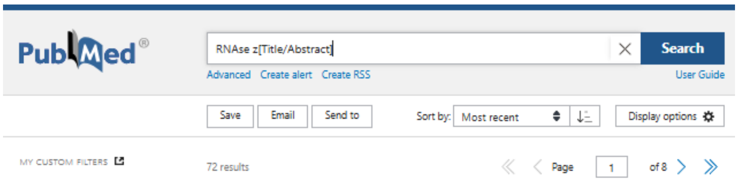
1.1 Vseh člankov je 72.



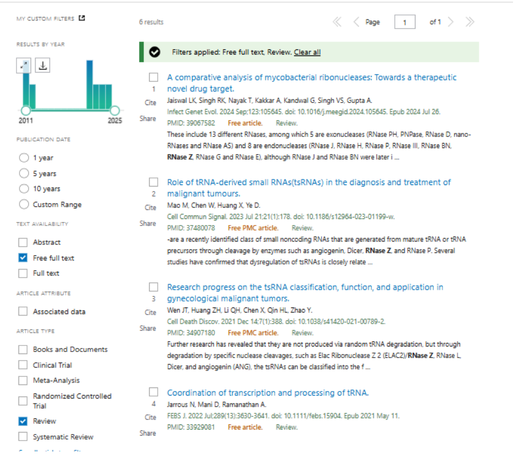
RNAse z[Title/Abstract]

Sort by: Most recent

72 results

Page 1 of 8

1.2 Takih člankov je 6.



6 results

Page 1 of 1

○ 1 year
○ 5 years
○ 10 years
○ Custom Range

☐ Abstract
☑ Free full text
☐ Full text

☐ Associated data

☐ Books and Documents
☐ Clinical Trial
☐ Meta-Analysis
☐ Randomized Controlled Trial
☑ Review
☐ Systematic Review

Filters applied: Free full text, Review. Clear all

1 A comparative analysis of mycobacterial ribonucleases: Towards a therapeutic novel drug target.
Jaiswal LK, Singh RK, Nayak T, Kakkar A, Kandwal G, Singh VS, Gupta A.
Infect Genet Evol. 2024 Sep;123:105645. doi: 10.1016/j.meegid.2024.105645. Epub 2024 Jul 26.
PMID: 39067582 Free article. Review.
These include 13 different RNases, among which 5 are exonucleases (RNase PH, PNPase, RNase D, nano-RNases and RNase AS) and 8 are endonucleases (RNase J, RNase H, RNase P, RNase III, RNase BN, **RNase Z**, RNase G and RNase E), although RNase J and RNase BN were later i ...

2 Role of tRNA-derived small RNAs(tsRNAs) in the diagnosis and treatment of malignant tumours.
Mao M, Chen W, Huang X, Ye D.
Cell Commun Signal. 2023 Jul 21;21(1):178. doi: 10.1186/s12964-023-01199-w.
PMID: 37480078 Free PMC article. Review.
-are a recently identified class of small noncoding RNAs that are generated from mature tRNA or tRNA precursors through cleavage by enzymes such as angiogenin, Dicer, **RNase Z**, and RNase P. Several studies have confirmed that dysregulation of tsRNAs is closely relate ...

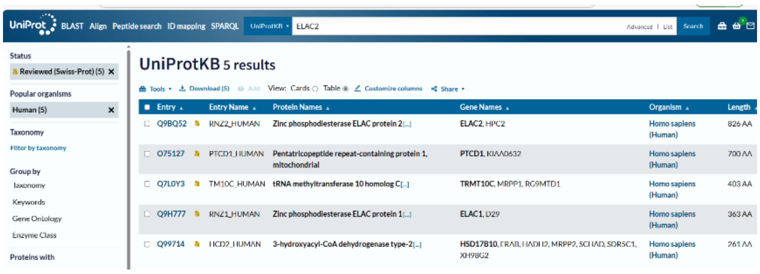
3 Research progress on the tsRNA classification, function, and application in gynecological malignant tumors.
Wen JT, Huang ZH, Li QH, Chen X, Qin HL, Zhao Y.
Cell Death Discov. 2021 Dec 14;7(1):388. doi: 10.1038/s41420-021-00789-2.
PMID: 34907180 Free PMC article. Review.
Further research has revealed that they are not produced via random tRNA degradation, but through degradation by specific nuclease cleavages, such as Elac Ribonuclease Z 2 (ELAC2)/**RNase Z**, RNase L, Dicer, and angiogenin (ANG), the tsRNAs can be classified into the f ...

4 Coordination of transcription and processing of tRNA.
Jarrous N, Mani D, Ramanathan A.
FEBS J. 2022 Jul;289(13):3630-3641. doi: 10.1111/febs.15904. Epub 2021 May 11.
PMID: 33929081 Free article. Review.

2.1 UniProt ID: **Q9BQ52**

Dolžina: 826 ak

Funkcija: sodeluje pri tRNA 3'-procesiranju.



ELAC2

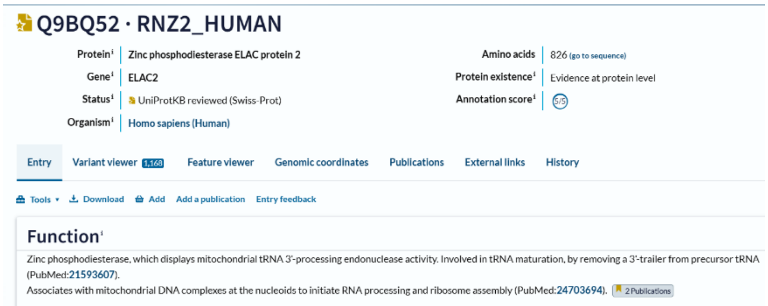
Status: Reviewed (Swiss-Prot) (5)

Popular organisms: Human (5)

UniProtKB 5 results

View: Cards ○ Table ●

| Entry | Entry Name | Protein Names | Gene Names | Organism | Length |
|---|---|---|---|---|---|
| Q9BQ52 | RNZ2_HUMAN | Zinc phosphodiesterase ELAC protein 2[...] | ELAC2, HPC2 | Homo sapiens (Human) | 826 AA |
| O75127 | PTCD1_HUMAN | Pentatricopeptide repeat-containing protein 1, mitochondrial | PTCD1, KIAA0632 | Homo sapiens (Human) | 700 AA |
| Q7L0Y3 | TM10C_HUMAN | tRNA methyltransferase 10 homolog C[...] | TRMT10C, MRPP1, RG9MTD1 | Homo sapiens (Human) | 403 AA |
| Q9H777 | RNZ1_HUMAN | Zinc phosphodiesterase ELAC protein 1[...] | ELAC1, D29 | Homo sapiens (Human) | 363 AA |
| Q99714 | HCD2_HUMAN | 3-hydroxyacyl-CoA dehydrogenase type-2[...] | HSD17B10, ERAB, HADH2, MRPP2, SCHAD, SDR5C1, XH98G2 | Homo sapiens (Human) | 261 AA |



Q9BQ52 · RNZ2_HUMAN

Protein: Zinc phosphodiesterase ELAC protein 2
Gene: ELAC2
Status: UniProtKB reviewed (Swiss-Prot)
Organism: Homo sapiens (Human)
Amino acids: 826 (go to sequence)
Protein existence: Evidence at protein level
Annotation score: 5/5

Function

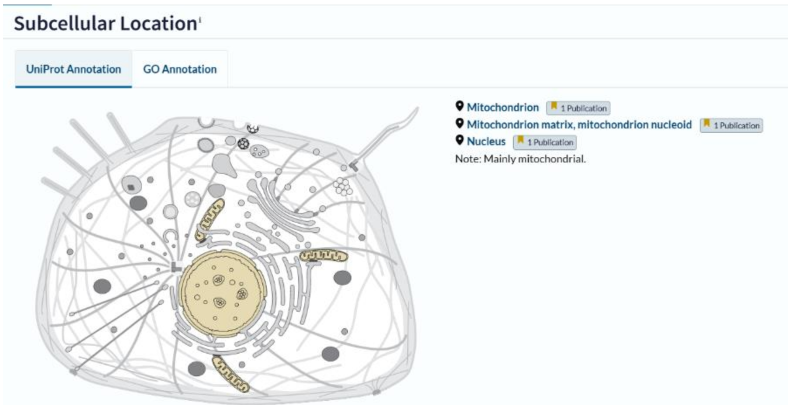
Zinc phosphodiesterase, which displays mitochondrial tRNA 3'-processing endonuclease activity. Involved in tRNA maturation, by removing a 3'-trailer from precursor tRNA (PubMed:21593607).
Associates with mitochondrial DNA complexes at the nucleoids to initiate RNA processing and ribosome assembly (PubMed:24703694).

2.2 Kofaktor je $Zn^{2+}$

Cofactor

$Zn^{2+}$ (UniProtKB | Rhea | CHEBI:29105 )

2.3 V jedru in mitohondriju.

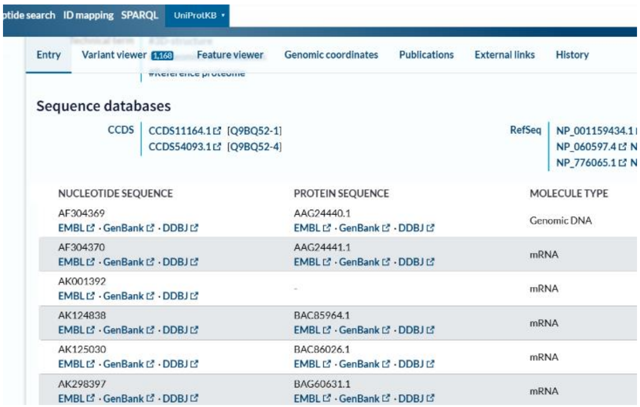


Subcellular Location

Mitochondrion
Mitochondrion matrix, mitochondrion nucleoid
Nucleus

Note: Mainly mitochondrial.

3.1 2908 bp

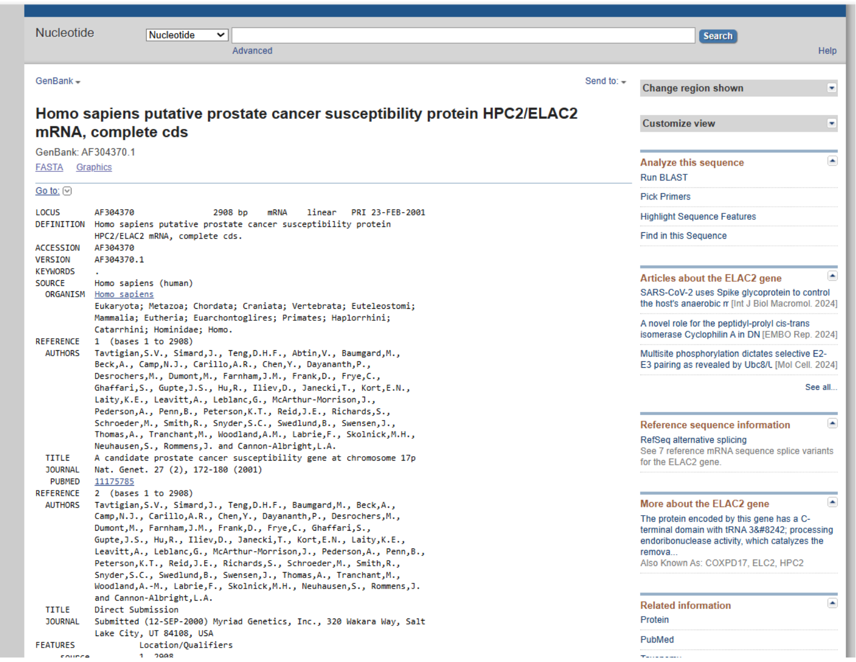


**Sequence databases**

CCDS: CCDS11164.1 [Q9BQ52-1]
CCDS54093.1 [Q9BQ52-4]

RefSeq: NP_001159434.1
NP_060597.4 N
NP_776065.1 N

| NUCLEOTIDE SEQUENCE | PROTEIN SEQUENCE | MOLECULE TYPE |
|---|---|---|
| AF304369<br>EMBL · GenBank · DDBJ | AAG24440.1<br>EMBL · GenBank · DDBJ | Genomic DNA |
| AF304370<br>EMBL · GenBank · DDBJ | AAG24441.1<br>EMBL · GenBank · DDBJ | mRNA |
| AK001392<br>EMBL · GenBank · DDBJ | - | mRNA |
| AK124838<br>EMBL · GenBank · DDBJ | BAC85964.1<br>EMBL · GenBank · DDBJ | mRNA |
| AK125030<br>EMBL · GenBank · DDBJ | BAC86026.1<br>EMBL · GenBank · DDBJ | mRNA |
| AK298397<br>EMBL · GenBank · DDBJ | BAG60631.1<br>EMBL · GenBank · DDBJ | mRNA |



**Homo sapiens putative prostate cancer susceptibility protein HPC2/ELAC2 mRNA, complete cds**

GenBank: AF304370.1

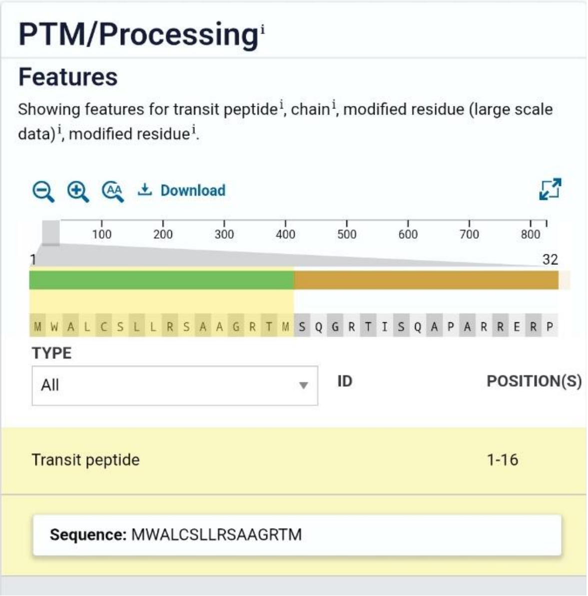
FASTA Graphics

Go to:

```
LOCUS       AF304370                2908 bp    mRNA    linear   PRI 23-FEB-2001
DEFINITION  Homo sapiens putative prostate cancer susceptibility protein
            HPC2/ELAC2 mRNA, complete cds.
ACCESSION   AF304370
VERSION     AF304370.1
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2908)
  AUTHORS   Tavtigian,S.V., Simard,J., Teng,D.H.F., Abtin,V., Baumgard,M.,
            Beck,A., Camp,N.J., Carillo,A.R., Chen,Y., Dayananth,P.,
            Desrochers,M., Dumont,M., Farnham,J.M., Frank,D., Frye,C.,
            Ghaffari,S., Gupte,J.S., Hu,R., Iliev,D., Janecki,T., Kort,E.N.,
            Laity,K.E., Leavitt,A., Leblanc,G., McArthur-Morrison,J.,
            Pederson,A., Penn,B., Peterson,K.T., Reid,J.E., Richards,S.,
            Schroeder,M., Smith,R., Snyder,S.C., Swedlund,B., Swensen,J.,
            Thomas,A., Tranchant,M., Woodland,A.M., Labrie,F., Skolnick,M.H.,
            Neuhausen,S., Rommens,J. and Cannon-Albright,L.A.
  TITLE     A candidate prostate cancer susceptibility gene at chromosome 17p
  JOURNAL   Nat. Genet. 27 (2), 172-180 (2001)
   PUBMED   11175785
REFERENCE   2  (bases 1 to 2908)
  AUTHORS   Tavtigian,S.V., Simard,J., Teng,D.H.F., Baumgard,M., Beck,A.,
            Camp,N.J., Carillo,A.R., Chen,Y., Dayananth,P., Desrochers,M.,
            Dumont,M., Farnham,J.M., Frank,D., Frye,C., Ghaffari,S.,
            Gupte,J.S., Hu,R., Iliev,D., Janecki,T., Kort,E.N., Laity,K.E.,
            Leavitt,A., Leblanc,G., McArthur-Morrison,J., Pederson,A., Penn,B.,
            Peterson,K.T., Reid,J.E., Richards,S., Schroeder,M., Smith,R.,
            Snyder,S.C., Swedlund,B., Swensen,J., Thomas,A., Tranchant,M.,
            Woodland,A.-M., Labrie,F., Skolnick,M.H., Neuhausen,S., Rommens,J.
            and Cannon-Albright,L.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
            Lake City, UT 84108, USA
FEATURES             Location/Qualifiers
```

The protein encoded by this gene has a C-terminal domain with tRNA 3&#8242; processing endoribonuclease activity, which catalyzes the remova...
Also Known As: COXPD17, ELC2, HPC2

3.2 Ta zapis vsebuje 6 triptofanov.



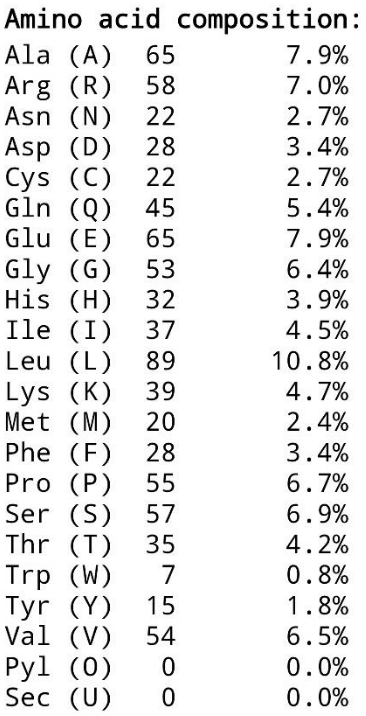
**PTM/Processing**

**Features**

Showing features for transit peptide, chain, modified residue (large scale data), modified residue.

| TYPE | ID | POSITION(S) |
|---|---|---|
| All | | |
| Transit peptide | | 1-16 |

**Sequence:** MWALCSLLRSAAGRTM



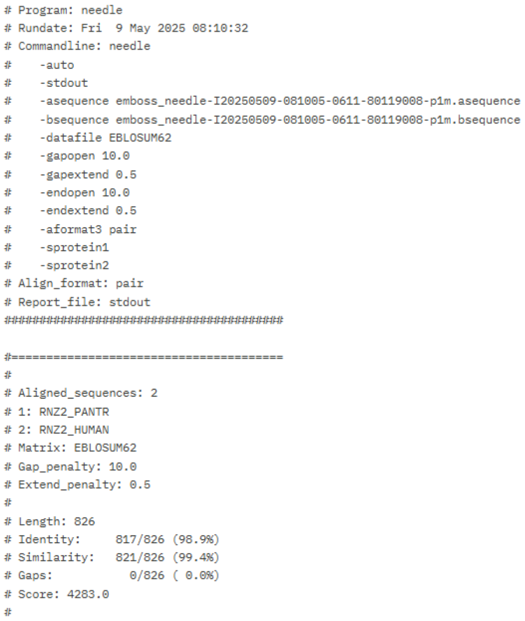
```
Amino acid composition:
Ala (A)  65        7.9%
Arg (R)  58        7.0%
Asn (N)  22        2.7%
Asp (D)  28        3.4%
Cys (C)  22        2.7%
Gln (Q)  45        5.4%
Glu (E)  65        7.9%
Gly (G)  53        6.4%
His (H)  32        3.9%
Ile (I)  37        4.5%
Leu (L)  89       10.8%
Lys (K)  39        4.7%
Met (M)  20        2.4%
Phe (F)  28        3.4%
Pro (P)  55        6.7%
Ser (S)  57        6.9%
Thr (T)  35        4.2%
Trp (W)   7        0.8%
Tyr (Y)  15        1.8%
Val (V)  54        6.5%
Pyl (O)   0        0.0%
Sec (U)   0        0.0%
```

3.3 Ocena poravnave je 4283. Evolucija je uvedla 7 točkovnih mutacij.

**Sequences producing significant alignments**

☑ select all *2 sequences selected*

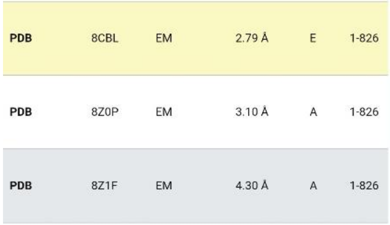
| | Description | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. Ident | Acc. Len | Accession |
|---|---|---|---|---|---|---|---|---|---|
| ☑ | zinc phosphodiesterase ELAC protein 2 [Gorilla gorilla gorilla] | Gorilla gorilla gorilla | 1568 | 1568 | 100% | 0.0 | 98.55% | 826 | NP_001266674.1 |
| ☑ | zinc phosphodiesterase ELAC protein 2 isoform X1 [Gorilla gorilla gorilla] | Gorilla gorilla gorilla | 1563 | 1563 | 100% | 0.0 | 98.55% | 825 | XP_018868441.4 |



```
# Program: needle
# Rundate: Fri  9 May 2025 08:10:32
# Commandline: needle
#    -auto
#    -stdout
#    -asequence emboss_needle-I20250509-081005-0611-80119008-p1m.asequence
#    -bsequence emboss_needle-I20250509-081005-0611-80119008-p1m.bsequence
#    -datafile EBLOSUM62
#    -gapopen 10.0
#    -gapextend 0.5
#    -endopen 10.0
#    -endextend 0.5
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: RNZ2_PANTR
# 2: RNZ2_HUMAN
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 826
# Identity:     817/826 (98.9%)
# Similarity:   821/826 (99.4%)
# Gaps:           0/826 ( 0.0%)
# Score: 4283.0
#
```

```
RNZ2_PANTR         1 MWALCSLLRSAAGRTMSQGRTISQAPARRERPRKDPLRHLRTREKRGPSG     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
RNZ2_HUMAN         1 MWALCSLLRSAAGRTMSQGRTISQAPARRERPRKDPLRHLRTREKRGPSG     50

RNZ2_PANTR        51 CSGGPNTVYLQVVAAGSRDSGAALYVFSEFNRYLFNCGEGIQRLMQEHKL    100
                     |||||||||||||||||||||||||||||||||||||||:||||||||||
RNZ2_HUMAN        51 CSGGPNTVYLQVVAAGSRDSGAALYVFSEFNRYLFNCGEGVQRLMQEHKL    100

RNZ2_PANTR       101 KVARLDNIFLTRMHWSNVGGLSGMILTLKETGLPKCVLSGPPQLEKYLEA    150
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
RNZ2_HUMAN       101 KVARLDNIFLTRMHWSNVGGLSGMILTLKETGLPKCVLSGPPQLEKYLEA    150

RNZ2_PANTR       151 IKIFSGPLKGIELAVRPHSAPEYEDETMTVYQIPIHSEQRRGKHQPWQSP    200
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
RNZ2_HUMAN       151 IKIFSGPLKGIELAVRPHSAPEYEDETMTVYQIPIHSEQRRGKHQPWQSP    200

RNZ2_PANTR       201 ERPLSRLSPERSSDSESNENEPHLPHGVSQRRGVRDSSLVVAFICKLHLK    250
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
RNZ2_HUMAN       201 ERPLSRLSPERSSDSESNENEPHLPHGVSQRRGVRDSSLVVAFICKLHLK    250

RNZ2_PANTR       251 RGNFLVLKAKEMGLPVGTAAIAPIIAAVKDGKSITHEGREILAEELCTPP    300
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
RNZ2_HUMAN       251 RGNFLVLKAKEMGLPVGTAAIAPIIAAVKDGKSITHEGREILAEELCTPP    300

RNZ2_PANTR       301 DPGAAFVVVECPDESFIQPICENATFQRYQGKADAPVALVVHMAPESVLV    350
                     |||||||||||||||||||||||||||||||||||||||||||||.||||
RNZ2_HUMAN       301 DPGAAFVVVECPDESFIQPICENATFQRYQGKADAPVALVVHMAPASVLV    350
```

## 4.1 8CBL



| | | | | | |
|---|---|---|---|---|---|
| **PDB** | 8CBL | EM | 2.79 Å | E | 1-826 |
| **PDB** | 8Z0P | EM | 3.10 Å | A | 1-826 |
| **PDB** | 8Z1F | EM | 4.30 Å | A | 1-826 |

## 4.2 Metoda: elektronski mikroskop

Ekspresijski sistem:  Escherichia coli

8CBL | pdb_00008cbl

Structure of human mitochondrial RNase Z in complex with mitochondrial pre-tRNA-His(0,Ser)

**PDB DOI:** https://doi.org/10.2210/pdb8CBL/pdb **EM Map EMD-16544:** EMDB EMDataResource **NAKB:** 8CBL

**Classification:** RNA BINDING PROTEIN
**Organism(s):** Homo sapiens
**Expression System:** Escherichia coli, in vitro transcription vector pT7-TP(deltai)
**Mutation(s):** Yes

**Deposited:** 2023-01-25 **Released:** 2024-06-12
**Deposition Author(s):** MEYNIER, V., HARDWICK, S., CATALA, M., ROSKE, J., OERUM, S., CHIRGADZE, D., BARRAUD, P., YU, W., LUISI, B., TISNE, C.
**Funding Organization(s):** Agence Nationale de la Recherche (ANR)

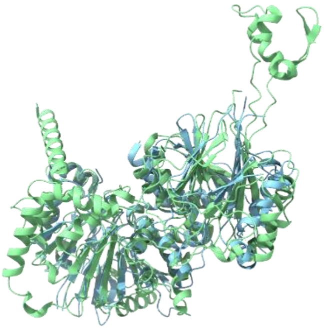
**Experimental Data Snapshot**

**Method:** ELECTRON MICROSCOPY
**Resolution:** 2.79 Å
**Aggregation State:** PARTICLE
**Reconstruction Method:** SINGLE PARTICLE

**wwPDB Validation**

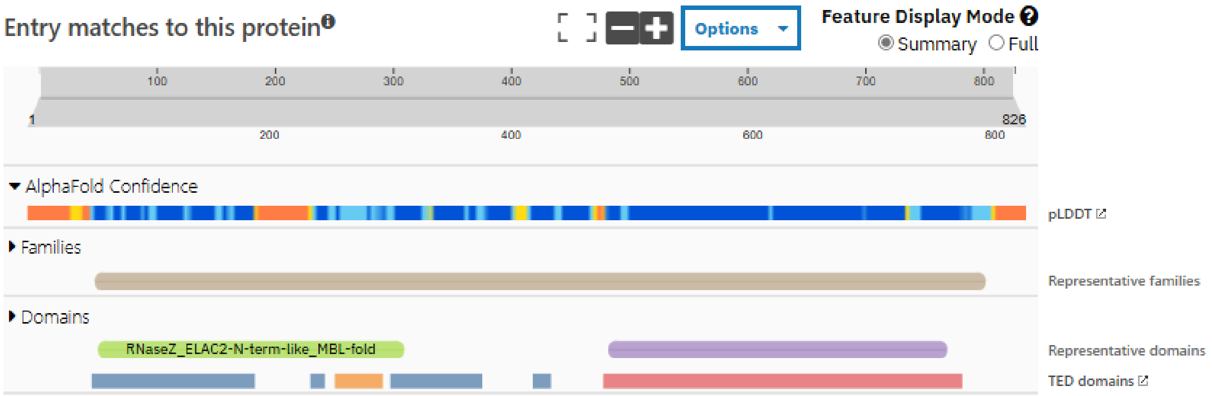
## 4.3

(Vir:



https://pmc.ncbi.nlm.nih.gov/articles/PMC7067598/)

5.1



ELAC2: 249 ak

ELAC1: 353 ak

6.1