Trouvez une Protéine par son Nom

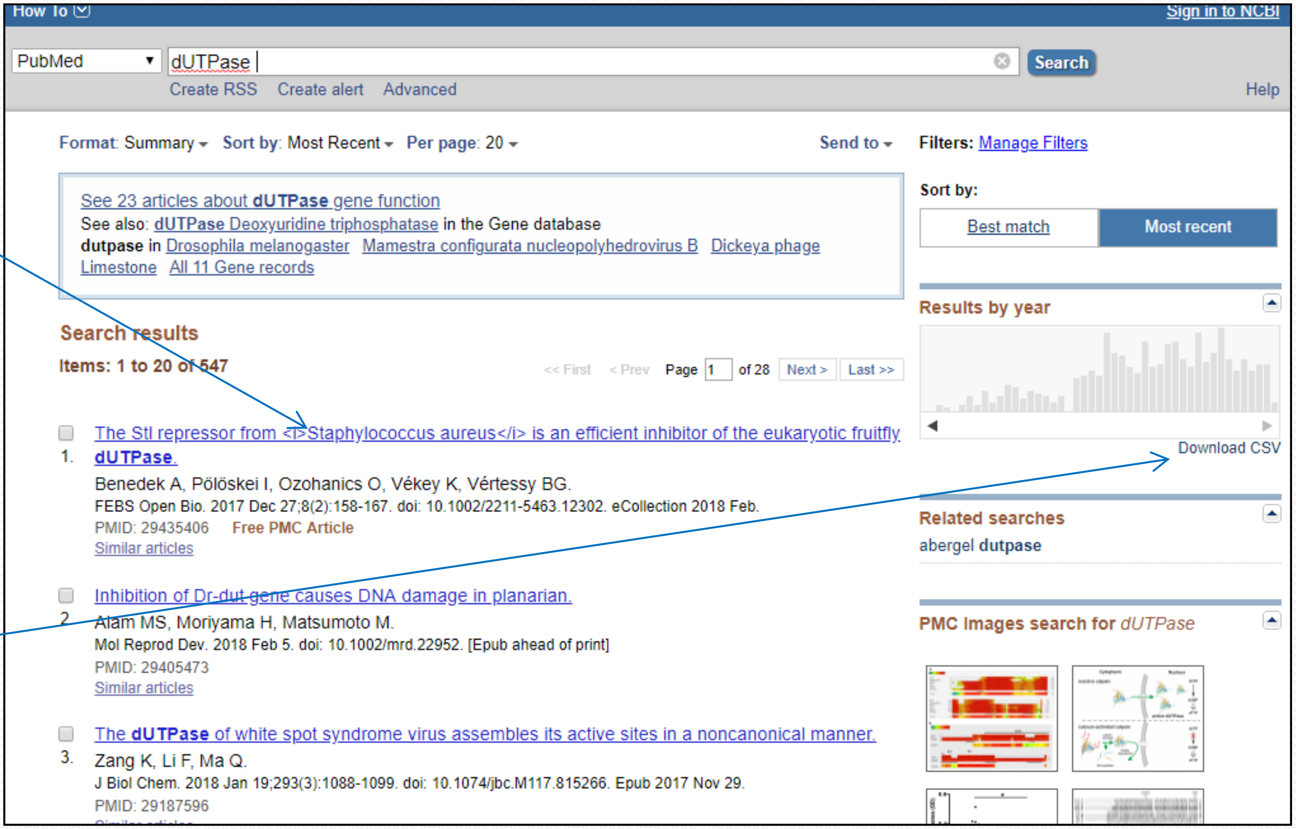
Par Joel Sandé

Prenom la protéine dUTPase

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

Vous pouvez clicker sur le lien pour voir l'article

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



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

☐ 1. The Stl repressor from <i>Staphylococcus aureus</i> is an efficient inhibitor of the eukaryotic fruitfly **dUTPase**.
Benedek A, Pölöskei 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.
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Alam MS, Moriyama H, Matsumoto M.
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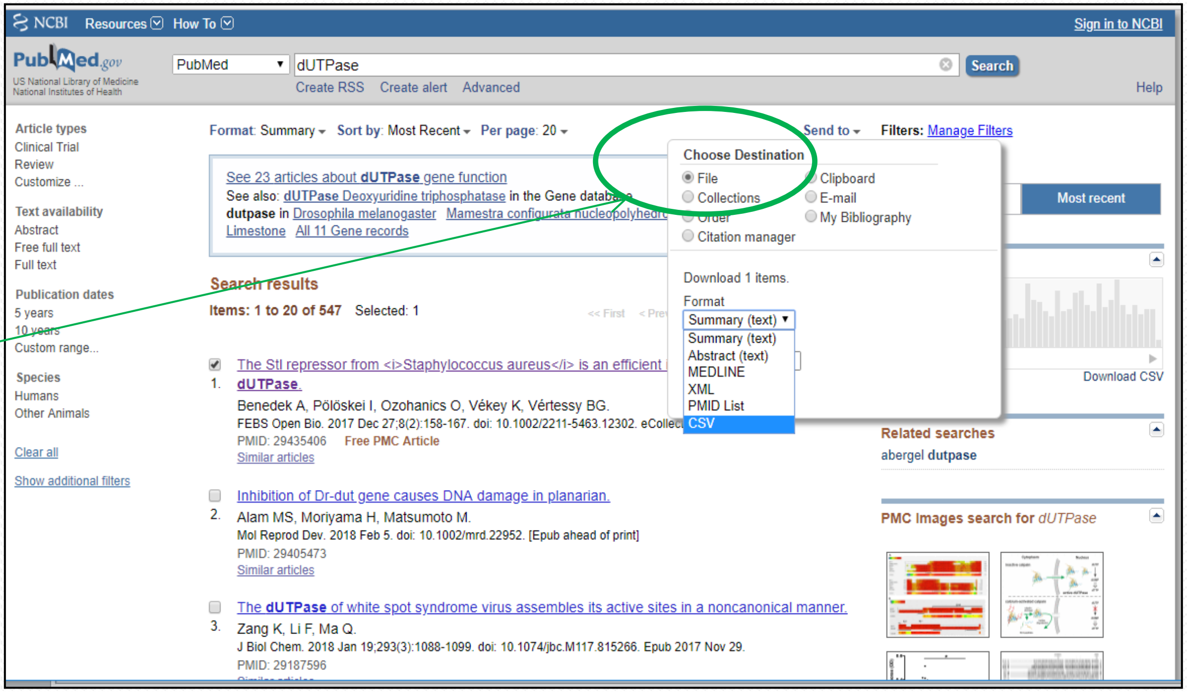
Zang K, Li F, Ma Q.
J Biol Chem. 2018 Jan 19;293(3):1088-1099. doi: 10.1074/jbc.M117.815266. Epub 2017 Nov 29.
PMID: 29187596

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).



dUTPase

See 23 articles about **dUTPase** gene function

See also: **dUTPase** Deoxyuridine triphosphatase in the Gene database

dutpase in Drosophila melanogaster Mamestra configurata nucleopolyhedr

Limestone All 11 Gene records

Choose Destination: ● File

Download 1 items.

Format
Summary (text)

Search results

Items: 1 to 20 of 547 Selected: 1

☑ 1. The Stl repressor from <i>Staphylococcus aureus</i> is an efficient i **dUTPase.**
Benedek A, Pölöskei I, Ozohanics O, Vékey K, Vértessy BG.
FEBS Open Bio. 2017 Dec 27;8(2):158-167. doi: 10.1002/2211-5463.12302. eCollec
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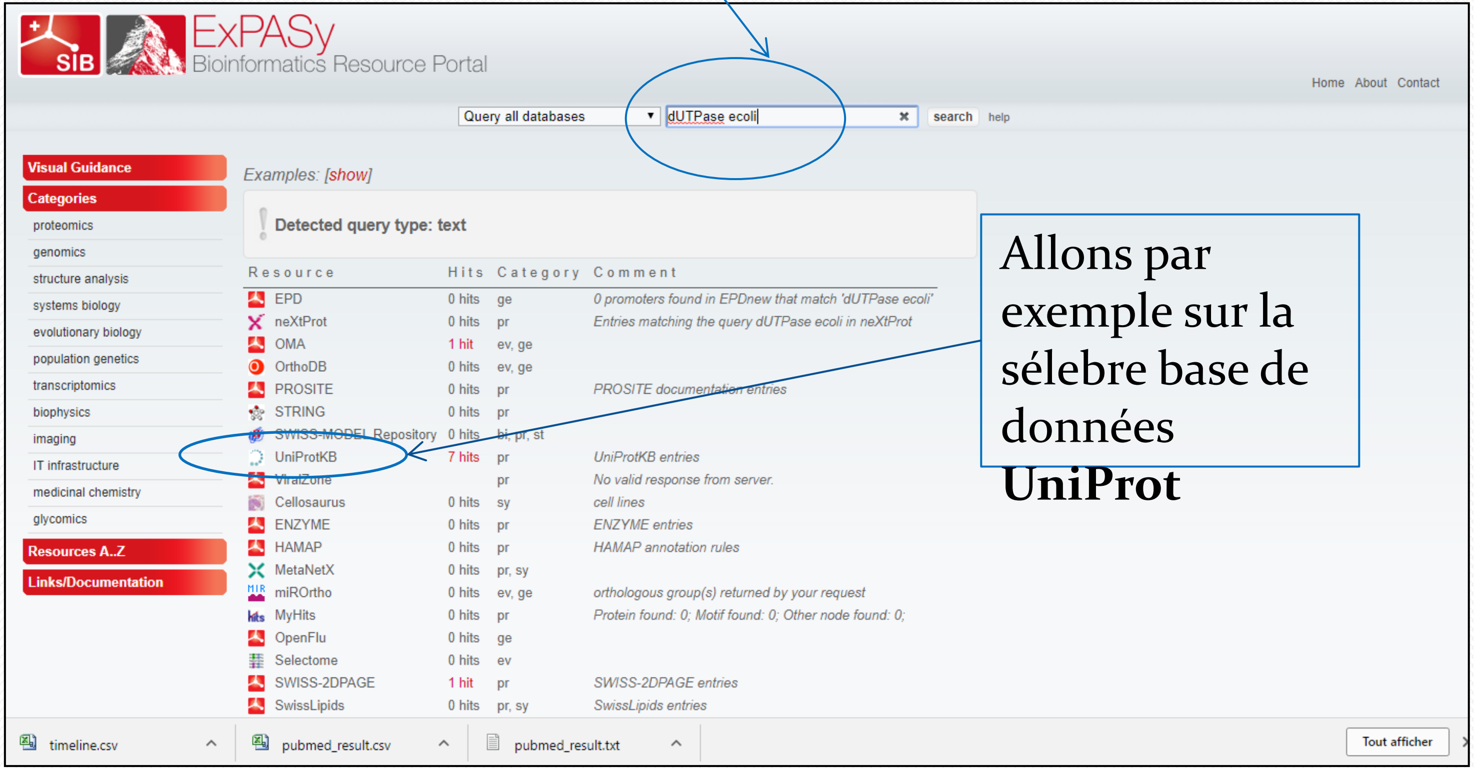
PMID: 29187596

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.

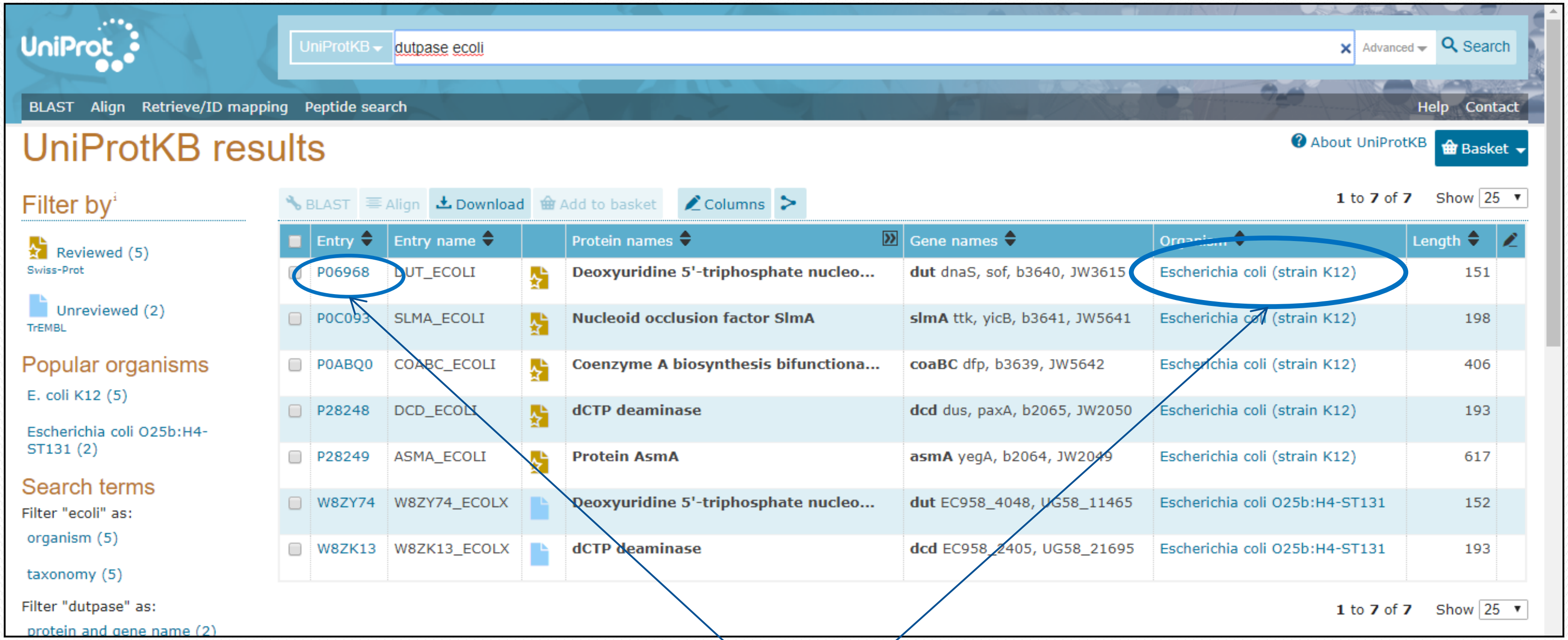


Detected query type: text

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*
ViralZone		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*

Allons par exemple sur la sélebre base de données **UniProt**

Informations sur la Protéine dUTPase



UniProtKB: dutpase ecoli

UniProtKB results

1 to 7 of 7 Show 25

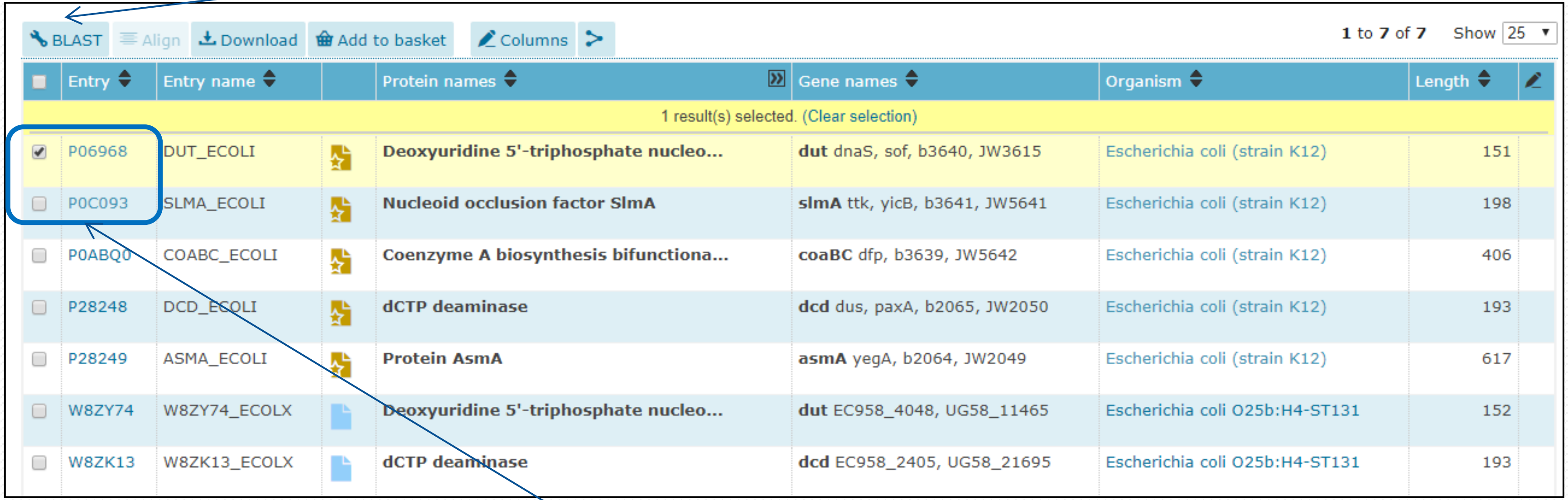
☐	Entry	Entry name	Protein names	Gene names	Organism	Length
☐	P06968	DUT_ECOLI	Deoxyuridine 5'-triphosphate nucleo...	**dut** dnaS, sof, b3640, JW3615	Escherichia coli (strain K12)	151
☐	P0C093	SLMA_ECOLI	Nucleoid occlusion factor SlmA	**slmA** ttk, yicB, b3641, JW5641	Escherichia coli (strain K12)	198
☐	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 Selectionnez la protéine et la Blaster pour voir ces homologues de séquence.



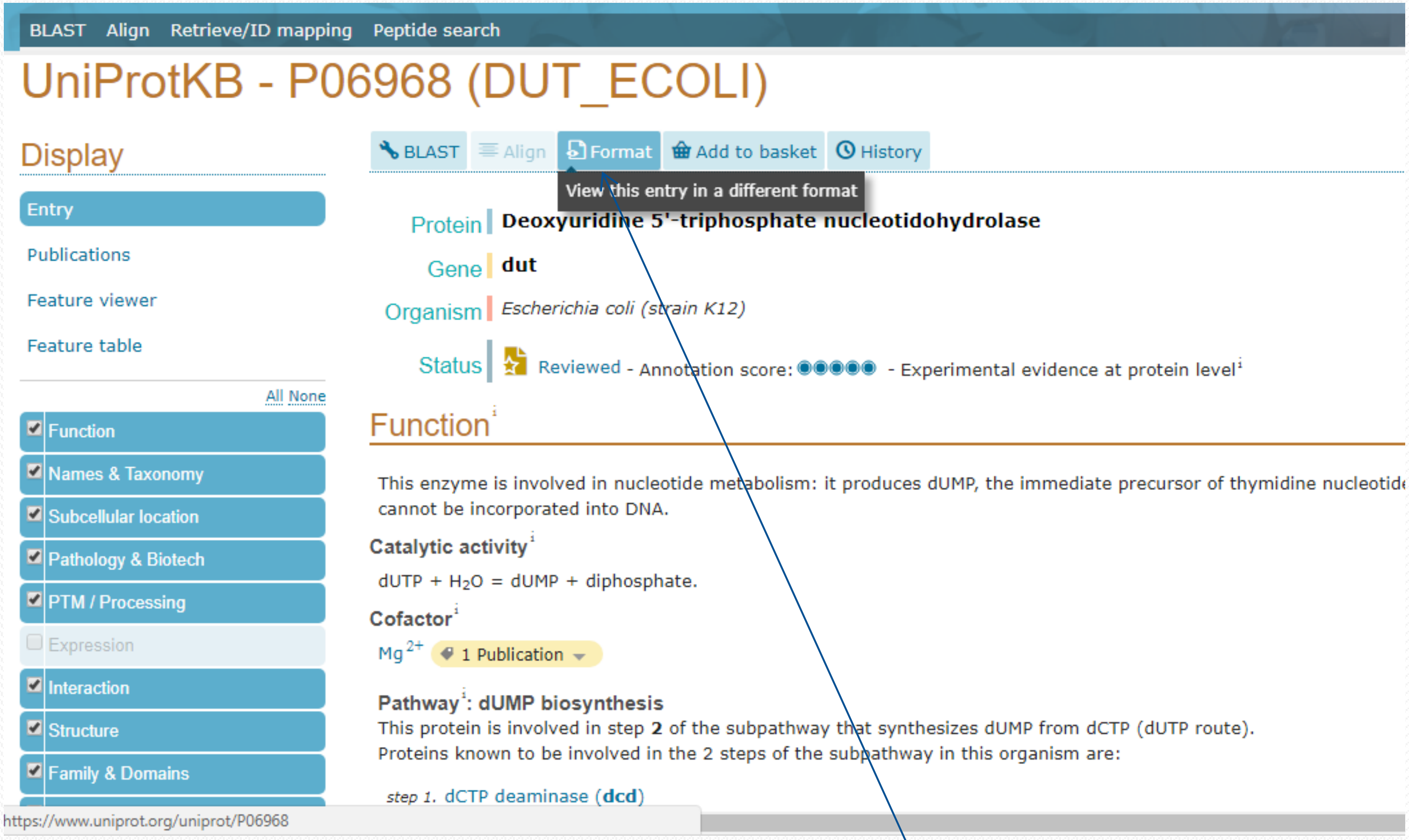
1 to **7** of **7** Show 25

1 result(s) selected. (Clear selection)

☐	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

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



UniProtKB - P06968 (DUT_ECOLI)

Protein Deoxyuridine 5'-triphosphate nucleotidohydrolase

Gene dut

Organism *Escherichia coli (strain K12)*

Status Reviewed - Annotation score: ●●●●● - Experimental evidence at protein level

Function

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

Catalytic activity

dUTP + H_2O = dUMP + diphosphate.

Cofactor

Mg^{2+} 1 Publication

Pathway: 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:

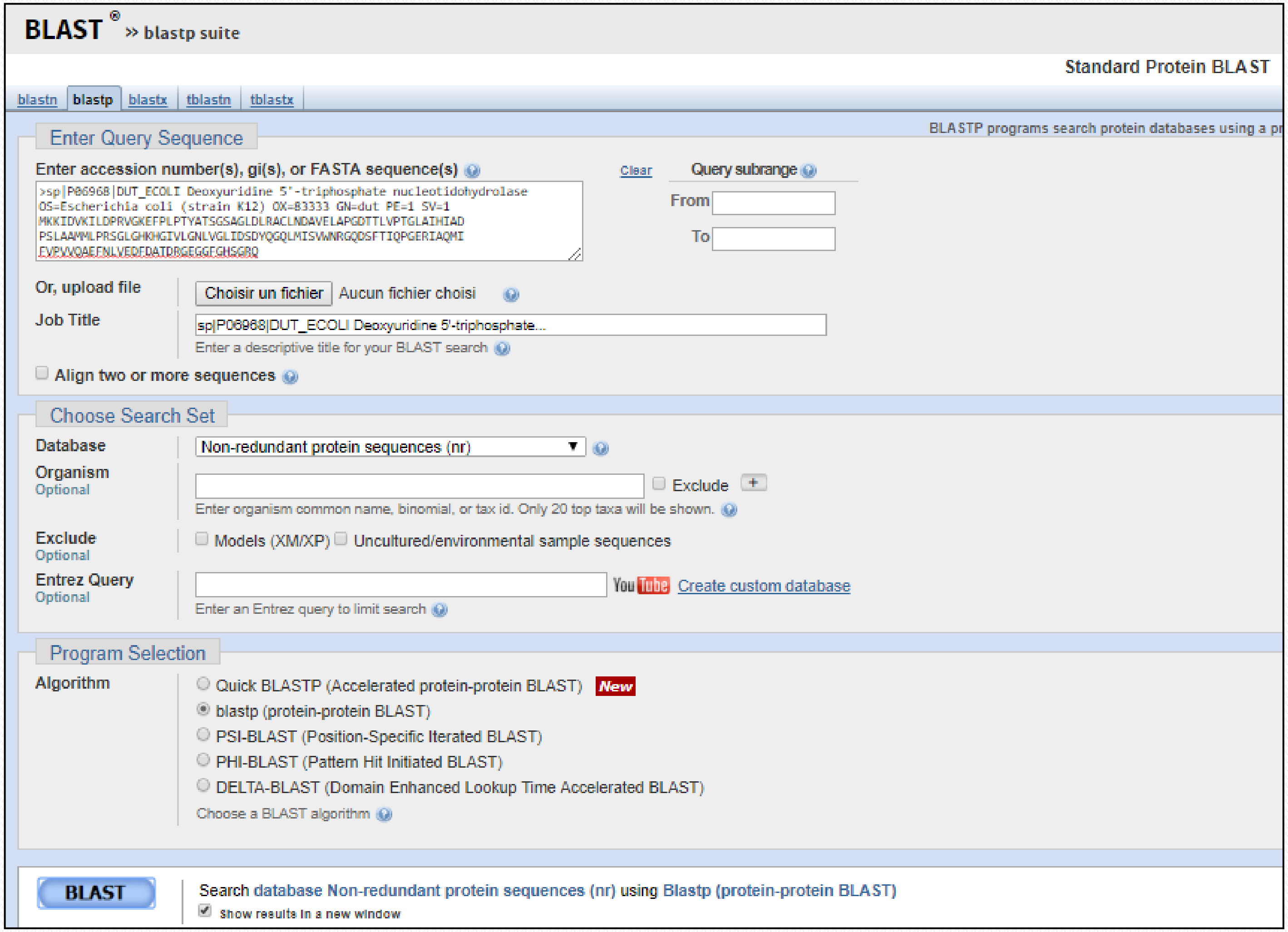
step 1. dCTP deaminase (**dcd**)

Clikez 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=

Copier-coller
ou
importer votre
fichier Fasta



BLAST® » blastp suite

Standard Protein BLAST

BLASTP programs search protein databases using a pr

Enter 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
MKKIDVKILDPRVGKEFPLPTYATSGSAGLDLRACLNDAVELAPGDTTLVPTGLAIHIAD
PSLAAMMLPRSGLGHKHGIVLGNLVGLIDSDYQGQLMISVWNRGQDSFTIQPGERIAQMI
FVPVVQAEFNLVEDFDATDRGEGGFGHSGRQ
```

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

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude Optional: ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Entrez Query Optional:

Enter an Entrez query to limit search

Program Selection

Algorithm:

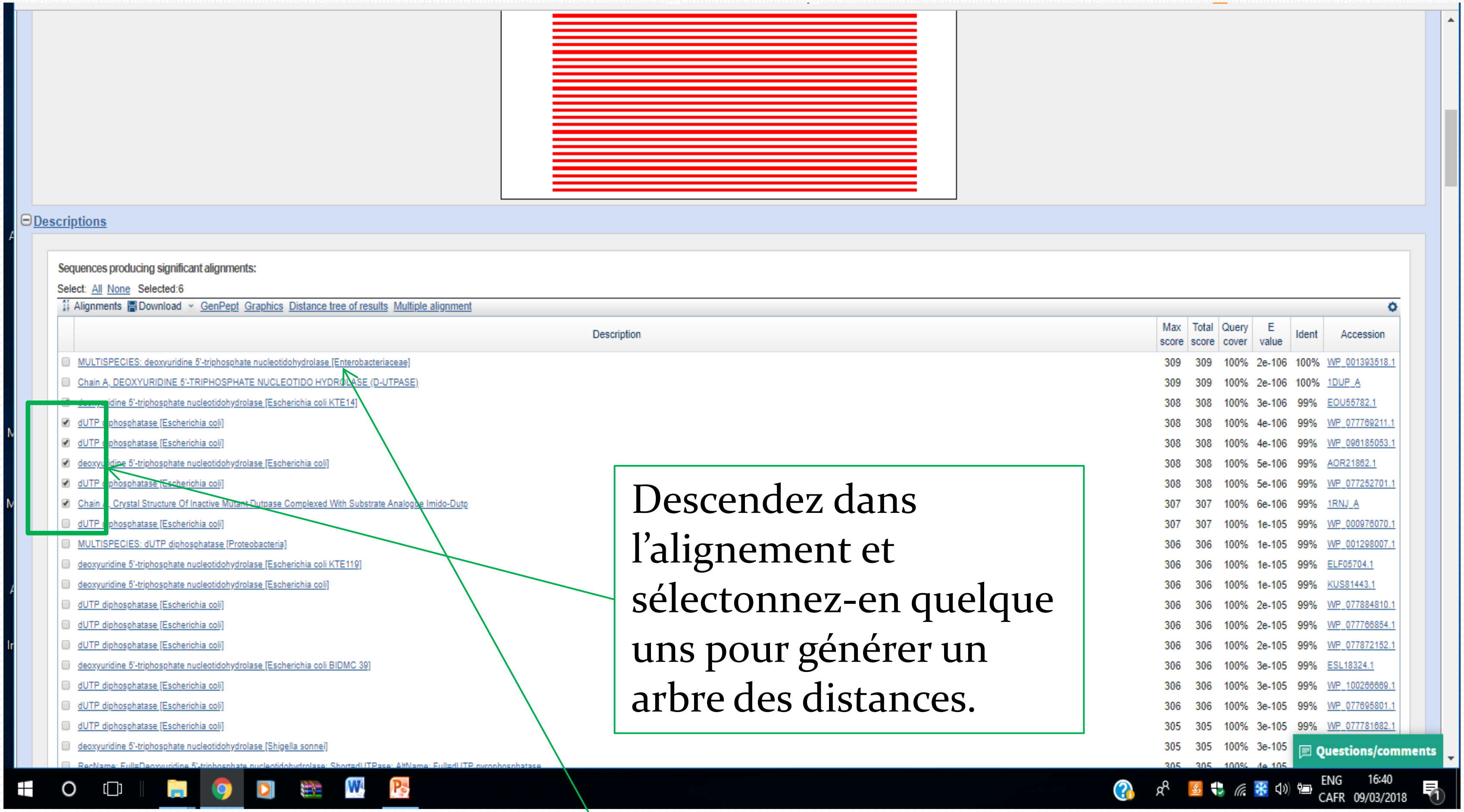
- ○ Quick BLASTP (Accelerated protein-protein BLAST) New
- ● blastp (protein-protein BLAST)
- ○ PSI-BLAST (Position-Specific Iterated BLAST)
- ○ PHI-BLAST (Pattern Hit Initiated BLAST)
- ○ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm

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

☑ Show results in a new window

Alignement de Séquences Protéiques



Descriptions

Sequences producing significant alignments:

Select: All None Selected:6

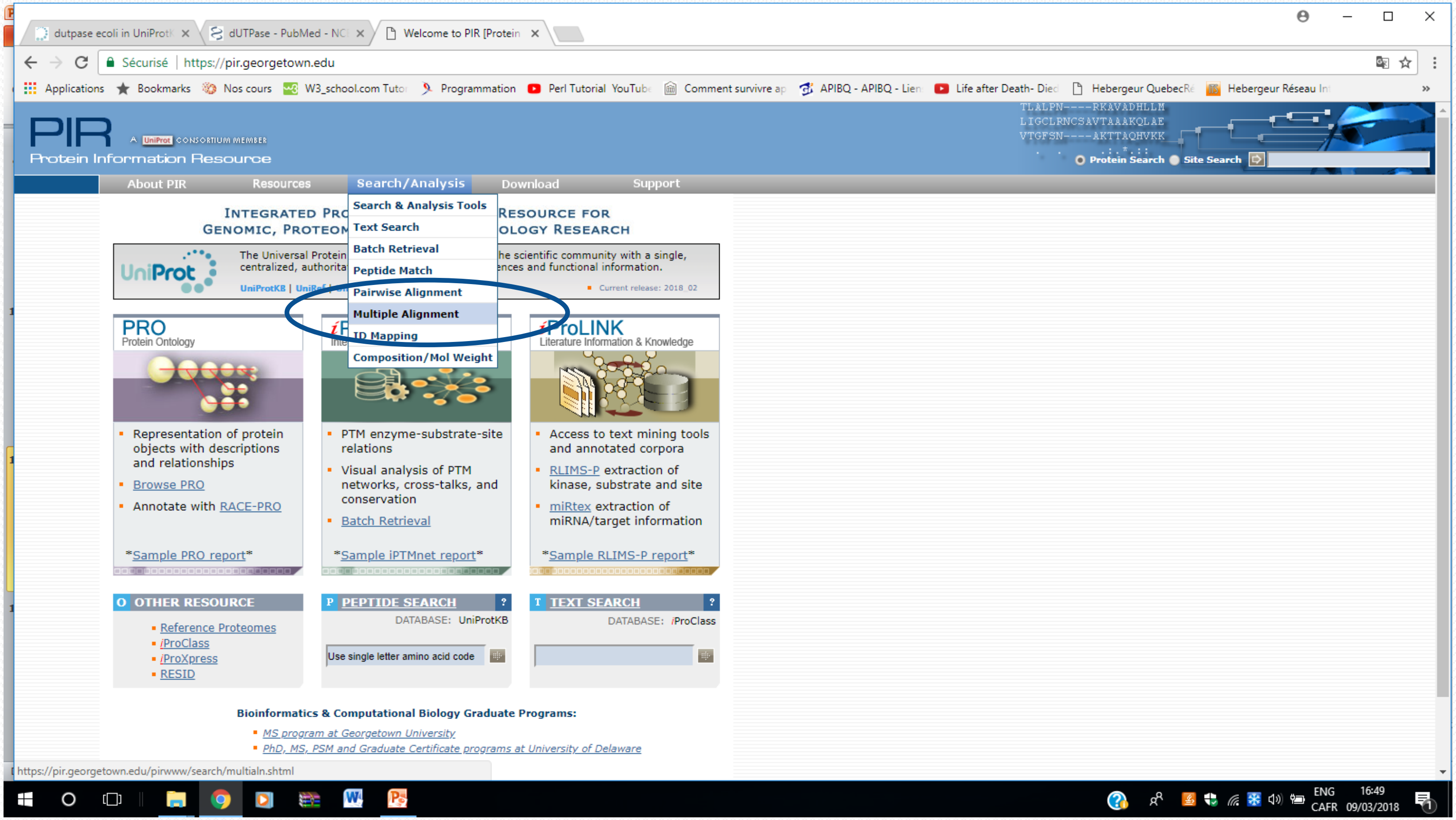
	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	MULTISPECIES: deoxyuridine 5'-triphosphate nucleotidohydrolase [Enterobacteriaceae]	309	309	100%	2e-106	100%	WP_001393518.1
☐	Chain A, DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDO HYDROLASE (D-UTPASE)	309	309	100%	2e-106	100%	1DUP_A
☑	deoxyuridine 5'-triphosphate nucleotidohydrolase [Escherichia coli KTE14]	308	308	100%	3e-106	99%	EOU55782.1
☑	dUTP diphosphatase [Escherichia coli]	308	308	100%	4e-106	99%	WP_077769211.1
☑	dUTP diphosphatase [Escherichia coli]	308	308	100%	4e-106	99%	WP_096185053.1
☑	deoxyuridine 5'-triphosphate nucleotidohydrolase [Escherichia coli]	308	308	100%	5e-106	99%	AOR21862.1
☑	dUTP diphosphatase [Escherichia coli]	308	308	100%	5e-106	99%	WP_077252701.1
☑	Chain A, Crystal Structure Of Inactive Mutant Dutpase Complexed With Substrate Analogue Imido-Dutp	307	307	100%	6e-106	99%	1RNJ_A
☐	dUTP diphosphatase [Escherichia coli]	307	307	100%	1e-105	99%	WP_000976070.1
☐	MULTISPECIES: dUTP diphosphatase [Proteobacteria]	306	306	100%	1e-105	99%	WP_001298007.1
☐	deoxyuridine 5'-triphosphate nucleotidohydrolase [Escherichia coli KTE119]	306	306	100%	1e-105	99%	ELF05704.1
☐	deoxyuridine 5'-triphosphate nucleotidohydrolase [Escherichia coli]	306	306	100%	1e-105	99%	KUS81443.1
☐	dUTP diphosphatase [Escherichia coli]	306	306	100%	2e-105	99%	WP_077884810.1
☐	dUTP diphosphatase [Escherichia coli]	306	306	100%	2e-105	99%	WP_077766854.1
☐	dUTP diphosphatase [Escherichia coli]	306	306	100%	2e-105	99%	WP_077872152.1
☐	deoxyuridine 5'-triphosphate nucleotidohydrolase [Escherichia coli BIDMC 39]	306	306	100%	3e-105	99%	ESL18324.1
☐	dUTP diphosphatase [Escherichia coli]	306	306	100%	3e-105	99%	WP_100266669.1
☐	dUTP diphosphatase [Escherichia coli]	306	306	100%	3e-105	99%	WP_077695801.1
☐	dUTP diphosphatase [Escherichia coli]	305	305	100%	3e-105	99%	WP_077781682.1
☐	deoxyuridine 5'-triphosphate nucleotidohydrolase [Shigella sonnei]	305	305	100%	3e-105		
☐	RecName: Full=Deoxyuridine 5'-triphosphate nucleotidohydrolase; Short=dUTPase; AltName: Full=dUTP pyrophosphatase	305	305	100%	4e-105		

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

Clicker ensuite sur Distance Tree

Alignement de Séquences Protéiques

https://pir.georgetown.edu/



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Sample PRO report

- PTM enzyme-substrate-site relations
- Visual analysis of PTM networks, cross-talks, and conservation
- Batch Retrieval

Sample iPTMnet report

iProLINK
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

TEXT SEARCH

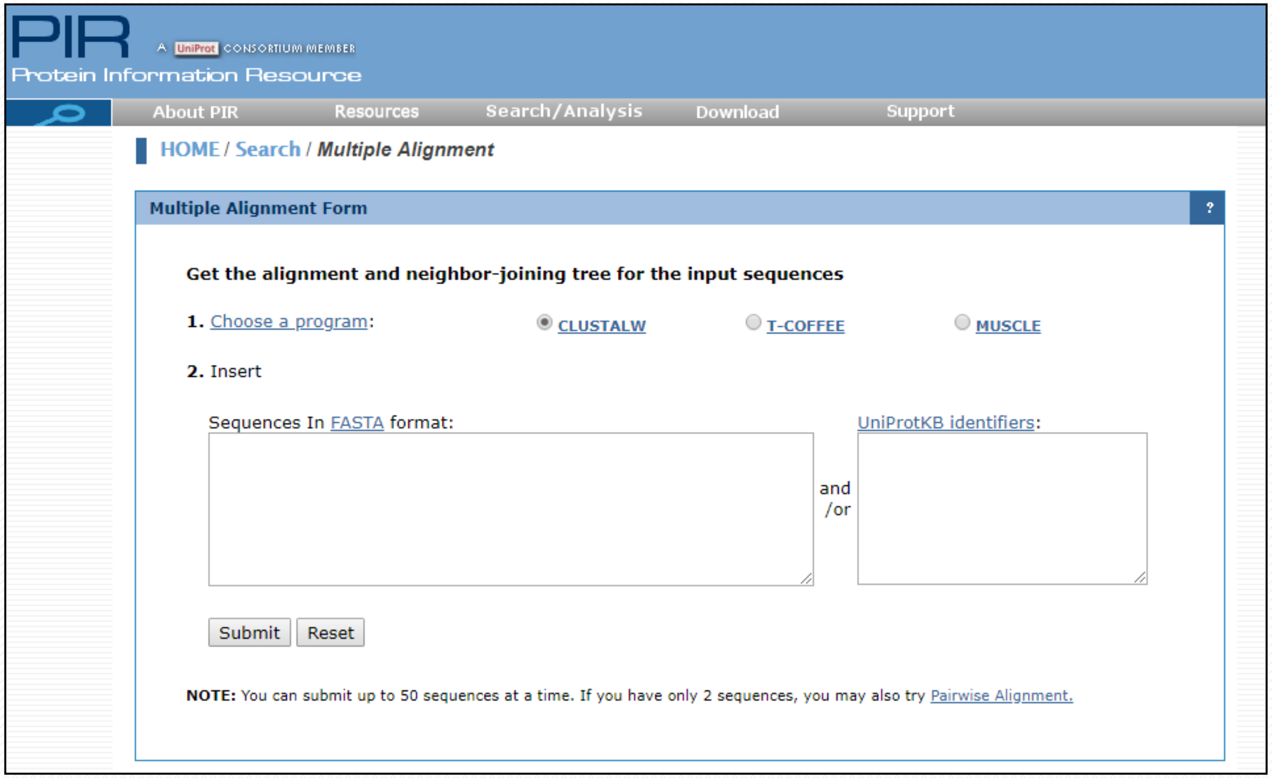
DATABASE: iProClass

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.



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:

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

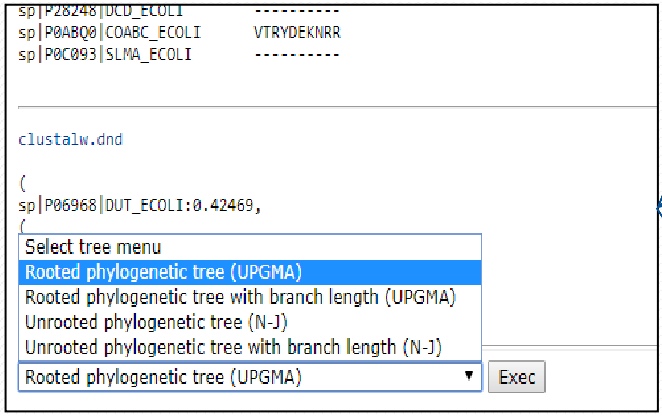
Alignement de Séquences Protéiques

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        ----MRLCDRDIEAWLDEGRLSINPRPPVERINGATVDVRLGNKFRTFRG
sp|P0ABQ0|COABC_ECOLI      ----MSLAGKKIVLGVSGGIAAYKTPELVRRLRDRGADVRVAMTEAAKAF
sp|P0C093|SLMA_ECOLI       MAEKQTAKRNRREEILQSLALMLESSDGSQRITTAKLAASVGVSEAALYR
                                                        .::        :.

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

sp|P06968|DUT_ECOLI        PTGLAIHIADPSLAAMMLPRSGLG-----HKHGIVLGNLVGLIDSDYQGQ
sp|P28248|DCD_ECOLI        PGELALAVTLESVTLPADLVGWLDGRSSLARLGLMVHVTAHRIDPGWSGC
sp|P0ABQ0|COABC_ECOLI      RVAAGMANDLVSTICLATPAPVAVLPAMNQQMYRAAATQHNLEVLASRGL
sp|P0C093|SLMA_ECOLI       LIVLLLLGFGERNPGLTRILTGHALMFEQDRLQGRINQLFERIEAQLRQV
                                :                        :

sp|P06968|DUT_ECOLI        LMISVWNRGQDSFTIQPGERIAQMIFVPVVQAEFN-LVEDFDATDRGEGG
sp|P28248|DCD_ECOLI        IVLEFYNSGKLPLALRPGMLIGALSFEPLSGPAVRPYNRREDAKYRNQQG
sp|P0ABQ0|COABC_ECOLI      LIWGPDSGSQACGDIGPGRMLDPLTIVDMAVAHFSPVNDLKHLNIMITAG
sp|P0C093|SLMA_ECOLI       LREKRMREGEGYTTDETLLASQILAFCEGMLSRFVRSEFKYRPTDDFDAR
                           :       .:      .      : :     . .         .

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

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


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

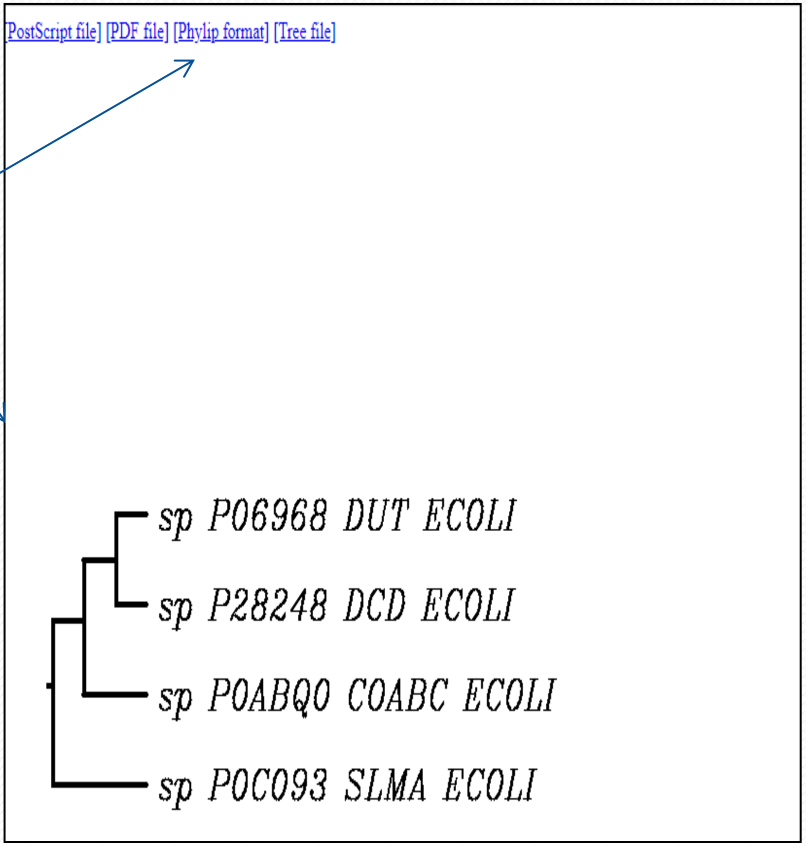
Alignement de Séquences Protéiques



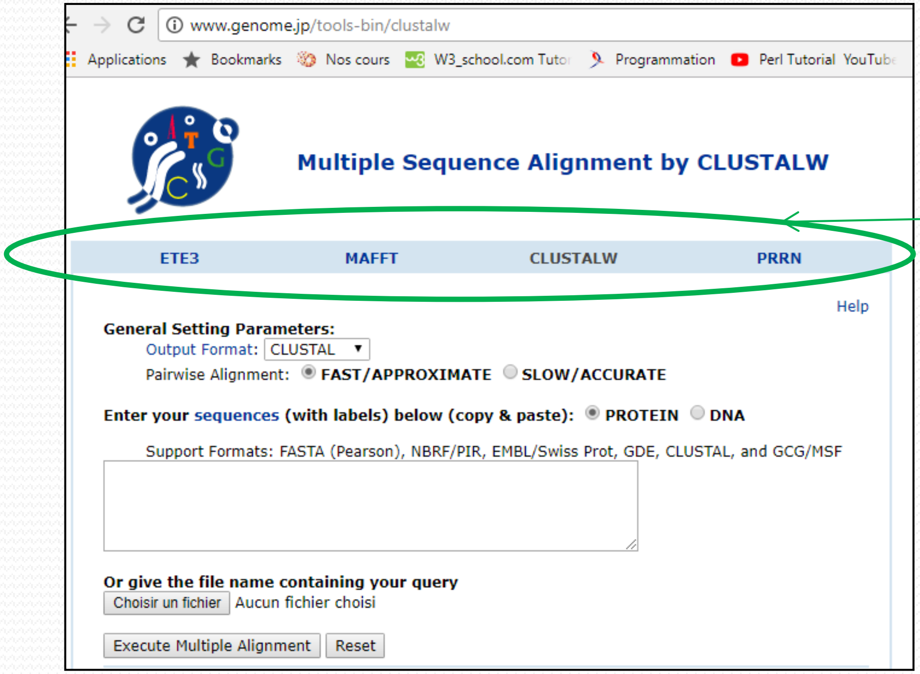
```
sp|P28248|DCD_ECOLI        ----------
sp|P0ABQ0|COABC_ECOLI      VTRYDEKNRR
sp|P0C093|SLMA_ECOLI       ----------

clustalw.dnd

(
sp|P06968|DUT_ECOLI:0.42469,
(
```

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

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



Qu’y a-t-il d’autre à par ClustalW ?



Multiple Sequence Alignment by CLUSTALW

General Setting Parameters:
Output Format: CLUSTAL ▾
Pairwise Alignment: ● FAST/APPROXIMATE ○ SLOW/ACCURATE

Enter your sequences (with labels) below (copy & paste): ● PROTEIN ○ DNA

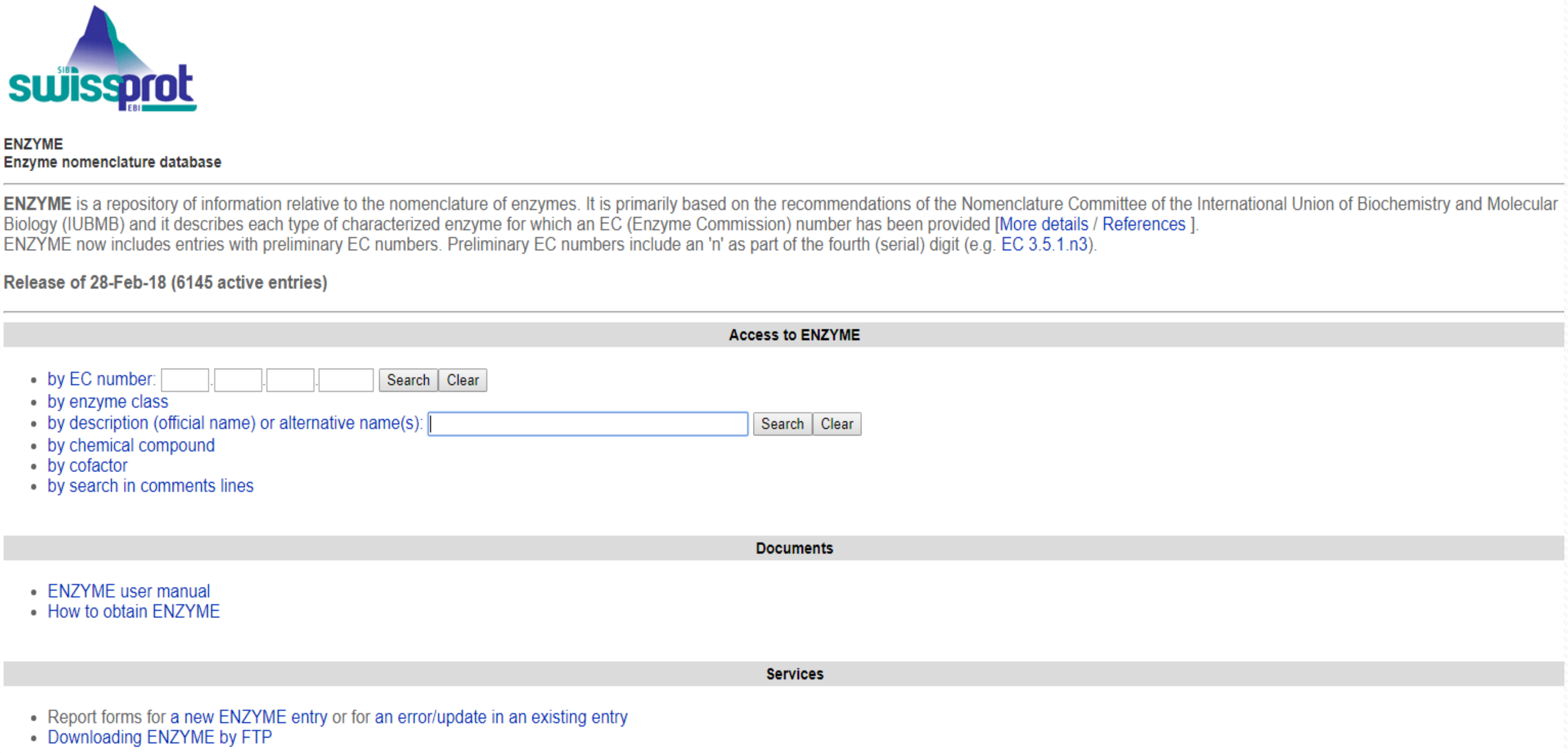
Support Formats: FASTA (Pearson), NBRF/PIR, EMBL/Swiss Prot, GDE, CLUSTAL, and GCG/MSF

Or give the file name containing your query
Aucun fichier choisi

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

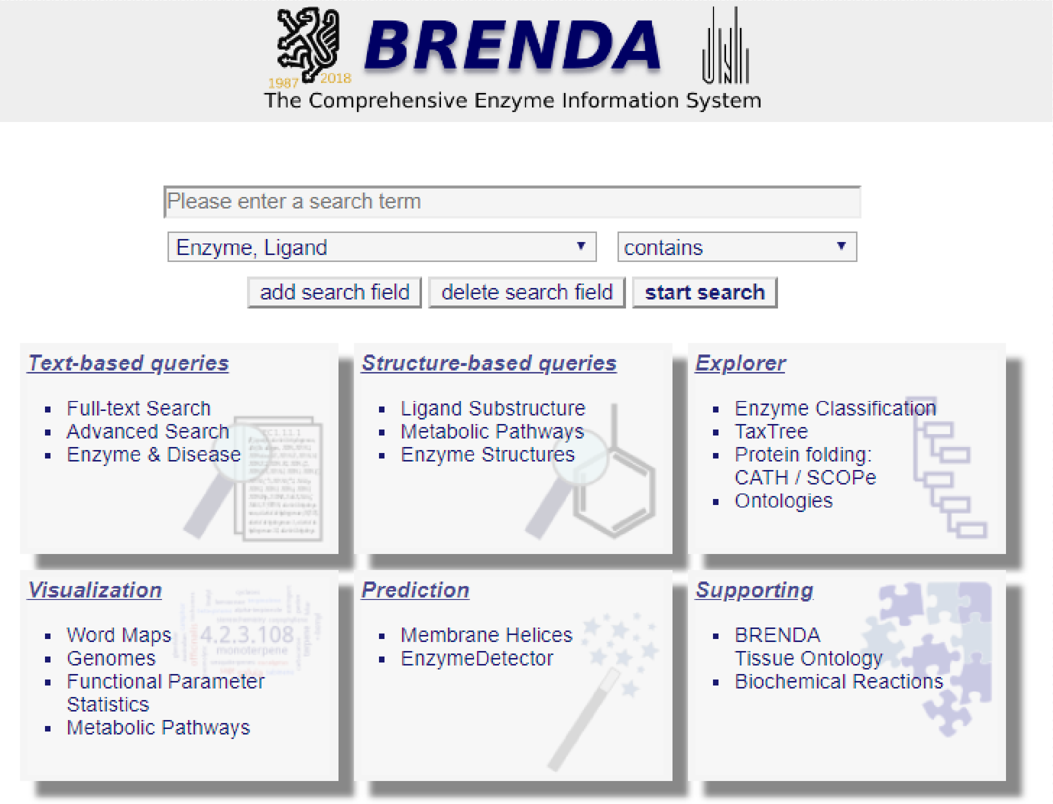
Services

- 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.



Text-based queries
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- Advanced Search
- Enzyme & Disease

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- Metabolic Pathways
- Enzyme Structures

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

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

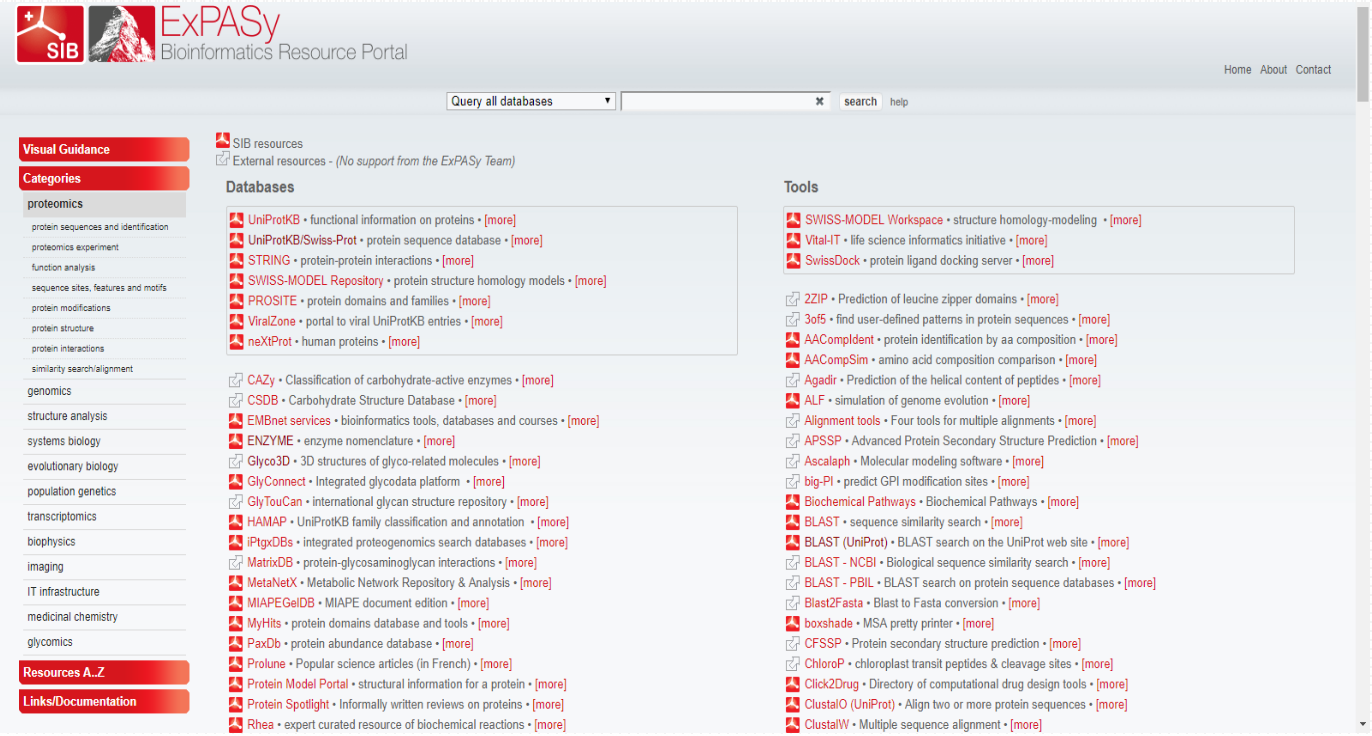
Prediction
- Membrane Helices
- EnzymeDetector

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.



SIB resources
External resources - *(No support from the ExPASy Team)*

Databases

UniProtKB • functional information on proteins • [more]
UniProtKB/Swiss-Prot • protein sequence database • [more]
STRING • protein-protein interactions • [more]
SWISS-MODEL Repository • protein structure homology models • [more]
PROSITE • protein domains and families • [more]
ViralZone • portal to viral UniProtKB entries • [more]
neXtProt • human proteins • [more]

CAZy • Classification of carbohydrate-active enzymes • [more]
CSDB • Carbohydrate Structure Database • [more]
EMBnet services • bioinformatics tools, databases and courses • [more]
ENZYME • enzyme nomenclature • [more]
Glyco3D • 3D structures of glyco-related molecules • [more]
GlyConnect • Integrated glycodata platform • [more]
GlyTouCan • international glycan structure repository • [more]
HAMAP • UniProtKB family classification and annotation • [more]
iPtgxDBs • integrated proteogenomics search databases • [more]
MatrixDB • protein-glycosaminoglycan interactions • [more]
MetaNetX • Metabolic Network Repository & Analysis • [more]
MIAPEGelDB • MIAPE document edition • [more]
MyHits • protein domains database and tools • [more]
PaxDb • protein abundance database • [more]
Prolune • Popular science articles (in French) • [more]
Protein Model Portal • structural information for a protein • [more]
Protein Spotlight • Informally written reviews on proteins • [more]
Rhea • expert curated resource of biochemical reactions • [more]

Tools

SWISS-MODEL Workspace • structure homology-modeling • [more]
Vital-IT • life science informatics initiative • [more]
SwissDock • protein ligand docking server • [more]

2ZIP • Prediction of leucine zipper domains • [more]
3of5 • find user-defined patterns in protein sequences • [more]
AACompIdent • protein identification by aa composition • [more]
AACompSim • amino acid composition comparison • [more]
Agadir • Prediction of the helical content of peptides • [more]
ALF • simulation of genome evolution • [more]
Alignment tools • Four tools for multiple alignments • [more]
APSSP • Advanced Protein Secondary Structure Prediction • [more]
Ascalaph • Molecular modeling software • [more]
big-PI • predict GPI modification sites • [more]
Biochemical Pathways • Biochemical Pathways • [more]
BLAST • sequence similarity search • [more]
BLAST (UniProt) • BLAST search on the UniProt web site • [more]
BLAST - NCBI • Biological sequence similarity search • [more]
BLAST - PBIL • BLAST search on protein sequence databases • [more]
Blast2Fasta • Blast to Fasta conversion • [more]
boxshade • MSA pretty printer • [more]
CFSSP • Protein secondary structure prediction • [more]
ChloroP • chloroplast transit peptides & cleavage sites • [more]
Click2Drug • Directory of computational drug design tools • [more]
ClustalO (UniProt) • Align two or more protein sequences • [more]
ClustalW • Multiple sequence alignment • [more]

Fiche d’Autoévaluation

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