

# Trouvez une Protéine par son Nom

Par Joel Sandé

# Prenom la protéine dUTPase

Allez sur <https://www.ncbi.nlm.nih.gov/pubmed>

Vous pouvez  
cliquer sur le lien  
pour voir  
l'article

Si ça vous tente,  
vous pouvez cliquer  
sur Download pour  
faire une analyse de  
données des  
publications sur le  
sujet

The screenshot shows the PubMed search results for the query 'dUTPase'. The search bar at the top contains 'dUTPase' and the 'Search' button is visible. Below the search bar, there are links for 'Create RSS', 'Create alert', and 'Advanced'. The results are displayed in a list format, with the first three results visible. The first result is titled 'The Stl repressor from Staphylococcus aureus is an efficient inhibitor of the eukaryotic fruitfly dUTPase' and includes the authors 'Benedek A, Póloskei I, Ozohanics O, Vékey K, Vértessy BG.' and the journal 'FEBS Open Bio. 2017 Dec 27;8(2):158-167. doi: 10.1002/2211-5463.12302. eCollection 2018 Feb. PMID: 29435406 Free PMC Article'. The second result is titled 'Inhibition of Dr-dut gene causes DNA damage in planarian' and includes the authors 'Atam MS, Moriyama H, Matsumoto M.' and the journal 'Mol Reprod Dev. 2018 Feb 5. doi: 10.1002/mrd.22952. [Epub ahead of print] PMID: 29405473'. The third result is titled 'The dUTPase of white spot syndrome virus assembles its active sites in a noncanonical manner' and includes the authors 'Zang K, Li F, Ma Q.' and the journal 'J Biol Chem. 2018 Jan 19;293(3):1088-1099. doi: 10.1074/jbc.M117.815266. Epub 2017 Nov 29. PMID: 29187596'. On the right side of the page, there is a 'Results by year' bar chart, a 'Download CSV' button, and a 'Related searches' section with the query 'abergel dutpase'. At the bottom right, there is a 'PMC Images search for dUTPase' section showing several thumbnail images of scientific figures.

How to Sign in to NCBI

PubMed

Create RSS Create alert Advanced Help

Format: Summary Sort by: Most Recent Per page: 20 Send to Filters: [Manage Filters](#)

Sort by:

Results by year

Download CSV

Related searches  
abergel dutpase

PMC Images search for dUTPase

See 23 articles about [dUTPase gene function](#)  
See also: [dUTPase Deoxyuridine triphosphatase in the Gene database](#)  
[dUTPase in Drosophila melanogaster](#) [Mamestra configurata nucleopolyhedrovirus B](#) [Dickeya phage Limestone](#) [All 11 Gene records](#)

**Search results**  
Items: 1 to 20 of 547

<< First < Prev Page 1 of 28 Next > Last >>

1. [The Stl repressor from Staphylococcus aureus is an efficient inhibitor of the eukaryotic fruitfly dUTPase.](#)  
Benedek A, Póloskei I, Ozohanics O, Vékey K, Vértessy BG.  
FEBS Open Bio. 2017 Dec 27;8(2):158-167. doi: 10.1002/2211-5463.12302. eCollection 2018 Feb.  
PMID: 29435406 [Free PMC Article](#)  
[Similar articles](#)

2. [Inhibition of Dr-dut gene causes DNA damage in planarian.](#)  
Atam MS, Moriyama H, Matsumoto M.  
Mol Reprod Dev. 2018 Feb 5. doi: 10.1002/mrd.22952. [Epub ahead of print]  
PMID: 29405473  
[Similar articles](#)

3. [The dUTPase of white spot syndrome virus assembles its active sites in a noncanonical manner.](#)  
Zang K, Li F, Ma Q.  
J Biol Chem. 2018 Jan 19;293(3):1088-1099. doi: 10.1074/jbc.M117.815266. Epub 2017 Nov 29.  
PMID: 29187596

# Protéine dUTPase

Vous pouvez le sauver dans le format que vous désirez.

J'aime bien les formats .csv et .xml parce qu'ils sont très pratiques pour le traitement Python (.csv) ou PHP (.xml).

NCBI Resources How To Sign in to NCBI

PubMed.gov PubMed dUTPase Search

Create RSS Create alert Advanced Help

Article types  
Clinical Trial  
Review  
Customize ...

Text availability  
Abstract  
Free full text  
Full text

Publication dates  
5 years  
10 years  
Custom range...

Species  
Humans  
Other Animals

Clear all  
Show additional filters

Format: Summary Sort by: Most Recent Per page: 20

See 23 articles about **dUTPase** gene function  
See also: **dUTPase** Deoxyuridine triphosphatase in the Gene database  
**dutpase** in *Drosophila melanogaster* *Mamestra configurata* *nucleopolyhe-*  
*Limestone* *All 11 Gene records*

**Search results**  
Items: 1 to 20 of 547 Selected: 1

1. ☒ [The \*Sti\* repressor from \*Staphylococcus aureus\* is an efficient \*\*dUTPase\*\*.](#)  
Benedek A, Polóskai I, Ozohanics O, Vékey K, Vértessy BG.  
FEBS Open Bio. 2017 Dec 27;8(2):158-167. doi: 10.1002/2211-5463.12302. eCollection 2017.  
PMID: 29435406 Free PMC Article  
[Similar articles](#)

2. ☐ [Inhibition of Dr-dut gene causes DNA damage in planarian.](#)  
Alam MS, Moriyama H, Matsumoto M.  
Mol Reprod Dev. 2018 Feb 5. doi: 10.1002/mrd.22952. [Epub ahead of print]  
PMID: 29405473  
[Similar articles](#)

3. ☐ [The \*\*dUTPase\*\* of white spot syndrome virus assembles its active sites in a noncanonical manner.](#)  
Zang K, Li F, Ma Q.  
J Biol Chem. 2018 Jan 19;293(3):1088-1099. doi: 10.1074/jbc.M117.815266. Epub 2017 Nov 29.  
PMID: 29187596  
[Similar articles](#)

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Summary (text)  
Abstract (text)  
MEDLINE  
XML  
PMID List  
CSV

Related searches  
abergel dutpase

PMC Images search for dUTPase

# Protéine dUTPase

Vous pouvez aller aussi sur <https://www.expasy.org/>  
et insérer le nom de notre protéine.  
La chercher par exemple en rapport avec la Bactérie Ecoli.

The screenshot shows the ExPASy Bioinformatics Resource Portal search results for the query 'dUTPase ecoli'. The search bar at the top contains the query, and a blue circle highlights it. Below the search bar, a message indicates 'Detected query type: text'. The results are displayed in a table with columns: Resource, Hits, Category, and Comment. The table lists various databases and their corresponding hit counts. A blue circle highlights the 'UniProtKB' entry, which shows 7 hits. A blue arrow points from the text box on the right to the UniProtKB entry. The text box on the right contains the text: 'Allons par exemple sur la célèbre base de données UniProt'.

Resource	Hits	Category	Comment
EPD	0 hits	ge	0 promoters found in EPDnew that match 'dUTPase ecoli'
neXtProt	0 hits	pr	Entries matching the query dUTPase ecoli in neXtProt
OMA	1 hit	ev, ge	
OrthoDB	0 hits	ev, ge	
PROSITE	0 hits	pr	PROSITE documentation entries
STRING	0 hits	pr	
SWISS-MODEL Repository	0 hits	bi, pr, st	
UniProtKB	7 hits	pr	UniProtKB entries
ViratZone	0 hits	pr	No valid response from server.
Cellosaurus	0 hits	sy	cell lines
ENZYME	0 hits	pr	ENZYME entries
HAMAP	0 hits	pr	HAMAP annotation rules
MetaNetX	0 hits	pr, sy	
miROrtho	0 hits	ev, ge	orthologous group(s) returned by your request
MyHits	0 hits	pr	Protein found: 0; Motif found: 0; Other node found: 0;
OpenFlu	0 hits	ge	
Selectome	0 hits	ev	
SWISS-2DPAGE	1 hit	pr	SWISS-2DPAGE entries
SwissLipids	0 hits	pr, sy	SwissLipids entries

Timeline: timeline.csv | pubmed\_result.csv | pubmed\_result.txt | Tout afficher

# Informations sur la Protéine dUTPase

UniProtKB results

Filter by:

- Reviewed (5) Swiss-Prot
- Unreviewed (2) TrEMBL

Popular organisms

- E. coli K12 (5)
- Escherichia coli O25b:H4-ST131 (2)

Search terms

Filter "ecoli" as:

- organism (5)
- taxonomy (5)

Filter "dutpase" as:

- protein and gene name (2)

UniProtKB results

1 to 7 of 7 Show 25

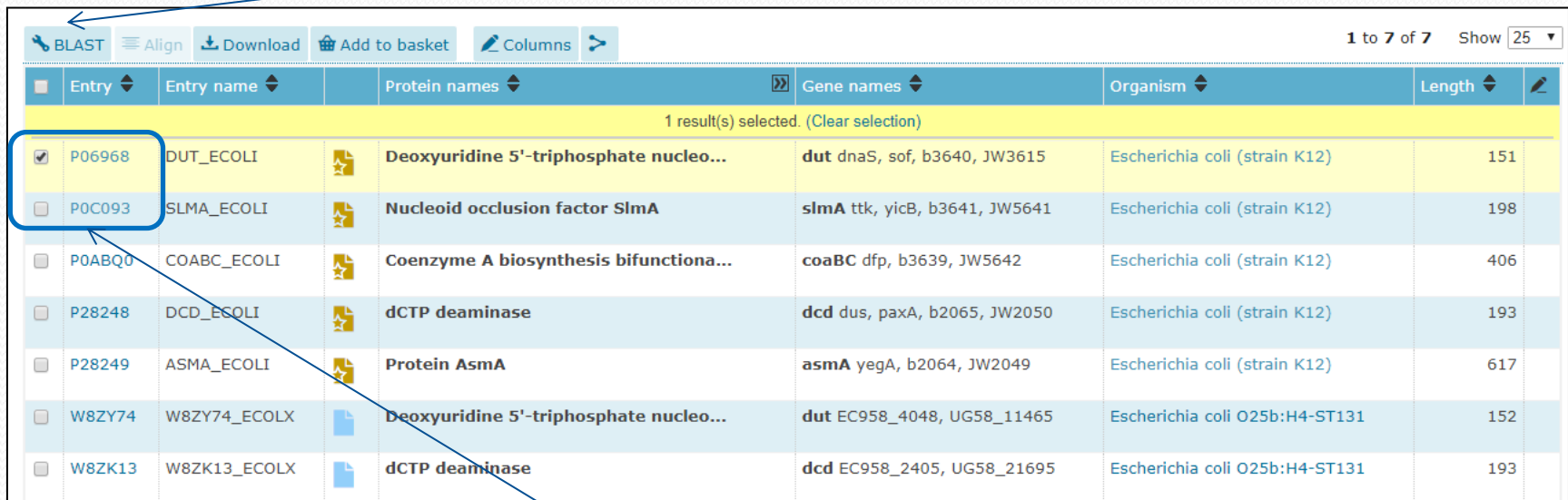
Entry	Entry name	Protein names	Gene names	Organism	Length
P06968	DUT_ECOLI	Deoxyuridine 5'-triphosphate nucleo...	dut dnaS, sof, b3640, JW3615	Escherichia coli (strain K12)	151
P0C093	SLMA_ECOLI	Nucleoid occlusion factor SlmA	slmA ttk, yicB, b3641, JW5641	Escherichia coli (strain K12)	198
P0ABQ0	COABC_ECOLI	Coenzyme A biosynthesis bifunctiona...	coaBC dfp, b3639, JW5642	Escherichia coli (strain K12)	406
P28248	DCD_ECOLI	dCTP deaminase	dcd dus, paxA, b2065, JW2050	Escherichia coli (strain K12)	193
P28249	ASMA_ECOLI	Protein AsmA	asmA yegA, b2064, JW2049	Escherichia coli (strain K12)	617
W8ZY74	W8ZY74_ECOLX	Deoxyuridine 5'-triphosphate nucleo...	dut EC958_4048, UG58_11465	Escherichia coli O25b:H4-ST131	152
W8ZK13	W8ZK13_ECOLX	dCTP deaminase	dcd EC958_2405, UG58_21695	Escherichia coli O25b:H4-ST131	193

1 to 7 of 7 Show 25

Vous avez accès à toutes les informations désirées sur votre Protéine

# Informations sur la Protéine dUTPase

Vous le Sélectionnez la protéine et la Blaster pour voir ces homologues de séquence.



1 result(s) selected. (Clear selection)

Entry	Entry name	Protein names	Gene names	Organism	Length
<input checked="" type="checkbox"/> P06968	DUT_ECOLI	Deoxyuridine 5'-triphosphate nucleo...	dut dnaS, sof, b3640, JW3615	Escherichia coli (strain K12)	151
<input type="checkbox"/> P0C093	SLMA_ECOLI	Nucleoid occlusion factor SlmA	slmA ttk, yicB, b3641, JW5641	Escherichia coli (strain K12)	198
<input type="checkbox"/> P0ABQ0	COABC_ECOLI	Coenzyme A biosynthesis bifunctiona...	coaBC dfp, b3639, JW5642	Escherichia coli (strain K12)	406
<input type="checkbox"/> P28248	DCD_ECOLI	dCTP deaminase	dcd dus, paxA, b2065, JW2050	Escherichia coli (strain K12)	193
<input type="checkbox"/> P28249	ASMA_ECOLI	Protein AsmA	asma yegA, b2064, JW2049	Escherichia coli (strain K12)	617
<input type="checkbox"/> W8ZY74	W8ZY74_ECOLX	Deoxyuridine 5'-triphosphate nucleo...	dut EC958_4048, UG58_11465	Escherichia coli O25b:H4-ST131	152
<input type="checkbox"/> W8ZK13	W8ZK13_ECOLX	dCTP deaminase	dcd EC958_2405, UG58_21695	Escherichia coli O25b:H4-ST131	193

Sélectionnez-en au moins 2 pour les aligner. Vous verrez des fichiers au format Fasta qui ont été générés pour faire cet alignement.

# Format Fasta

BLAST Align Retrieve/ID mapping Peptide search

## UniProtKB - P06968 (DUT\_ECOLI)

Display

- Entry
- Publications
- Feature viewer
- Feature table

Function

Names & Taxonomy

Subcellular location

Pathology & Biotech

PTM / Processing

Expression

Interaction

Structure

Family & Domains

BLAST Align **Format** Add to basket History

View this entry in a different format

**Protein** Deoxyuridine 5'-triphosphate nucleotidohydrolase

**Gene** dut

**Organism** *Escherichia coli* (strain K12)

**Status** Reviewed - Annotation score: ●●●●●● - Experimental evidence at protein level<sup>i</sup>

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

This enzyme is involved in nucleotide metabolism: it produces dUMP, the immediate precursor of thymidine nucleotide, which cannot be incorporated into DNA.

**Catalytic activity<sup>i</sup>**

dUTP + H<sub>2</sub>O = dUMP + diphosphate.

**Cofactor<sup>i</sup>**

Mg<sup>2+</sup> 1 Publication ▼

**Pathway<sup>i</sup>: dUMP biosynthesis**

This protein is involved in step 2 of the subpathway that synthesizes dUMP from dCTP (dUTP route). Proteins known to be involved in the 2 steps of the subpathway in this organism are:

step 1. dCTP deaminase (**dcd**)

<https://www.uniprot.org/uniprot/P06968>

Cliquez sur P06968 et sur et cherchez le format Fasta

# Alignement de Séquences Protéiques

[https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Proteins&PROGRAM=blastp&BLAST\\_PROGRAMS=blastp&PAGE\\_TYPE=BlastSearch&DBSEARCH=true&QUERY=&SUBJECTS=](https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Proteins&PROGRAM=blastp&BLAST_PROGRAMS=blastp&PAGE_TYPE=BlastSearch&DBSEARCH=true&QUERY=&SUBJECTS=)

Copier-coller  
ou  
importer votre  
fichier Fasta

**BLAST** » blastp suite

Standard Protein BLAST

blastn blastp blastx tblastn tblastx

Enter Query Sequence

BLASTP programs search protein databases using a protein query sequence.

Enter accession number(s), gi(s), or FASTA sequence(s)

>sp|P06968|DUT\_ECOLI Deoxyuridine 5'-triphosphate nucleotidohydrolase  
OS=Escherichia coli (strain K12) OX=83333 GN=dut PE=1 SV=1  
MKKIDVKTLDPRVGKEFLPTVATSGSAGLDLRACLNDAVELAPGDTTLVPTGLAIHID  
PSLAAMMLPRSGLGKHGIVLGNLVGLIDSDVQGLMISVWNRGQDSFTIQGERTIAQMI  
EVPVQAEFNILVEDFDATDREGGEGGHSGRQ

Clear

Query subrange

From

To

Or, upload file

Choisir un fichier

Aucun fichier choisi

Job Title

sp|P06968|DUT\_ECOLI Deoxyuridine 5'-triphosphate...

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Database

Non-redundant protein sequences (nr)

Organism

Optional

Exclude

Optional

Entrez Query

Optional

Exclude

Optional

Models (XM/XP)

Uncultured/environmental sample sequences

You Tube

Create custom database

Enter an Entrez query to limit search

Program Selection

Algorithm

☐ Quick BLASTP (Accelerated protein-protein BLAST) **New**

☒ blastp (protein-protein BLAST)

☐ PSI-BLAST (Position-Specific Iterated BLAST)

☐ PHI-BLAST (Pattern Hit Initiated BLAST)

☐ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm

**BLAST**

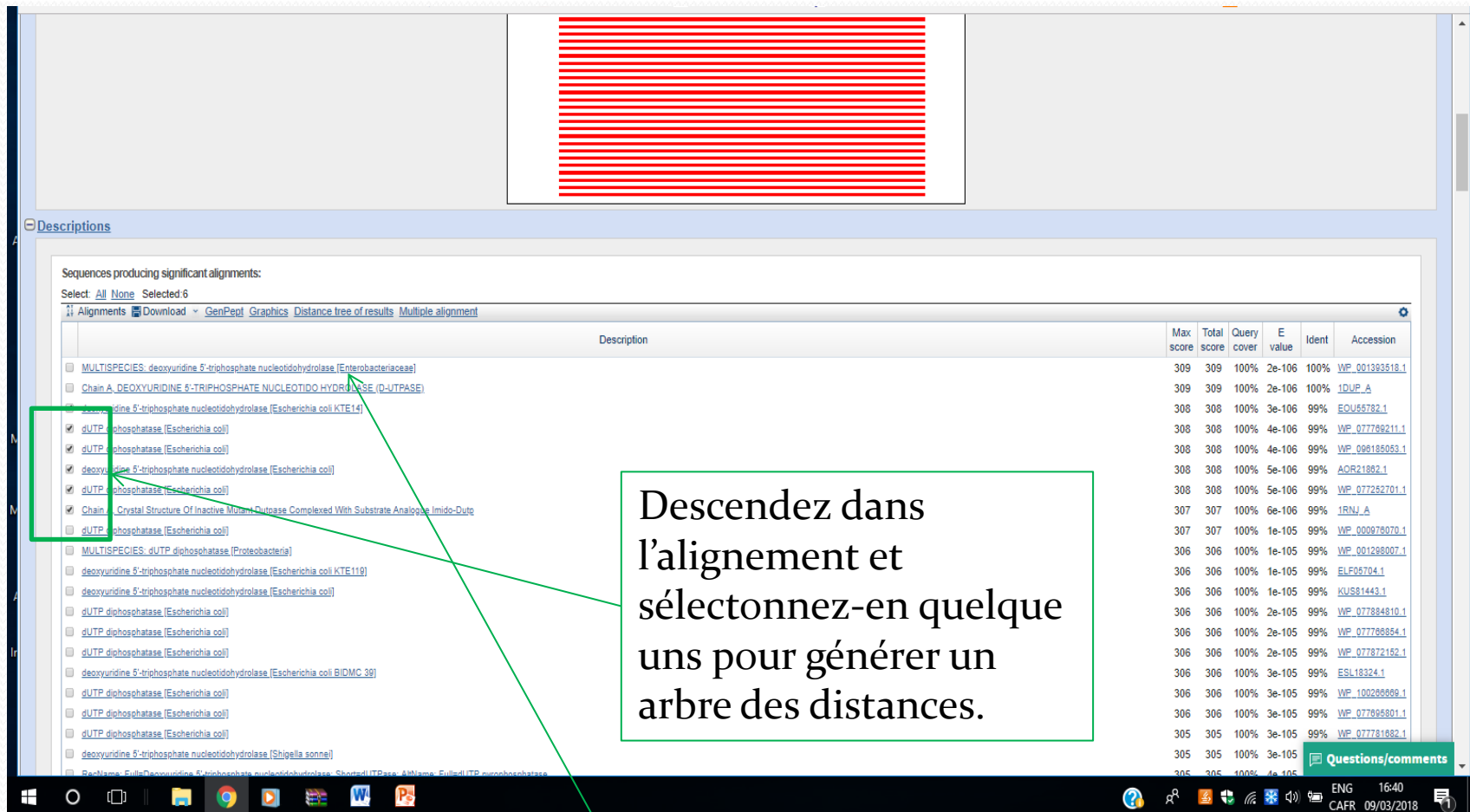
Search database Non-redundant protein sequences (nr) using Blastp (protein-protein BLAST)

☒ Show results in a new window



# Alignement de séquences

## Protéiques



The screenshot shows a bioinformatics alignment tool interface. At the top, there is a header with a red and white striped pattern. Below the header, there is a section titled "Descriptions" with a sub-header "Sequences producing significant alignments:". Under this, there is a "Select:" dropdown menu with "All" and "None" options, and a "Selected: 6" indicator. Below the selection options, there are tabs for "Alignments", "Download", "GenPept", "Graphics", "Distance tree of results", and "Multiple alignment". The "Alignments" tab is active, showing a list of sequences with checkboxes. A green box highlights the first six sequences in the list. To the right of the list is a table with columns: "Description", "Max score", "Total score", "Query cover", "E value", "Ident", and "Accession". The table contains 24 rows of data. A green box highlights the first six rows of the table. A green arrow points from the text "Descendez dans l'alignement et sélectionnez-en quelque uns pour générer un arbre des distances." to the green box highlighting the first six sequences in the list. Another green arrow points from the text "Clicker ensuite sur Distance Tree" to the "Distance tree of results" tab.

Descriptions

Sequences producing significant alignments:

Select: **All** None Selected: 6

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> MULTISPECIES: deoxyuridine 5'-triphosphate nucleotidohydrolase [Enterobacteriaceae]	309	309	100%	2e-106	100%	<a href="#">WP_001383518.1</a>
<input type="checkbox"/> Chain A: DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDO HYDROLASE (D-UTPASE)	309	309	100%	2e-106	100%	<a href="#">1DUP_A</a>
<input type="checkbox"/> deoxyuridine 5'-triphosphate nucleotidohydrolase [Escherichia coli KTE14]	308	308	100%	3e-106	99%	<a href="#">EQU55782.1</a>
<input checked="" type="checkbox"/> dUTP_diphosphatase [Escherichia coli]	308	308	100%	4e-106	99%	<a href="#">WP_077769211.1</a>
<input checked="" type="checkbox"/> dUTP_diphosphatase [Escherichia coli]	308	308	100%	4e-106	99%	<a href="#">WP_098185053.1</a>
<input checked="" type="checkbox"/> deoxyuridine 5'-triphosphate nucleotidohydrolase [Escherichia coli]	308	308	100%	5e-106	99%	<a href="#">AQR21862.1</a>
<input checked="" type="checkbox"/> dUTP_diphosphatase [Escherichia coli]	308	308	100%	5e-106	99%	<a href="#">WP_077252701.1</a>
<input checked="" type="checkbox"/> Chain: Crystal Structure Of Inactive Muramidase Complexed With Substrate Analogue Imido-Dutp	307	307	100%	6e-106	99%	<a href="#">1RNJ_A</a>
<input type="checkbox"/> dUTP_diphosphatase [Escherichia coli]	307	307	100%	1e-105	99%	<a href="#">WP_000978070.1</a>
<input type="checkbox"/> MULTISPECIES: dUTP diphosphatase [Proteobacteria]	306	306	100%	1e-105	99%	<a href="#">WP_001298007.1</a>
<input type="checkbox"/> deoxyuridine 5'-triphosphate nucleotidohydrolase [Escherichia coli KTE119]	306	306	100%	1e-105	99%	<a href="#">ELF05704.1</a>
<input type="checkbox"/> deoxyuridine 5'-triphosphate nucleotidohydrolase [Escherichia coli]	306	306	100%	1e-105	99%	<a href="#">KUS81443.1</a>
<input type="checkbox"/> dUTP_diphosphatase [Escherichia coli]	306	306	100%	2e-105	99%	<a href="#">WP_077884810.1</a>
<input type="checkbox"/> dUTP_diphosphatase [Escherichia coli]	306	306	100%	2e-105	99%	<a href="#">WP_077786854.1</a>
<input type="checkbox"/> dUTP_diphosphatase [Escherichia coli]	306	306	100%	2e-105	99%	<a href="#">WP_077872152.1</a>
<input type="checkbox"/> deoxyuridine 5'-triphosphate nucleotidohydrolase [Escherichia coli BIDMC 39]	306	306	100%	3e-105	99%	<a href="#">ESL18324.1</a>
<input type="checkbox"/> dUTP_diphosphatase [Escherichia coli]	306	306	100%	3e-105	99%	<a href="#">WP_100289669.1</a>
<input type="checkbox"/> dUTP_diphosphatase [Escherichia coli]	306	306	100%	3e-105	99%	<a href="#">WP_077695801.1</a>
<input type="checkbox"/> dUTP_diphosphatase [Escherichia coli]	305	305	100%	3e-105	99%	<a href="#">WP_077781882.1</a>
<input type="checkbox"/> deoxyuridine 5'-triphosphate nucleotidohydrolase [Shigella sonnei]	305	305	100%	3e-105	99%	<a href="#">WP_077781882.1</a>
<input type="checkbox"/> dUTP_diphosphatase [Escherichia coli]	305	305	100%	3e-105	99%	<a href="#">WP_077781882.1</a>

Questions/comments

ENG 16:40  
CAFR 09/03/2018

Descendez dans l'alignement et sélectionnez-en quelque uns pour générer un arbre des distances.

Clicker ensuite sur Distance Tree

# Alignement de Séquences Protéiques

<https://pir.georgetown.edu/>

The screenshot displays the PIR Protein Information Resource website. The browser's address bar shows the URL <https://pir.georgetown.edu/>. The website's header includes the PIR logo and navigation tabs: About PIR, Resources, Search/Analysis, Download, and Support. The Search/Analysis dropdown menu is open, listing various tools: Search & Analysis Tools, Text Search, Batch Retrieval, Peptide Match, Pairwise Alignment (highlighted with a blue circle), Multiple Alignment, ID Mapping, and Composition/Mol Weight. The main content area features three columns of resources: UniProt (The Universal Protein Resource), PRO (Protein Ontology), and ProLINK (Literature Information & Knowledge). Each column lists specific services and provides links to sample reports. At the bottom, there are sections for OTHER RESOURCE, PEPTIDE SEARCH, and TEXT SEARCH, along with information about Bioinformatics & Computational Biology Graduate Programs.

PIR  
A UNIPROT CONJUNCTION MEMBER  
Protein Information Resource

Search/Analysis

- Search & Analysis Tools
- Text Search
- Batch Retrieval
- Peptide Match
- Pairwise Alignment
- Multiple Alignment
- ID Mapping
- Composition/Mol Weight

UniProt  
The Universal Protein Resource  
centralized, authoritative  
UniProtKB | UniProt

PRO  
Protein Ontology  
Representation of protein objects with descriptions and relationships  
Browse PRO  
Annotate with RACE-PRO  
Sample PRO report

ProLINK  
Literature Information & Knowledge  
Access to text mining tools and annotated corpora  
RLIMS-P extraction of kinase, substrate and site  
miRtex extraction of miRNA/target information  
Sample RLIMS-P report

OTHER RESOURCE

- Reference Proteomes
- iProClass
- iProXpress
- RESID

PEPTIDE SEARCH  
DATABASE: UniProtKB  
Use single letter amino acid code

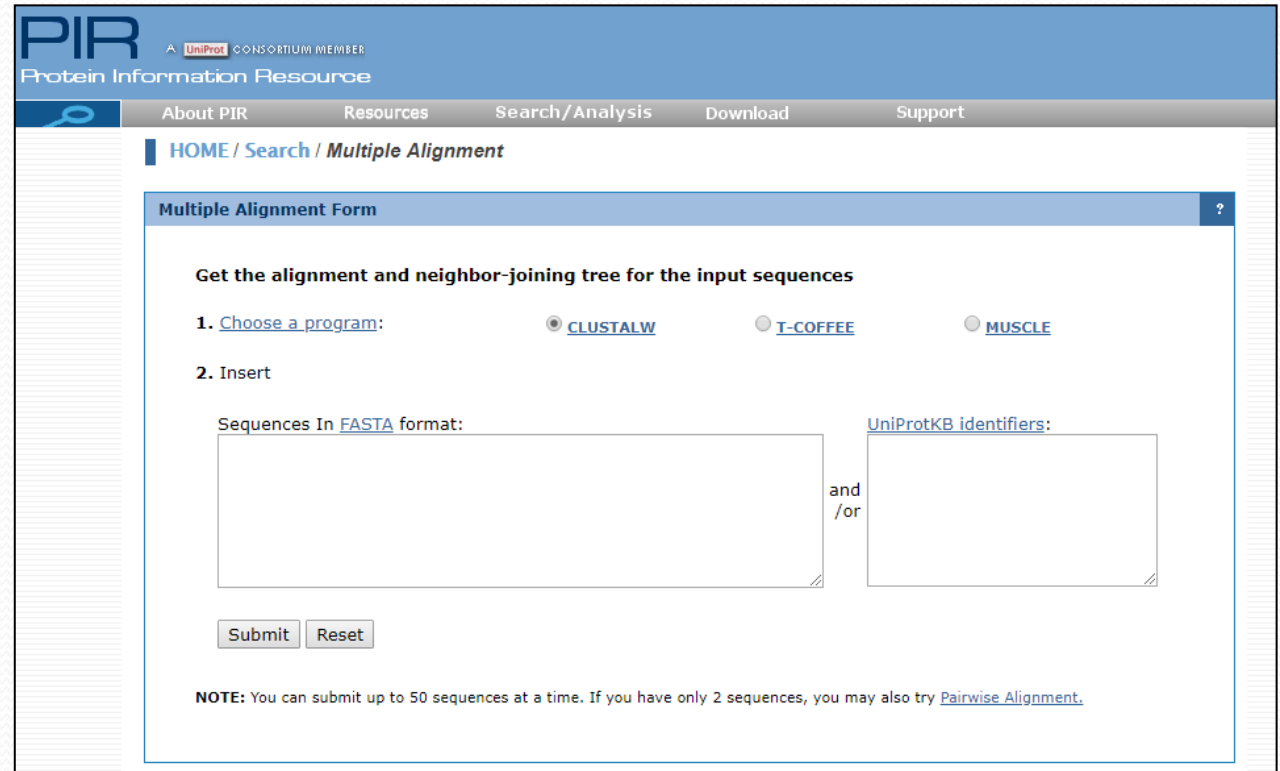
TEXT SEARCH  
DATABASE: iProClass

Bioinformatics & Computational Biology Graduate Programs:

- MS program at Georgetown University
- PhD, MS, PSM and Graduate Certificate programs at University of Delaware

# Alignement de Séquences Protéiques

Mais tu dois t'enregistrer avant.



The screenshot shows the PIR (Protein Information Resource) website's Multiple Alignment Form. The header includes the PIR logo, a UniProt Consortium Member badge, and navigation links: About PIR, Resources, Search/Analysis, Download, and Support. The breadcrumb trail is HOME / Search / Multiple Alignment. The form title is 'Multiple Alignment Form'. The instructions state: 'Get the alignment and neighbor-joining tree for the input sequences'. Step 1, 'Choose a program:', has three radio buttons: CLUSTALW (selected), T-COFFEE, and MUSCLE. Step 2, 'Insert', has two input fields: 'Sequences In FASTA format:' and 'UniProtKB identifiers:'. Between these fields is the text 'and /or'. Below the fields are 'Submit' and 'Reset' buttons. A note at the bottom states: 'NOTE: You can submit up to 50 sequences at a time. If you have only 2 sequences, you may also try Pairwise Alignment.'

PIR A UniProt CONSORTIUM MEMBER  
Protein Information Resource

About PIR Resources Search/Analysis Download Support

HOME / Search / Multiple Alignment

Multiple Alignment Form ?

Get the alignment and neighbor-joining tree for the input sequences

1. Choose a program: ☒ CLUSTALW ☐ T-COFFEE ☐ MUSCLE

2. Insert

Sequences In FASTA format: and /or UniProtKB identifiers:

Submit Reset

NOTE: You can submit up to 50 sequences at a time. If you have only 2 sequences, you may also try [Pairwise Alignment](#).

# Alignement de Séquences Protéiques

J'en ai un autre : ClustalW

<http://www.genome.jp/tools-bin/clustalw>

CLUSTAL-Alignment file created [clustalw.aln]

clustalw.aln

CLUSTAL 2.1 multiple sequence alignment

```
sp|P06968|DUT_ECOLI      -----MKKIDVKILDPRVGKEFP----
sp|P28248|DCD_ECOLI      ---MRLCDRDIEAWLDEGRLSINPRPPVERINGATVDVRLGNKFRFTFRG
sp|P0ABQ0|COABC_ECOLI    ---MSLAGKKIVLGVSGGIAAYKTPELVRRLRDRGADVRAVMTAAKAF
sp|P0C093|SLMA_ECOLI     MAEKQTAKRNRREETLQSLALMLESSDGSQRITTAASVGVSEAAALYR
                               .:. .:

sp|P06968|DUT_ECOLI      -----LPTYA-----TSGSAGLDLRACLNDAVELAPG-DTTLV
sp|P28248|DCD_ECOLI      HTAAFIDLSG-----PKDEVSAALDRVMSDEIVLDEGEAFYLH
sp|P0ABQ0|COABC_ECOLI    ITPLSLQAVSGYPVSDSLDPAEEAAMGHIELGKWADLVILAPATADLIA
sp|P0C093|SLMA_ECOLI     HFPSKTRMFDS-----LIEFIEDSLITRINLILKDEKDTTARLR
                               :  :

sp|P06968|DUT_ECOLI      PTGLAIHIADPSLAAMMLPRSGLG-----HKHGIVLGNLVGLIDSDYQGQ
sp|P28248|DCD_ECOLI      PGELALAVTLESVTLPADLVGWLDRSSLARLGLMVHTAHRIDPGWSGC
sp|P0ABQ0|COABC_ECOLI    RVAAGMANDLVSTICLATPAPVAVLPAMNQMYRAAATQHNLVLAASRGL
sp|P0C093|SLMA_ECOLI     LIVLLLLGFGERNPGLTRILTGHALMFEQDRLQGRINQLFERIEAQLRQV
                               :  :

sp|P06968|DUT_ECOLI      LMISVNNRGQDSFTIQPGERIAQMIFVPVVQAEFN-LVEDFDATDRGEGG
sp|P28248|DCD_ECOLI      IVLEFYNSGKLPALARPGMLIGALSFEPLSGPAVRPNYRREDAKYRNQOG
sp|P0ABQ0|COABC_ECOLI    LIWGPDSGSQACGDIGPGRMLDPLTIIDMAVAHFSPVNDLKHLNIMITAG
sp|P0C093|SLMA_ECOLI     LREKRMREGEGYTTDETLLASQILAFCEGMLSFRVSRSEFKYRPTDDFDAR
                               :  .: . : : .

sp|P06968|DUT_ECOLI      FGHSGRQ-----
sp|P28248|DCD_ECOLI      AVASRIDKD-----
sp|P0ABQ0|COABC_ECOLI    PTREPLDPVRYISNHSSGKMGFATAAAAAARRGAINVLVSGVPVSLPTPPFV
sp|P0C093|SLMA_ECOLI     WPLIAAQLQ-----
                               :

sp|P06968|DUT_ECOLI      -----
sp|P28248|DCD_ECOLI      -----
sp|P0ABQ0|COABC_ECOLI    KRVDVMTALEMEAAVNASVQQQNIIFIGCAAVADYRAATVAPEKIKKQATQ
sp|P0C093|SLMA_ECOLI     -----

sp|P06968|DUT_ECOLI      -----
sp|P28248|DCD_ECOLI      -----
```

# Alignement de Séquences Protéiques

Vas tout en bas et choisis l'option que tu veux pour afficher ton arbre

```
sp|P28248|DCD_ECOLI
sp|P0ABQ0|COABC_ECOLI
sp|P0C093|SLMA_ECOLI
```

-----  
VTRYDEKNRR  
-----

clustalw.dnd

(  
sp|P06968|DUT\_ECOLI:0.42469,  
(

Select tree menu  
Rooted phylogenetic tree (UPGMA)  
Rooted phylogenetic tree with branch length (UPGMA)  
Unrooted phylogenetic tree (N-J)  
Unrooted phylogenetic tree with branch length (N-J)  
Rooted phylogenetic tree (UPGMA) ▼

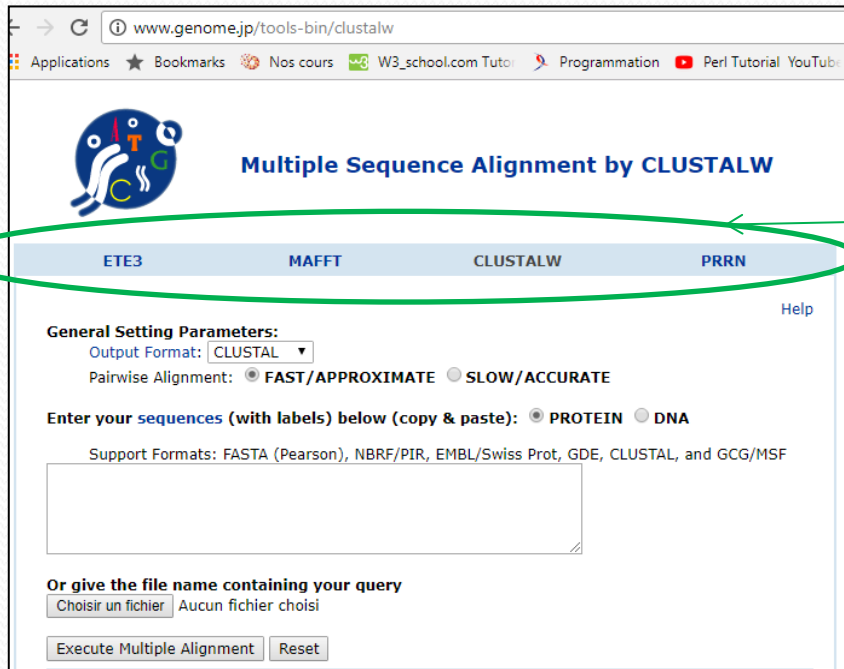
Exec

La tu as accès à plusieurs formats de cet alignement, inclus le format Philip .phy et le Fichier de l'arbre, pour utilisation future

[PostScript file](#) [\[PDF file\]](#) [\[Phylip format\]](#) [\[Tree file\]](#)

```
graph TD
    A["sp P06968 DUT ECOLI"] --- B["sp P28248 DCD ECOLI"]
    A --- C["sp P0ABQ0 COABC ECOLI"]
    A --- D["sp P0C093 SLMA ECOLI"]
```

# Qu'y a-t-il d'autre à par ClustalW ?



The screenshot shows the ClustalW web interface at [www.genome.jp/tools-bin/clustalw](http://www.genome.jp/tools-bin/clustalw). A green oval highlights the navigation bar containing the following tools: ETE3, MAFFT, CLUSTALW, and PRRN. Below the navigation bar, the 'General Setting Parameters' section includes an 'Output Format' dropdown set to 'CLUSTAL', a 'Pairwise Alignment' section with 'FAST/APPROXIMATE' selected, and an 'Enter your sequences' section with 'PROTEIN' selected. A text area for pasting sequences is provided, along with a list of supported formats: FASTA (Pearson), NBRF/PIR, EMBL/Swiss Prot, GDE, CLUSTAL, and GCG/MSF. At the bottom, there is a file upload section with a 'Choisir un fichier' button and a 'Reset' button.

Remarque que ce site te propose d'autres outils d'alignement en plus de ClustalW

# Swiss-Prot

<https://enzyme.expasy.org/>



ENZYME  
Enzyme nomenclature database

ENZYME is a repository of information relative to the nomenclature of enzymes. It is primarily based on the recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB) and it describes each type of characterized enzyme for which an EC (Enzyme Commission) number has been provided [[More details](#) / [References](#)]. ENZYME now includes entries with preliminary EC numbers. Preliminary EC numbers include an 'n' as part of the fourth (serial) digit (e.g. [EC 3.5.1.n3](#)).

Release of 28-Feb-18 (6145 active entries)

## Access to ENZYME

- by EC number:
- by enzyme class
- by description (official name) or alternative name(s):
- by chemical compound
- by cofactor
- by search in comments lines

## Documents

- [ENZYME user manual](#)
- [How to obtain ENZYME](#)



## Services

- [Report forms for a new ENZYME entry](#) or for [an error/update in an existing entry](#)
- [Downloading ENZYME by FTP](#)

# Brenda

<http://www.brenda-enzymes.org/>

This website is HUUUGE ! In term of informations you can get. I am going to make a special course on Brenda.

**BRENDA**  
The Comprehensive Enzyme Information System

Enzyme, Ligand

contains


add search field

delete search field

start search

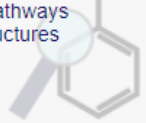
Text-based queries

- Full-text Search
- Advanced Search
- Enzyme & Disease




Structure-based queries

- Ligand Substructure
- Metabolic Pathways
- Enzyme Structures




Explorer

- Enzyme Classification
- TaxTree
- Protein folding: CATH / SCOPe
- Ontologies



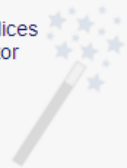
Visualization

- Word Maps
- Genomes
- Functional Parameter Statistics
- Metabolic Pathways




Prediction

- Membrane Helices
- EnzymeDetector



Supporting

- BRENDA Tissue Ontology
- Biochemical Reactions





# Expasy

- Back to Expasy.org.

<https://www.expasy.org/proteomics/> is a huge database tool for all kind of observation on Proteins. It is completely impossible to visit all of them.

The screenshot displays the Expasy Bioinformatics Resource Portal. The header includes the SIB logo, the Expasy logo, and the text 'Bioinformatics Resource Portal'. Navigation links for 'Home', 'About', and 'Contact' are in the top right. A search bar with a dropdown menu set to 'Query all databases' and a 'search' button is located below the header. The left sidebar contains a 'Visual Guidance' section with a 'Categories' dropdown menu currently set to 'proteomics'. Below this, a list of categories is visible: protein sequences and identification, proteomics experiment, function analysis, sequence sites, features and motifs, protein modifications, protein structure, protein interactions, similarity search/alignment, genomics, structure analysis, systems biology, evolutionary biology, population genetics, transcriptomics, biophysics, imaging, IT infrastructure, medicinal chemistry, and glycomics. The main content area is divided into three columns. The first column, 'SIB resources', lists various databases with links to more information: UniProtKB, UniProtKB/Swiss-Prot, STRING, SWISS-MODEL Repository, PROSITE, ViralZone, and neXtProt. The second column, 'Databases', lists: CAZy, CSDB, EMBnet services, ENZYME, Glyco3D, GlyConnect, GlyTouCan, HAMAP, iPTGDBs, MatrixDB, MetaNetX, MIAPEGelDB, MyHits, PaxDb, Prolune, Protein Model Portal, Protein Spotlight, and Rhea. The third column, 'Tools', lists: SWISS-MODEL Workspace, VIta-HT, SwissDock, 2ZIP, 3of5, AACompliment, AACompSim, Agadir, ALF, Alignment tools, APSSP, Ascalaph, big-PI, Biochemical Pathways, BLAST, BLAST (UniProt), BLAST - NCBI, BLAST - PBIL, Blast2Fasta, boxshade, CFSSP, ChloroP, Click2Drug, ClustalO, and ClustalW. Each tool entry includes a brief description and a link to more information.

# Fiche d'Autoévaluation

Question 1: . . . . .  
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Question 2: . . . . .  
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