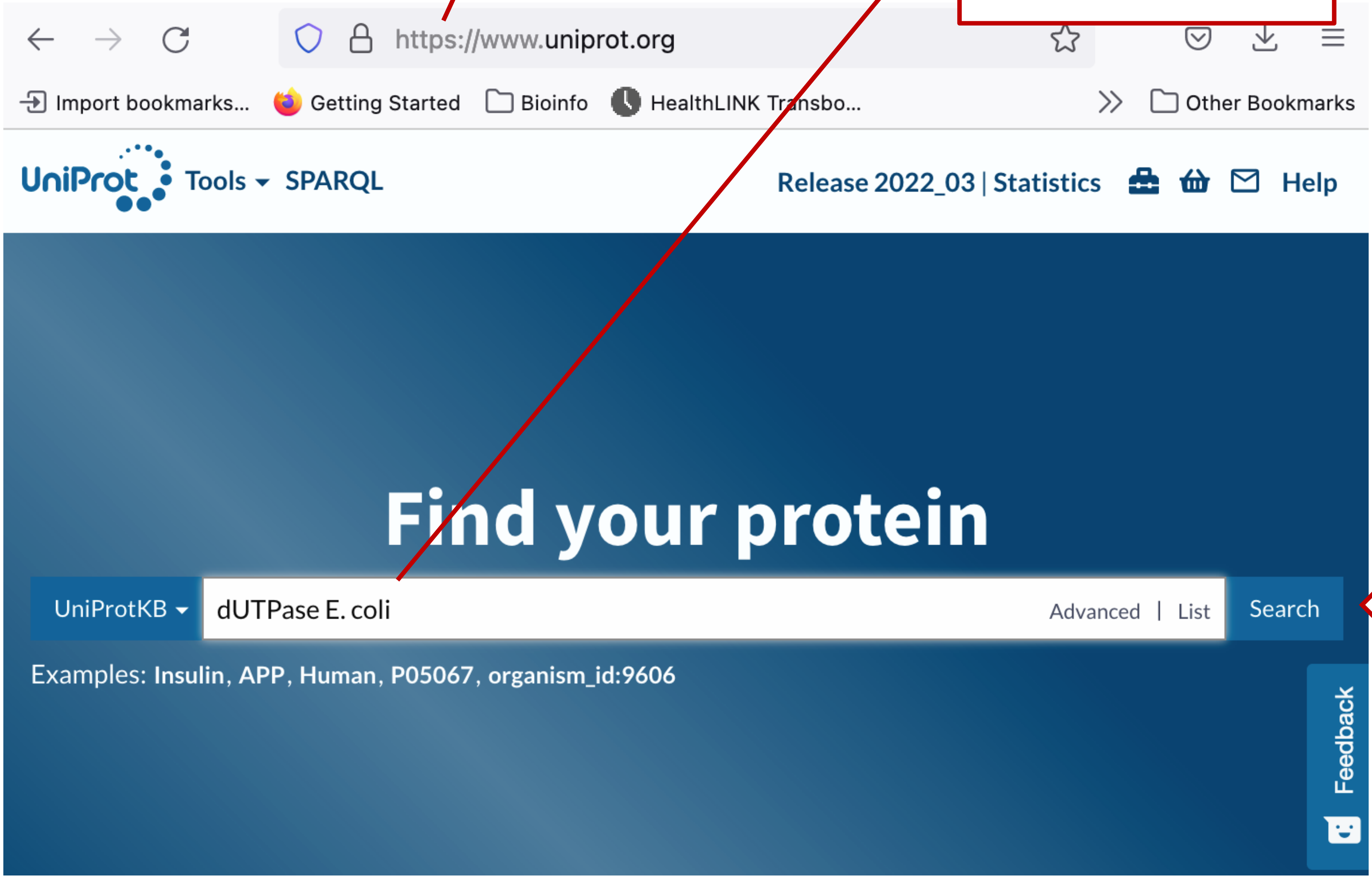
UniProt Beta Site for protein sequences

UniProt URL

Type search query

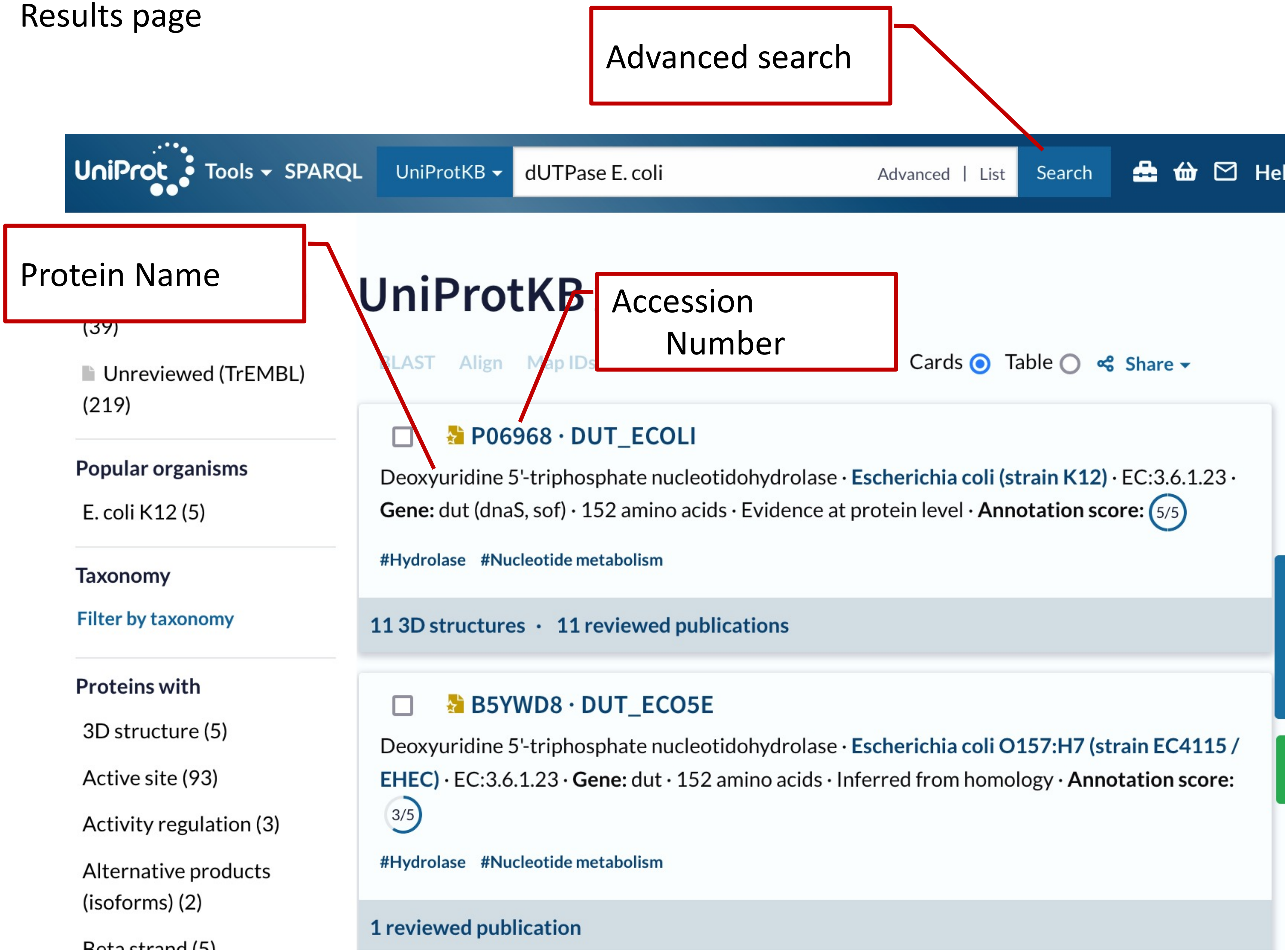


https://www.uniprot.org

dUTPase E. coli

Click

Results page



Advanced search

Protein Name

Accession Number

dUTPase E. coli

UniProtKB

(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)

☐ **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

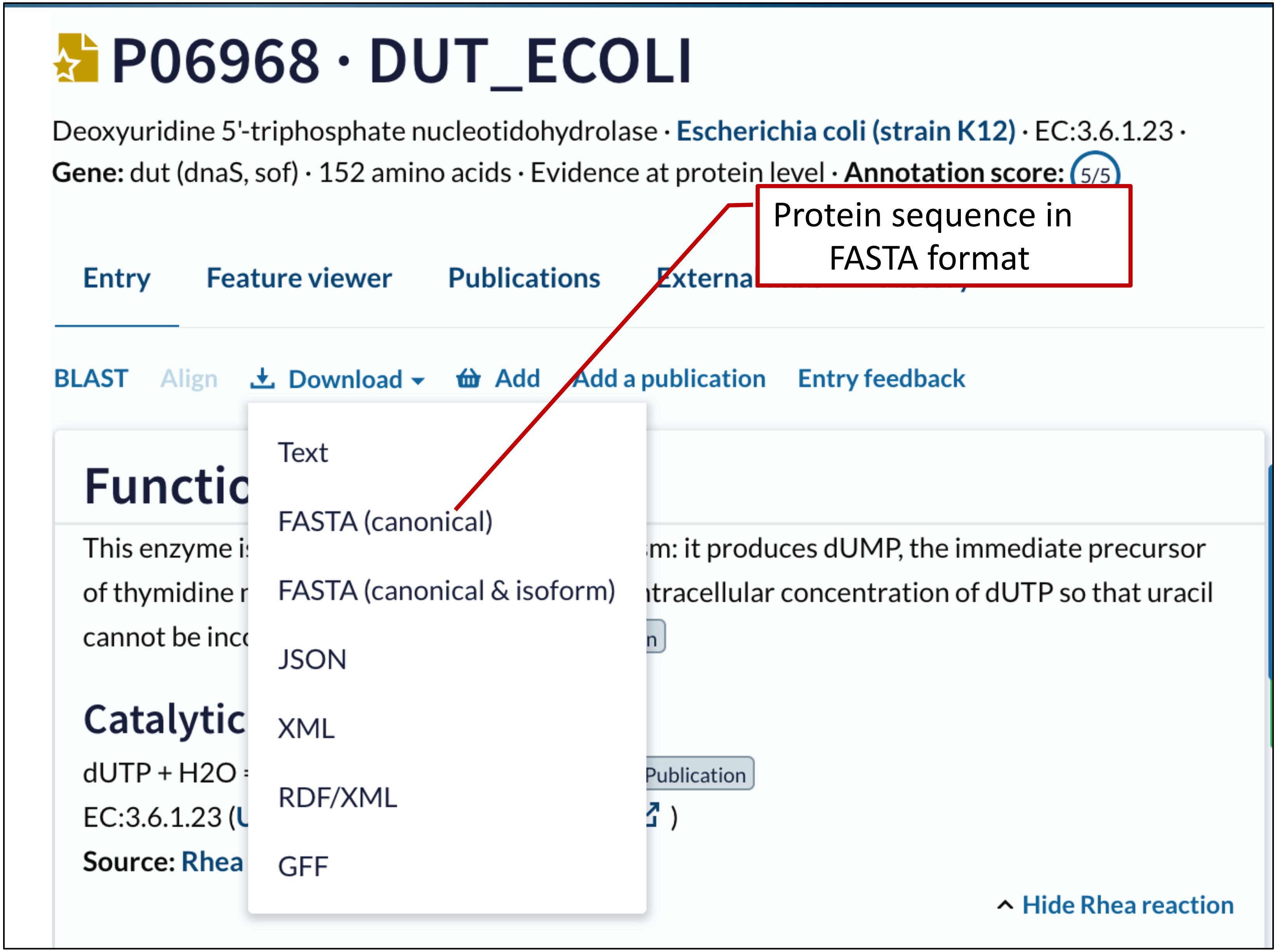
☐ **B5YWD8 · DUT_ECO5E**

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

Results page



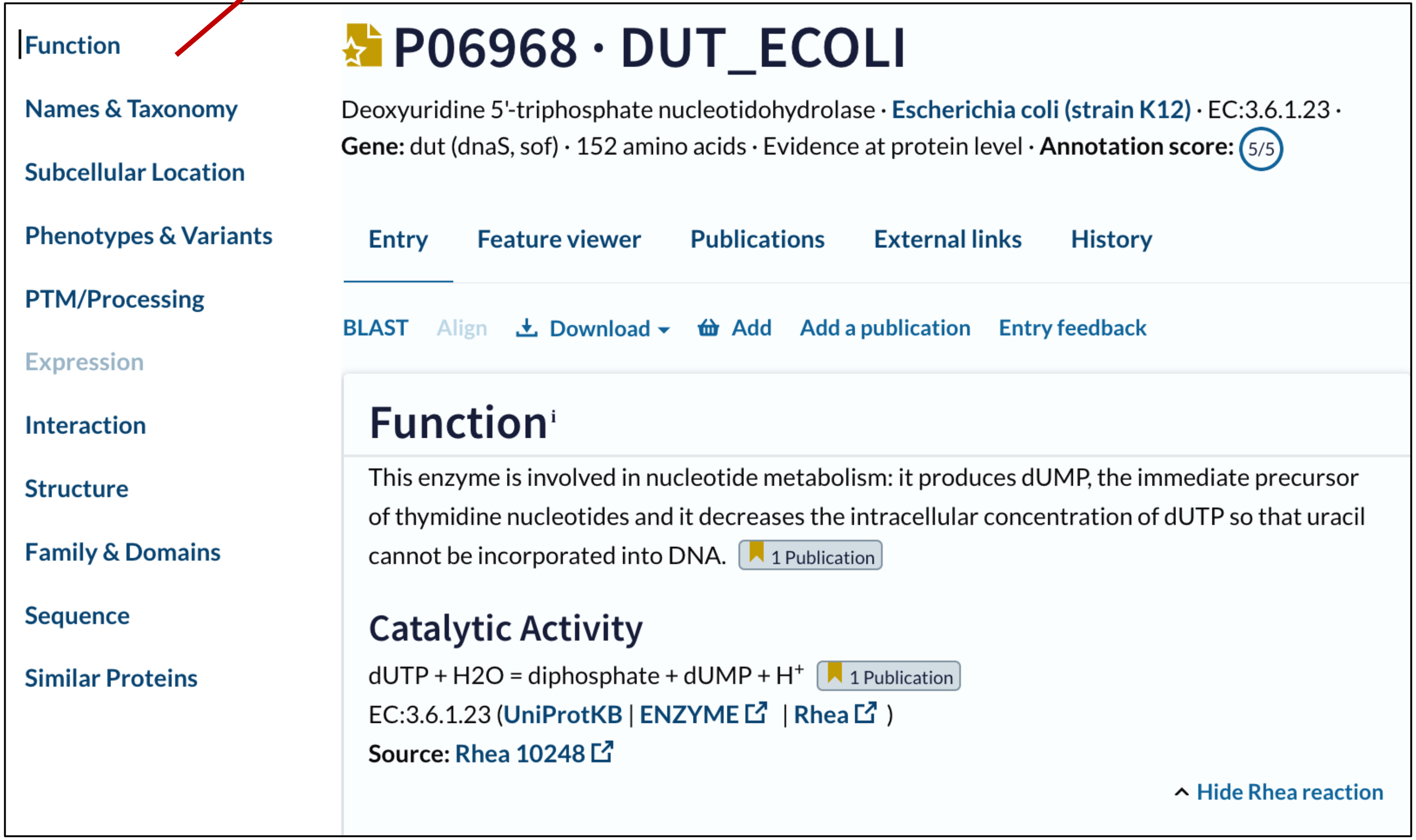
P06968 · DUT_ECOLI

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

Protein sequence in FASTA format

Detailed result page

Quick links



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

Function

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

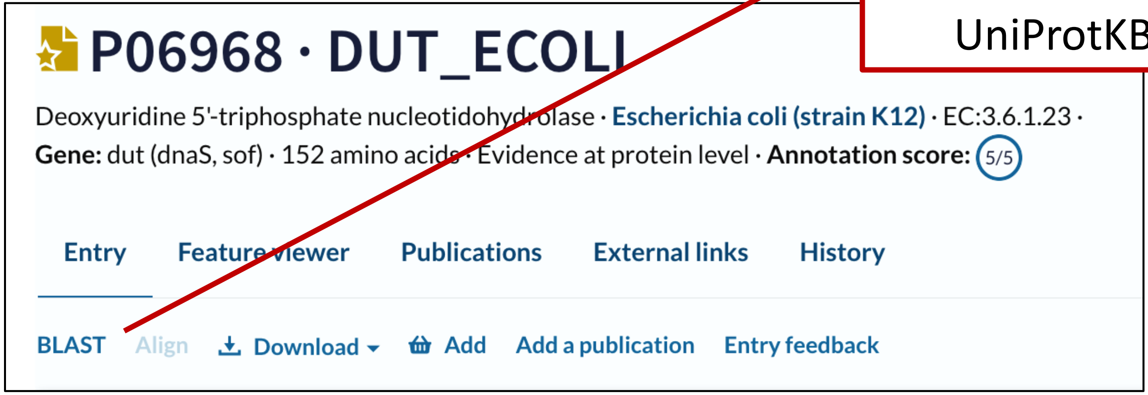
dUTP + H2O = diphosphate + dUMP + H^+ 1 Publication

EC:3.6.1.23 (UniProtKB | ENZYME | Rhea)

Source: Rhea 10248

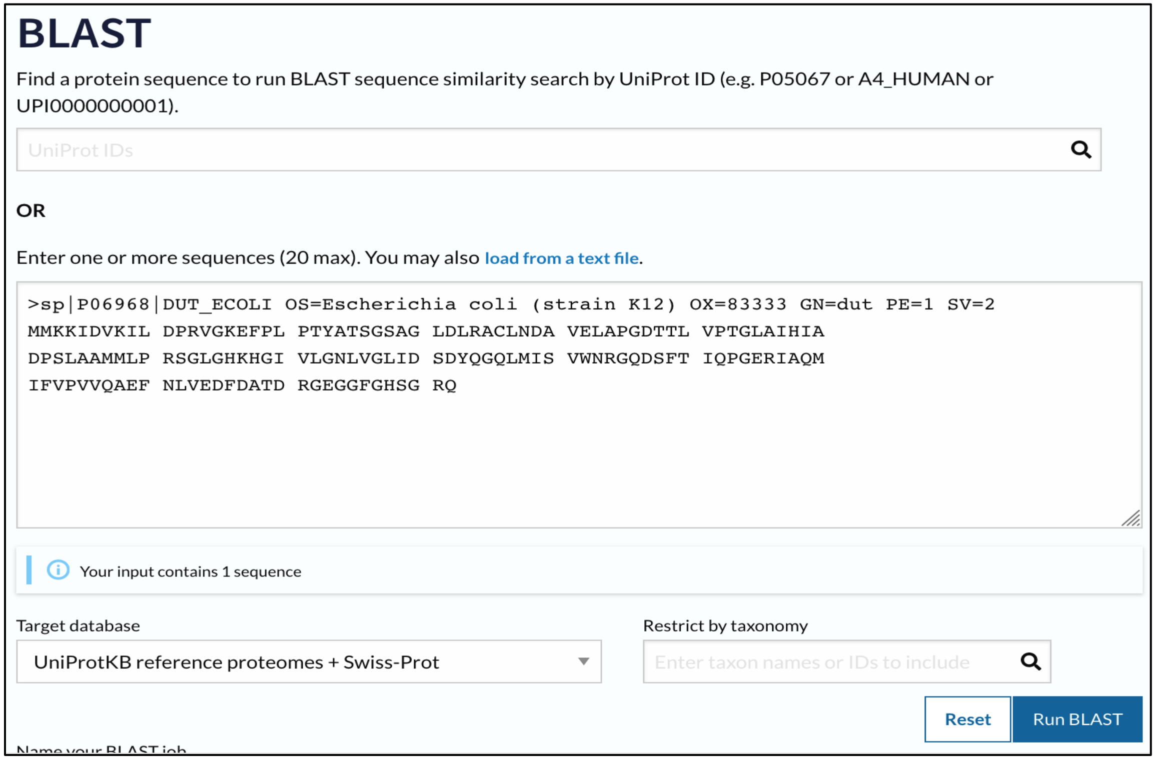
Find related sequences using BLAST

Run BLASTP against this UniProtKB sequence



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



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 SDYQGQLMIS VWNRGQDSFT IQPGERIAQM
IFVPVVQAEF NLVEDFDATD RGEGGFGHSG RQ
```

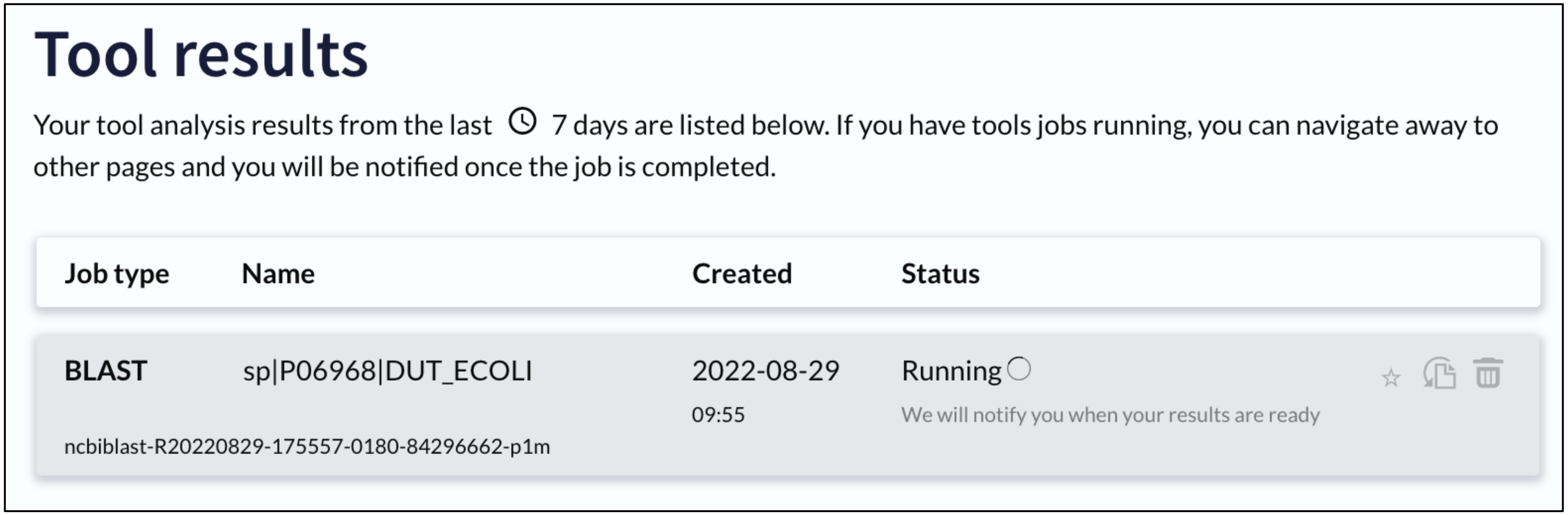
Your input contains 1 sequence

Target database: UniProtKB reference proteomes + Swiss-Prot

Restrict by taxonomy

Click

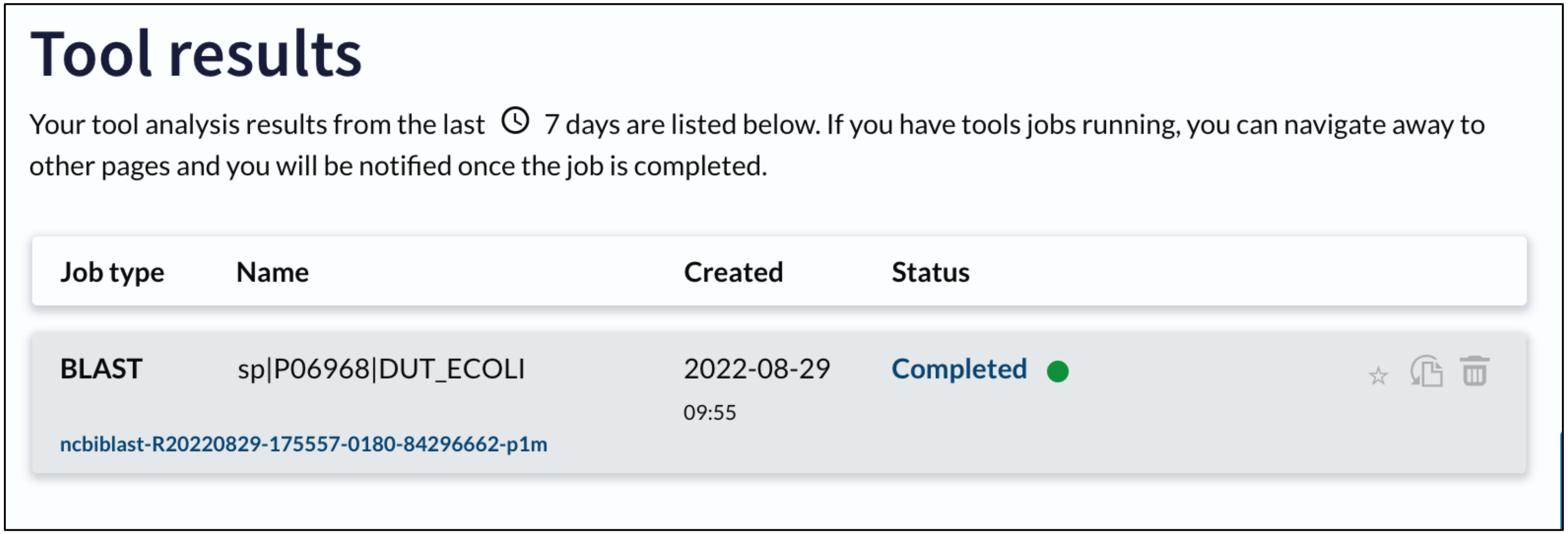
Wait patiently.....



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 ncbiblast-R20220829-175557-0180-84296662-p1m	sp|P06968|DUT_ECOLI	2022-08-29 09:55	Running ○ We will notify you when your results are ready



Tool results

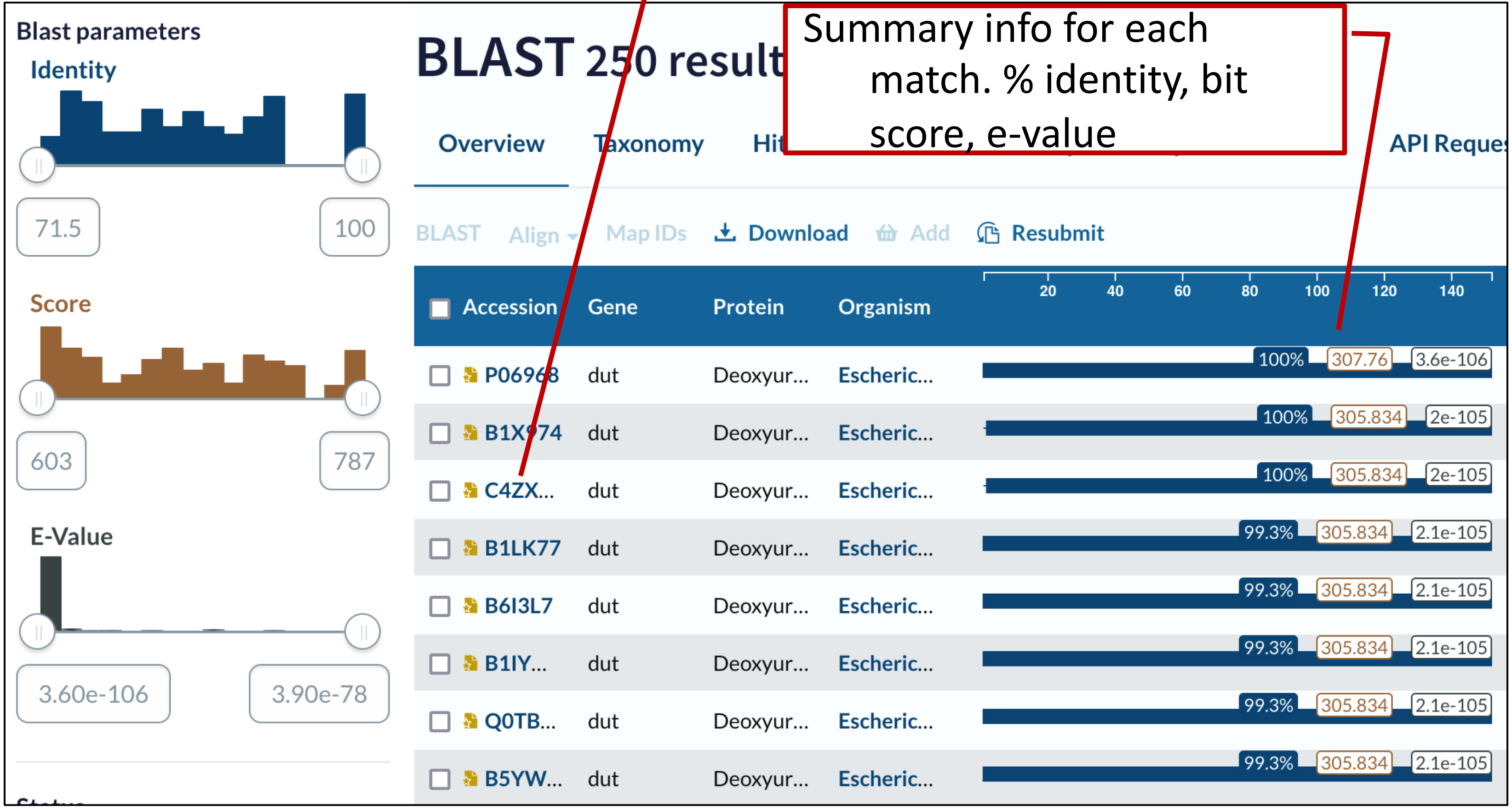
Your tool analysis results from the last 7 days are listed below. If you have tools jobs running, you can navigate away to other pages and you will be notified once the job is completed.

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

Alignment results

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

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



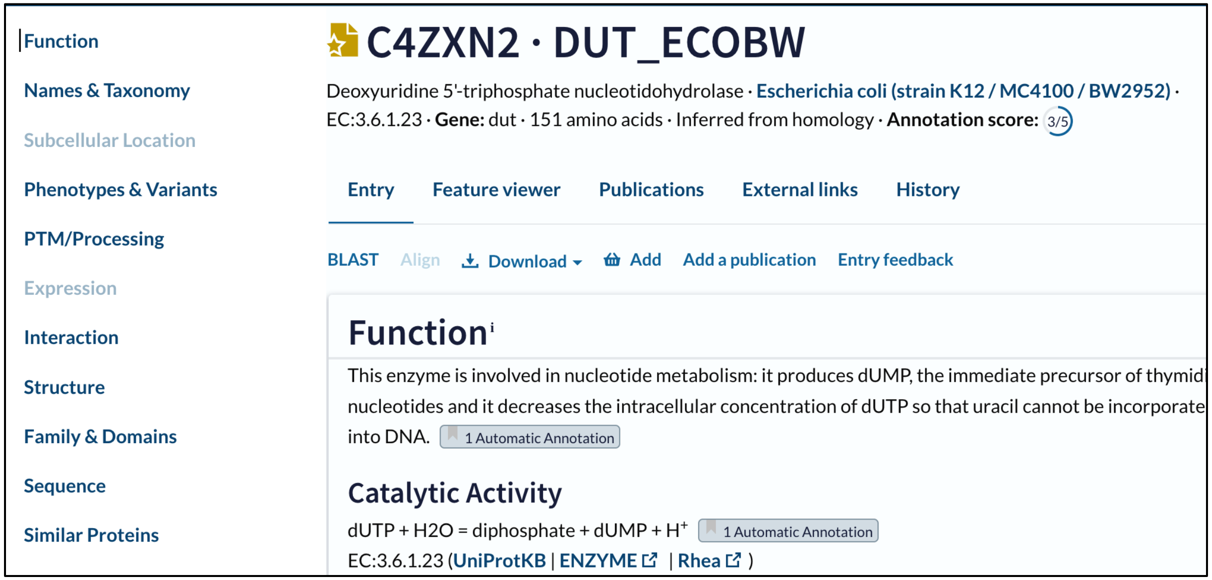
Identity: 71.5 – 100

Score: 603 – 787

E-Value: 3.60e-106 – 3.90e-78

☐ Accession	Gene	Protein	Organism	20 40 60 80 100 120 140
☐ P06968	dut	Deoxyur...	Escheric...	100% 307.76 3.6e-106
☐ B1X974	dut	Deoxyur...	Escheric...	100% 305.834 2e-105
☐ C4ZX...	dut	Deoxyur...	Escheric...	100% 305.834 2e-105
☐ B1LK77	dut	Deoxyur...	Escheric...	99.3% 305.834 2.1e-105
☐ B6I3L7	dut	Deoxyur...	Escheric...	99.3% 305.834 2.1e-105
☐ B1IY...	dut	Deoxyur...	Escheric...	99.3% 305.834 2.1e-105
☐ Q0TB...	dut	Deoxyur...	Escheric...	99.3% 305.834 2.1e-105
☐ B5YW...	dut	Deoxyur...	Escheric...	99.3% 305.834 2.1e-105

Getting the DNA that codes for the protein



Function

Names & Taxonomy

Subcellular Location

Phenotypes & Variants

PTM/Processing

Expression

Interaction

Structure

Family & Domains

Sequence

Similar Proteins

C4ZXN2 · DUT_ECOBW

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

Function

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 incorporate into DNA. 1 Automatic Annotation

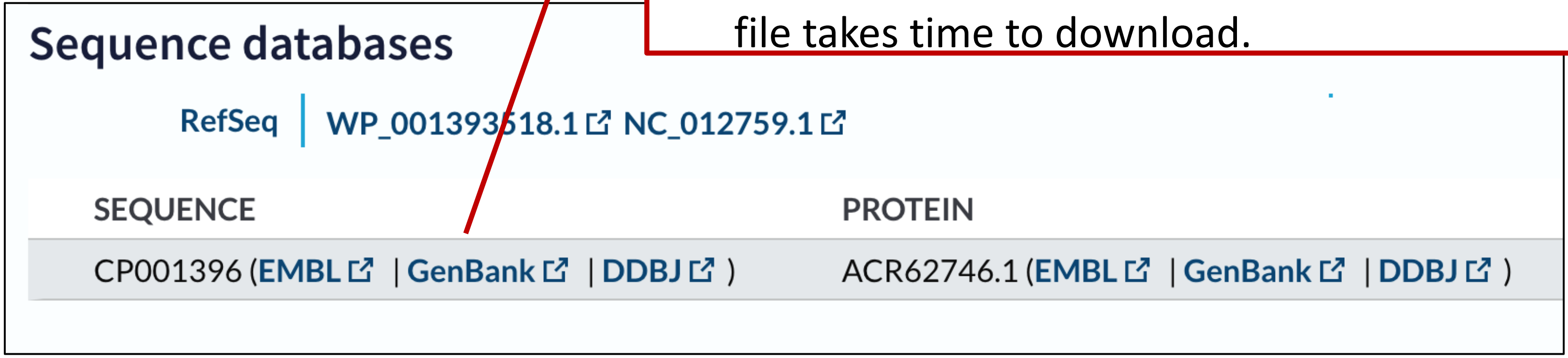
Catalytic Activity

dUTP + H2O = diphosphate + dUMP + H^+ 1 Automatic Annotation

EC:3.6.1.23 (UniProtKB | ENZYME | Rhea)

Click

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)