

UniProt Beta Site for protein sequences

UniProt URL

Type search query

The image shows a browser window with the UniProt website. The address bar contains 'https://www.uniprot.org'. The page header includes the UniProt logo, 'Tools ▾ SPARQL', 'Release 2022\_03 | Statistics', and icons for a printer, home, mail, and help. The main content area has a dark blue background with the text 'Find your protein' in white. Below this is a search bar with a dropdown menu set to 'UniProtKB', the text 'dUTPase E. coli', and buttons for 'Advanced | List' and 'Search'. A red arrow points from the 'Search' button to a red box labeled 'Click'. Another red arrow points from a red box labeled 'UniProt URL' to the address bar. A third red arrow points from a red box labeled 'Type search query' to the search input field. At the bottom left, there are examples: 'Examples: Insulin, APP, Human, P05067, organism\_id:9606'. A vertical 'Feedback' button is on the right side.

Click

Feedback

Advanced search

Protein Name

UniProtKB

Accession Number

- (39)
- Unreviewed (TrEMBL) (219)
- Popular organisms
  - E. coli K12 (5)
- Taxonomy
  - Filter by taxonomy
- Proteins with
  - 3D structure (5)
  - Active site (93)
  - Activity regulation (3)
  - Alternative products (isoforms) (2)
  - Beta strand (5)

BLAST Align Map IDs Cards  Table  Share ▾

 **P06968 · DUT\_ECOLI**  
Deoxyuridine 5'-triphosphate nucleotidohydrolase · **Escherichia coli (strain K12)** · EC:3.6.1.23 · **Gene:** dut (dnaS, sof) · 152 amino acids · Evidence at protein level · **Annotation score:** 5/5  
#Hydrolase #Nucleotide metabolism

**11 3D structures · 11 reviewed publications**

 **B5YWD8 · DUT\_ECO5E**  
Deoxyuridine 5'-triphosphate nucleotidohydrolase · **Escherichia coli O157:H7 (strain EC4115 / EHEC)** · EC:3.6.1.23 · **Gene:** dut · 152 amino acids · Inferred from homology · **Annotation score:** 3/5  
#Hydrolase #Nucleotide metabolism

**1 reviewed publication**

# P06968 · DUT\_ECOLI

Deoxyuridine 5'-triphosphate nucleotidohydrolase · [Escherichia coli \(strain K12\)](#) · EC:3.6.1.23 ·

**Gene:** dut (dnaS, sof) · 152 amino acids · Evidence at protein level · **Annotation score:** 5/5

[Entry](#) [Feature viewer](#) [Publications](#) [External links](#)

Protein sequence in FASTA format

[BLAST](#) [Align](#) [Download](#) [Add](#) [Add a publication](#) [Entry feedback](#)

## Function

This enzyme is involved in the synthesis of thymidine nucleotides. It cannot be induced.

## Catalytic

dUTP + H<sub>2</sub>O → dUMP + P<sub>i</sub>  
EC:3.6.1.23 (UniProt)

Source: [Rhea](#)

- Text
- FASTA (canonical)
- FASTA (canonical & isoform)
- JSON
- XML
- RDF/XML
- GFF

Function: it produces dUMP, the immediate precursor of dTMP. It also maintains intracellular concentration of dUTP so that uracil

[Publication](#) [↗](#)

[^ Hide Rhea reaction](#)

# Detailed result page

Quick links

**Function**

**Names & Taxonomy**

**Subcellular Location**

**Phenotypes & Variants**

**PTM/Processing**

**Expression**

**Interaction**

**Structure**

**Family & Domains**

**Sequence**

**Similar Proteins**

 **P06968 · DUT\_ECOLI**

Deoxyuridine 5'-triphosphate nucleotidohydrolase · [Escherichia coli \(strain K12\)](#) · EC:3.6.1.23 · **Gene:** dut (dnaS, sof) · 152 amino acids · Evidence at protein level · **Annotation score:** 5/5

[Entry](#) [Feature viewer](#) [Publications](#) [External links](#) [History](#)

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## Function<sup>i</sup>

This enzyme is involved in nucleotide metabolism: it produces dUMP, the immediate precursor of thymidine nucleotides and it decreases the intracellular concentration of dUTP so that uracil cannot be incorporated into DNA. 1 Publication

## Catalytic Activity

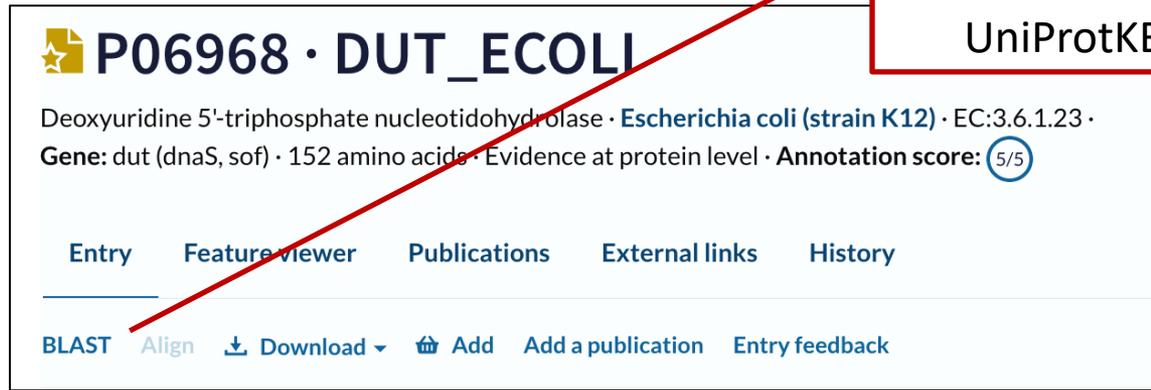
dUTP + H<sub>2</sub>O = diphosphate + dUMP + H<sup>+</sup> 1 Publication

EC:3.6.1.23 ([UniProtKB](#) | [ENZYME](#) | [Rhea](#) )

Source: [Rhea 10248](#)

[^ Hide Rhea reaction](#)

# Find related sequences using BLAST



**P06968 · DUT\_ECOLI**

Deoxyuridine 5'-triphosphate nucleotidohydrolase · **Escherichia coli (strain K12)** · EC:3.6.1.23 ·  
Gene: dut (dnaS, sof) · 152 amino acids · Evidence at protein level · Annotation score: 5/5

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Run BLASTP against this UniProtKB sequence

## BLAST

Find a protein sequence to run BLAST sequence similarity search by UniProt ID (e.g. P05067 or A4\_HUMAN or UPI0000000001).

OR

Enter one or more sequences (20 max). You may also [load from a text file](#).

```
>sp|P06968|DUT_ECOLI OS=Escherichia coli (strain K12) OX=83333 GN=dut PE=1 SV=2
MMKKIDVKIL DPRVGKEFPL PTYATSGSAG LDLRACLNDA VELAPGDTTL VPTGLAIHIA
DPSLAAMMLP RSGLGHKHGI VLGNLVGLID SDYQQLMIS VWNRGQDSFT IQPGERIAQM
IFVPVVQAEF NLVEDFDATD REGGGFGHSG RQ
```

ⓘ Your input contains 1 sequence

Target database: UniProtKB reference proteomes + Swiss-Prot

Restrict by taxonomy:

Name your BLAST job



Click

Wait patiently.....

## Tool results

Your tool analysis results from the last 🕒 7 days are listed below. If you have tools jobs running, you can navigate away to other pages and you will be notified once the job is completed.

Job type	Name	Created	Status	
BLAST	sp P06968 DUT_ECOLI	2022-08-29 09:55	Running ○ We will notify you when your results are ready	☆ 📄 🗑️
ncbiblast-R20220829-175557-0180-84296662-p1m				

## Tool results

Your tool analysis results from the last 🕒 7 days are listed below. If you have tools jobs running, you can navigate away to other pages and you will be notified once the job is completed.

Job type	Name	Created	Status	
BLAST	sp P06968 DUT_ECOLI	2022-08-29 09:55	Completed ●	☆ 📄 🗑️
ncbiblast-R20220829-175557-0180-84296662-p1m				

# Alignment results

List of related protein sequence IDs. Selected 3rd entry as an example.

Summary info for each match. % identity, bit score, e-value

**Blast parameters**

**Identity**  
71.5 100

**Score**  
603 787

**E-Value**  
3.60e-106 3.90e-78

## BLAST 250 results

Overview Taxonomy Hits API Request

BLAST Align Map IDs Download Add Resubmit

Accession	Gene	Protein	Organism	Identity	Bit Score	E-Value
<input type="checkbox"/> P06968	dut	Deoxyur...	Escheric...	100%	307.76	3.6e-106
<input type="checkbox"/> B1X974	dut	Deoxyur...	Escheric...	100%	305.834	2e-105
<input type="checkbox"/> C4ZX...	dut	Deoxyur...	Escheric...	100%	305.834	2e-105
<input type="checkbox"/> B1LK77	dut	Deoxyur...	Escheric...	99.3%	305.834	2.1e-105
<input type="checkbox"/> B6I3L7	dut	Deoxyur...	Escheric...	99.3%	305.834	2.1e-105
<input type="checkbox"/> B1IY...	dut	Deoxyur...	Escheric...	99.3%	305.834	2.1e-105
<input type="checkbox"/> Q0TB...	dut	Deoxyur...	Escheric...	99.3%	305.834	2.1e-105
<input type="checkbox"/> B5YW...	dut	Deoxyur...	Escheric...	99.3%	305.834	2.1e-105

# Getting the DNA that codes for the protein

**Function**  **C4ZXN2 · DUT\_ECOWB**

**Names & Taxonomy** Deoxyuridine 5'-triphosphate nucleotidohydrolase · *Escherichia coli* (strain K12 / MC4100 / BW2952) · EC:3.6.1.23 · **Gene:** dut · 151 amino acids · Inferred from homology · **Annotation score:** 3/5

**Subcellular Location**

**Phenotypes & Variants** [Entry](#) [Feature viewer](#) [Publications](#) [External links](#) [History](#)

**PTM/Processing**

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**Similar Proteins**

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### Function<sup>i</sup>

This enzyme is involved in nucleotide metabolism: it produces dUMP, the immediate precursor of thymid nucleotides and it decreases the intracellular concentration of dUTP so that uracil cannot be incorporated into DNA. 1 Automatic Annotation

### Catalytic Activity

dUTP + H<sub>2</sub>O = diphosphate + dUMP + H<sup>+</sup> 1 Automatic Annotation

EC:3.6.1.23 ([UniProtKB](#) | [ENZYME](#) | [Rhea](#) )



This link gets you an ENTIRE genome of *E. coli*. In this file is the DNA coding for this protein. The file takes time to download.

## Sequence databases

RefSeq | [WP\\_001393518.1](#) [NC\\_012759.1](#)

SEQUENCE

PROTEIN

CP001396 ([EMBL](#) | [GenBank](#) | [DDBJ](#) )

ACR62746.1 ([EMBL](#) | [GenBank](#) | [DDBJ](#) )