTACTTGTAA
GCGTCCACACGACTGCCGAGGAGGGTTCATGACAGATCCGCTGTTCCGCTTCCGTCGCCCTCCGTTT
CGGAGGACCTCTTGGCGGATCTTACGCCGGGTTCTCGATCCGAAACAGTGCAAGCTCTGTGGCCGCT
GGTACATGCAGACGCCGACGCCATGCATTGTCTACTACTCTCGACAGCGTCACAGCATCACTCGCGACA
CTGAACTCGCGCAGGCGCTCTACGAACGGATTCCGAATTCGCTTCCGAGCGAATCAATTCGGCATGG
ATCTACAGTCCGGTCAGGACGAGCGCTCAGCAGAGACAACCGTCTGCGCTTCCGGCGACGCCCAAGC
GTGGCTGCTCGGTGCCGAGCAGCGCTGTGGTGGCTTCTGATCGTTGTGATCGGAACCCGAGATTCC
GAACCTGCCGAAAGCGTTGTGCTCAACCAAGCACACCGGCGACATCTGCTGTGGACGATCCGGATTCCG
CGTCCCTGCTTCACTCATCGGATCCAAAACCTTGGACCACTGGATGATCCCAAGCTTCCGCGCTG
CCTGAGCGCAATGGATCGACGAGGCGAGCGCTGTGCTCGGCTCGGGTGAGGTTGCACTGACGGTGA
CCGGCGATAGTCTACTCTTCCGGGATCGCAGCCGCGTCAGATCACTGCACTCACTGTTGGCATCACT
GCAGCGCGTAATTCGAAATAGTTGTCAATCAAGACATCGGTTGACGTCGACGGTGTGACGCGGTGT
```

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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

```
gtgggtcaatgccttgacccggtacgcgcaacaaatcgcgggc
cggttctctctgtctccgagaatcgagggaacccggtgacccg
cgattacgcggcgggcggtggacagagcctgacgctcgaacaagc
gctggcatcgctgccccctgagcagcgcgctgctgctgctgctg
atgtcgaggggtatccggtggcgaggccgagaggttggcgctg
gcccgtaggagacggtgaagagtcgctgccccgcgacgcaagcg
cctcgccgccagttgaggacttgcgaaggcggaaccattcgt
gaaccgcccgcgtctatctgttaagcgctccacagcactgcccagg
gaggggtcatgacagatccgctgttcgcttcgctcctccgttttcg
aggaccttggcgatctcagccggggttctcgatcccgaaacca
```

### 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!

Results of translation

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### 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**

```
VVNACLDIRIRNKSRAAFSLSSNAEEPRDHRDYAAGVDRSLTVEQALASLPPEQRAAVVAVDVEGYPVAAEAERLGVFVGTVKSRC
ARARKRLAAQLEDFREGGNHS-TGRVLSCKRPHRLPREGS-QIRLFAFRRLRFRRTSWRIFTGFSIPKPVQLCGRWYMQTPTFMHL
SLISTASQHHSHR-TRARPLTNGFRIRLPSESIRHWIYSPVRSRQQRQPSRCRSGDAHKRGCSVPQQPCWFP-SL-SEPEIPNLPK
ALSLNQAHRRHLLWTIRIRPCFHSSDPKTLDHWMIRPSLPAA-APMASTRAGLCSARVRFASIVYR-SYSSRDRSRVRSLSHLLA
STAATVIRIRQQRSTSDVDGVSAPLPRAGARGFSRAMHPYRPRPLSDSKTSLRPPIPARPWHRAVPIRDLRHSEGTVACSAH-N
RATIRCVGRHGAAQPAVPATQHEPRAARRAEHFPFPNGSSRRDRCPRTVSGQVSHPGSTRELDVPSTAIVVTSRLG-PLFVPRSP
GD-VAPIRPGASLG-PRGLORRCVGLVGDILWRSSCRIVGQIGSRRIYVVVTSPLAS-RSGRRRKLMTTAPTSPISIFEPARLGPL
TLRNRIVKAATFEGVMPRGAVSDDLINFHAEVARGGAAMTVAYCAVSPGGRVHRDTLVMDERALPGLRRLTDAVHAEGALAAQIG
HAGLVANTLSNKTTLAPSTRLSPPAMGLVKATLAELDGVVSDFTARVAVDAGFDAIEVHLGHNYLLSFSFMSFNLNKRHRYGG
SVAKRAEYFRVIEAVRVAAGSSVAVTAKFNMSDGVKGLWLDQSLPIAQILEADGHLDAMQLTGGSSLLNGMYFFRGEVPLAEFVA
SQPKLVGYGLKFYGPRIFFTPYFEEGFFLPFARQFRQALRMPLILLGGINRVDTEHALDEGFEFVAMARALLRDPQLVNKFQAESV
DQGLCIHCNKMCTIYTGTTRCVVRDALVREAPRLGQ-VPRCELPAVSHFPSECGNNTYPGVDRYGSPPRSGGSALTIGRLA-PPSW
KPRPRSMTSSLSVDRPATPLVSTPRALSSSPCSREPPSSVAPS-PPPSRSTSPDSAKESWAPI-WNRCAHRCASTPTSPARTSKR
STSAARSRPSSRTAKPTPTRRSSPWAQQPATWAFPVKNASSAAASAPAPATASSSVTRTSSWSAAATPRWKKQSPSPASLARSFW
CTAARSSAPHGSCSSAPRPTRSAS-PTPSPSRCSVTASPASSCATPSPVKLPHSRSPACSSPSATTRAVNSSRARSISTTPTDCA
SLPVPFRPPTASSLPLVTWISITRVRSSPLPADAPQOSTPNAGWPTAATSPPTRSTQPATRSTSSALPDSPSCRTQPSRNSVEYR
HHHRRFLQAGRPQGRQARSGRFLGNLVRVQDGRPGPRGDRRREQREADRRQARHRCQPRGRARFPGHVDDDDFVQGRQADQDDRR
RQGGRAAQGFRRRL
```

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**Your selected amino-acid sequence**

[Pseudo-entry](#)

```
ID VIRT-15850 Unreviewed: 59 AA.
AC VIRT-15850;
DE Translation of nucleotide sequence generated on Expaty
DE 5'3' Frame 1, start_pos=188
DE on Wed Dec 13 19:14:52 CET 2023 by 156.212.44.207
CC -!- This virtual protein sequence will automatically be deleted
CC from the server after a few days.
SQ SEQUENCE 59 AA; A61488F1BCB18AEA CRC64.
TRARPLTNGF RIRLPSESIR HWIYSPVRS RQQRQPSRCS GDAHKRGCSV PQQPCWFP
//
```

[Fasta format](#)

```
> VIRT-15850:5'3' Frame 1, start_pos=188
TRARPLTNGF RIRLPSESIR HWIYSPVRS RQQRQPSRCS GDAHKRGCSV
PQQPCWFP
```

**Results of translation**

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web.expasy.org/cgi-bin/protparam/protparam?VIRT15850

# Expasy

## ProtParam

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### ProtParam

User-provided sequence:

10 20 30 40 50  
TRARPLTNGF RIRLPSESIR HWIYSPVPTS RQQRPSCRS GDAHKRGCSV PQQPCWIPS

References and documentation are available.

Number of amino acids: 59  
Molecular weight: 6916.85  
Theoretical pI: 11.64

Amino acid composition: [CSV format](#)

Ala (A)	2	3.4%
Arg (R)	10	16.9%
Asn (N)	1	1.7%
Asp (D)	1	1.7%
Cys (C)	3	5.1%
Gln (Q)	5	8.5%
Glu (E)	1	1.7%
Gly (G)	3	5.1%
His (H)	2	3.4%
Ile (I)	3	5.1%
Leu (L)	2	3.4%
Lys (K)	1	1.7%
Met (M)	0	0.0%
Phe (F)	1	1.7%
Pro (P)	7	11.9%
Ser (S)	8	13.6%
Thr (T)	3	5.1%
Trp (W)	3	5.1%

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### Start a New Modelling Project

Target Sequence(s): [Settings](#)

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

Target: VVNACLDRIRNKSRAAFSLSSENAEEPRDHRDYAAGVDRLTVEQALASLPPEQRAAVVAVDVEGYVPAEAAERLGVPGTVKSRCARARKRLAAQLED 100

Target: FREGGNHSTGRVLSCKRPHRLPREGSQIRLFAFRRLRFRTSWRIFTPGFSIPKPVQLCGRWYMQTPTPIHLSSLSTASQHSRHRTRARPLTNGFRIRLP 200

Target: SESIRHWIYSPVPTSRRQROPSCRSQDAHKRGCSVPQQPCWIPSSLSSEPIPNLPKALSLNQAHRRLHLLTIRIRRPCFHSSDPKTLQHWIRPSLPAAA 300

Target: PMASTRAGLCSARVRFASVTYRRSYSRDRSRVRLSHSLLASTAATVIRIRQSRSTVDVGSAVLPRAAAGARGFSAIHPYRPRPLSDSKTSLLRPPI 400

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- DeepView Project

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SummaryTemplates50Models4Project Data

Model ResultsOrder by: GMQE

11478

Model 04

Structure Assessment



Oligo-State Monomer

GMQE 0.08

QMEANDisCo Global: 0.45 ± 0.05

QMEANDisCo Local

QMEAN Z-Scores

Template

616j.1.A Oxidored\_FMN domain-containing protein

Structure of 6-hydroxypseudooxynicotine (6-HPON) amine oxidase (HisD) from Pseudomonas geniculata N1

Seq Identity 29.94%

Coverage

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