

BRENDA Exercises Quick Search



Federal Ministry of Education and Research



- How often can you find the term "glucosidase" in enzyme names?
- How many EC classes are connected with this term?

Exercise 2

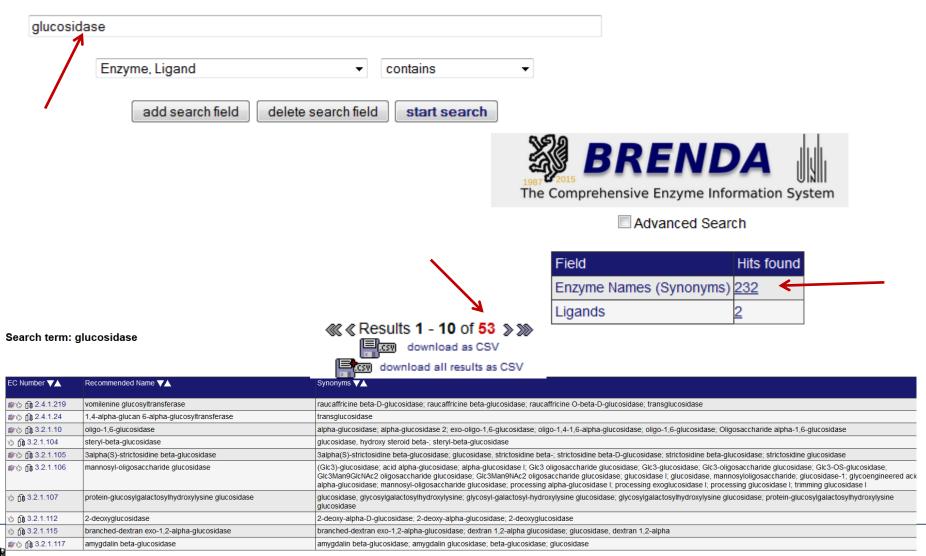
- How many enzymes accept molybdopterin as a cofactor?
- Display the results for exact matches for molybdopterin
- To which main EC class do the enzymes belong?

Exercise 3

- What is the EC number and the recommended name for the enzyme commonly termed RUBISCO?
- Display the wordmap
- RUBISCO is involved in a biological process. What is its name and what are the major metabolites of this process?
- Display the reaction diagram for RUBISCO
- How many protein sequences for RUBISCO are stored in BRENDA?





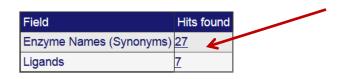


Search with "contains"

| | ybdopterin | | | | | | |
|---------------------|--|--|---|---|---|--|--|
| Cofacto | or | ▼ contain | IS 🔹 | | | | |
| | add search field | delete search field star | t search ≪ ≪ Results 1 - 10 o | | | | |
| | | | ew download | as CSV | | | |
| | EC Number 🔻 | Recommended Name 🔻 | | Cofactor VA | Structure VA | | |
| | 齡心 🕅 1.1.5.6 | formate dehydrogenase-N | | bis(molybdopterin guanine dinucleotide)molybdenum cofactor | r 🕆 🕼 🛄 | | |
| | 蒙诊 🏦 1.1.99.6 | D-lactate dehydrogenase (acc | • • | molybdopterin mononucleotide | - | | |
| | i∰ ⊚ jît 1.1.99.33 | formate dehydrogenase (acce | | bis(molybdopterin guanine dinucleotide)molybdenum cofactor | | | |
| | i∰ ⊘ jît 1.1.99.33 | formate dehydrogenase (acce | eptor) | molybdopterin | | | |
| | | formate dehydrogenase | | molybdopterin | | | |
| | ☆ ① 1.2.3.1 ☆ ① 1.2.3.1 | aldehyde oxidase aldehyde oxidase | | molybdopterin molybdopterin cytosine dinucleotide | | | |
| | | | | molybdopterin | | | |
| | | | | | | | |
| | | | uctase | Imolybdopterin | YAYA Emoti 🗄 | | |
| | ₩\$\$ ()) 1.2.7.5 ₩\$\$ ()) 1.2.7.5 | aldehyde ferredoxin oxidoredi aldehyde ferredoxin oxidoredi | | | | | |
| earch Cofa | ⊯⊚ î〕 1.2.7.5 actor | aldehyde ferredoxin oxidoredi | uctase ≪≪ Results 1 - 10 o | tungsten-molybdopterin of 51 >>> as CSV | | | |
| earch Cofa | <i>₩</i> ☆ f) 1.2.7.5 | aldehyde ferredoxin oxidoredi | uctase ≪≪ Results 1 - 10 o | tungsten-molybdopterin of 51 >>> as CSV as CSV | | | |
| earch Cofa | 献金 前 1.2.7.5 Actor Cofactor: molybdopt | aldehyde ferredoxin oxidoredi | vctase | tungsten-molybdopterin of 51 >>> as CSV as CSV | | | |
| earch Cofa | actor Cofactor: molybdopte ✓ Don't show of the state | aldehyde ferredoxin oxidoredi errin exact organism specific information | vctase | tungsten-molybdopterin of 51 >>> as CSV as CSV Search with "exact" | | | |
| earch Cofa | Cofactor: molybdopte | aldehyde ferredoxin oxidoredi rerin exact organism specific information anism in taxonomic tree (slow | vctase ≪ Results 1 - 10 c ↓ show 10 ▼ results n (fast!) v e c "mammalia" for rat human | tungsten-molybdopterin of 51 >>> as CSV as CSV Search with "exact" | | | |
| | actor Cofactor: molybdopte ✓ Don't show of the state | aldehyde ferredoxin oxidoredi rerin exact organism specific information anism in taxonomic tree (slow | vctase ≪ Results 1 - 10 c ∞ download | tungsten-molybdopterin of 51 >>> as CSV as CSV Search with "exact" | | | |
| fine your search | Cofactor: molybdopte Don't show of (Not possible | aldehyde ferredoxin oxidoredi rerin exact organism specific information anism in taxonomic tree (slow | v e α "mammalia" for rat huma | tungsten-molybdopterin of 51 >>> as CSV as CSV Search with "exact" n m Results 1 - 10 of 26 >>>> | | | |
| | Cofactor: molybdopte | erin exact organism specific information anism in taxonomic tree (slow | v e α "mammalia" for rat human we a "mammalia" or rat human we a "mammalia" for rat human we a "mammalia" for rat human we a "mammalia" for rat human we a mammalia or rat human | tungsten-molybdopterin of 51 >>> as CSV as CSV Search with "exact" n m Results 1 - 10 of 26 >>>> download as CSV download all results as CSV | | | |
| fine your search | Cofactor: molybdopte | erin exact organism specific information anism in taxonomic tree (slow le to EC Number VA | vctase Results 1 - 10 c Results 1 - 10 c Results n (fast!) v e c "mammalia" for rat humai w e c "mammalia" for rat humai w e c "mammalia" for rat humai w e c "mammalia" for rat humai | tungsten-molybdopterin of 51 >>> as CSV as CSV Cofactor | vorske te structure | | |
| fine your search | Cofactor: molybdopte | erin exact organism specific information anism in taxonomic tree (slow | v e α "mammalia" for rat human we a "mammalia" or rat human we a "mammalia" for rat human we a "mammalia" for rat human we a "mammalia" for rat human we a mammalia or rat human | tungsten-molybdopterin of 51 >>> as CSV as CSV Cofactor | ♦ ♦ ♦ ♦ ♦ ♦ ♦ ♦ • • • • • • • • • • • • | | |

LAALLA

| rub | isco | | | |
|-------|-----------------------|------------------|--------------|---|
| Enzym | ne, Ligand | • | contains | T |
| | add search field dele | ete search field | start search | |



≪ ≪ Results 1 - 4 of 4 ≫ ≫ and download as CSV and download all results as CSV

| EC Number VA | Recommended Name VA | Synonyms 🟹 📐 |
|---------------------|--|---|
| 齡心 🕅 2.1.1.127 | [ribulose-bisphosphate carboxylase]-lysine N-methyltransferase | Rubisco large subunit epsilonN-methyltransferase; Rubisco large subunit methyltrans dimethyltransferase; Rubisco LS methyltransferase; Rubisco LSMT; Rubisco methylt |
| ர்ற் பிழ் 2.1.1.259 | [fructose-bisphosphate aldolase]-lysine N-methyltransferase | large subunit of Rubisco methyltransferas; Rubisco methyltransferase |
| 齡心 頎 4.1.1.39 | Ribulose-bisphosphate carboxylase | archaeal Rubisco; barley rubisco; form I RubisCO; Form II Rubisco; Galdieria Rubisc red-type form I RuBisCO; Rubisco; RubisCO 1; RuBisCO 2; RubisCO redlike form I; Rubisco-LSU; RubiscoL; Tk-Rubisco; type III Rubisco |
| 📾 👌 🕦 5.3.2.5 | 2,3-diketo-5-methylthiopentyl-1-phosphate enolase | RuBisCO-like protein |

Sequences- 46425 protein sequences from UniProt

Reaction

Wordmap – The biological process is the photosynthesis. The main metabolites in this process are CO2, chlorophyll, 3-phosphoglycerate, and phosphoenolpyruvate



BRENDA Exercises The Enzyme Summery Page

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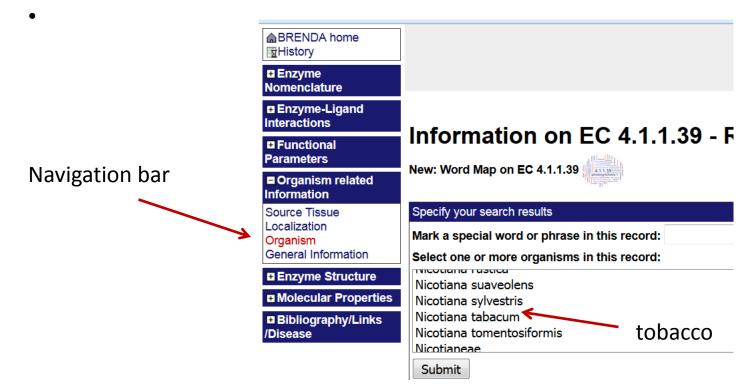


- Display the enzyme summary page for RUBISCO
- Open the menue organism-related information on the navigation bar and look at the section "organism"
- Then go back to the top of the flatfile and click Include FRENDA results (AMENDA + additional results, but less precise; more...)
- Again open the menue organism-related information on the navigation bar and look at the section "organism". What is different now?
- The optimal temperature for RUBISCO varies with the enzyme origin. What is the maximal value for optimal activity. In which organism has it been detected?
- You are only interested in RUBISCO from tobacco. How can you reduce the displayed data to show only those related to tobacco? (Note: if you do not know the scientific name for tobacco, you may need to study the tutorial on the Taxonomy Explorer first. If you know the name (or your instructor is willing to reveal it), you can go ahead with this task (2)





- Rubisco, EC 4.1.1.39
- The navigation bar is on the left side of the screen



In the organism section the BRENDA data are in dark blue. The textmining data are in light blue. The reliability of the textmining data is indicated by +, ++, +++





BRENDA Exercises Fulltext Search





- methylmalonyl-CoA is a frequently occuring metabolite. Display a list of all BRENDA data categories where this compound is mentioned.
- How many kinetic values are stored for this compound $(K_m, k_{cat}/K_m, K_i)$ ٠ turnover numbers)?

Exercise 6

 What are the EC numbers for enzymes that are related to lactate dehydrogenase deficiency?





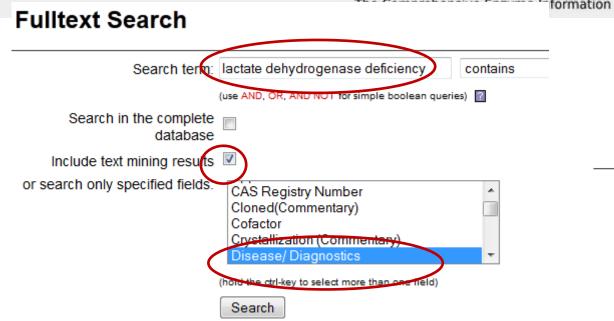
Fulltext Search

Search terne: methylmalonyl-CoA contains (use AND, OR, AND NOT for simple boolean queries) Search in the complete 📝 database Include text mining results or search only specified fields: Activating Compound Ξ Amino Acid Sequence Application CAS Registry Number Cloned(Commentary) (hold the ctrl-key to select more than one field) Search

| Field | Hits found |
|---|------------|
| Activating Compound | 1 |
| Cloned(Commentary) | 3 |
| Crystallization (Commentary) | 5 |
| Disease/ Diagnostics | 72 |
| Enzyme Names (Synonyms) | 30 |
| Inhibitors | 17 |
| KCat/KM [mM/s] | 3 |
| Ki Value [mM] | 2 |
| KM Value [mM] | 30 |
| Ligands | 118 |
| Natural Product | 5 |
| Natural Substrate | 13 |
| Natural Substrates/ Products (Substrates) | 93 |
| Product | 27 |
| Reaction | 25 |
| Recommended Name | 6 |
| Reference by Title | 329 |
| Renatured (Commentary) | 2 |
| Substrate | 60 |
| Substrates and Products (Substrate) | 390 |
| Synonyms | 19 |
| Systematic Name | 10 |
| Turnover Number [1/s] | 22 |







| Field | Hits found |
|----------------------|------------|
| Disease/ Diagnostics | 76 |





BRENDA Exercises Advanced Search

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- Search all acetyltransferases which have been crystallized.
- How many of these have a connected pdb entry?

Exercise 8

 Xylose from hydrolyzed wood components might be a good material for energy production or biofuel production. Find enzymes that may be useful in these processes.







Advanced Search results

New advanced search



pyruvate dehydrogenase (acetyl-transferring) (EC 1.2.4.1) from *Homo sapiens*

Crystallization (Commentary)

| Crystallization | Reference |
|---|-----------|
| recombinant enzyme, orthorhombic crystals in polyethylene glycol 3350 by vapor-diffusion method, space group P222 | 348993 |
| vapour diffusion method with 14-18% PEG 3350, 0.1 mM sodium azide, and 200 mM NaSCN in 50 mM potassium phosphate (pH 8.0) | 685160 |

pyruvate dehydrogenase (acetyl-transferring)

(EC 1.2.4.1) from *Escherichia coli* Crystallization (Commentary)

Crystallization

in complex with phosphonolactylthiamine diphosphate as structural and electrostatic analogue of alpha-lactylthiamin diphosphate. Presence of phosp

preparation of catalytic subunit E1 of pyruvate dehydrogenase complex, without cofactors thiamine diphosphate and Mg2+, no evidence of disorder/c complex with thiamine 2-thiazolone diphosphate

purified enzyme E1 in complex with inhibitor thiamine thiazolone diphosphate and Mg2+, sitting drop vapour diffusion method, reservoir solution: 15-:

Advanced Search results

New advanced search

pyruvate dehydrogenase (acetyl-transferring)

(EC 1.2.4.1) from *Homo sapiens* Crystallization (Commentary)



| Crystallization | Reference |
|---|-----------|
| recombinant enzyme, orthorhombic crystals in polyethylene glycol 3350 by vapor-diffusion method, space group P222 | 348993 |
| vapour diffusion method with 14-18% PEG 3350, 0.1 mM sodium azide, and 200 mM NaSCN in 50 mM potassium phosphate (pH 8.0) | 685160 |

PDB ID

| PDB ID | Chain | UniProt (1st accession) |
|--------|-------|-------------------------|
| 1ni4 | А | P08559 |
| 1ni4 | С | P08559 |
| 1ni4 | В | P08559 |



| EC Number: | exact | • | | use * as a wildcard |
|-----------------------|-------|------------|------------|---------------------------|
| Organism: | exact | • | | use * as a wildcard (* in |
| Enzyme Name: | exact | • | |] |
| Search in text fields | | | | |
| ٥ | | | | |
| 1. Application | - | contains • | production | |
| 2. Ligands | • | contains - | xylose | |
| • | | | | |

glucose 1-dehydrogenase (PQQ, quinone)

(EC 1.1.5.2) from *Pyrobaculum aerophilum* Application

| Application | Commentary |
|-------------|---|
| biofuel | construction of a long-life biofuel cell using a hyperthermophilic enzyme. For the cathode, the mul |
| production | glucose dehydrogenase from Pyrobaculum aerophilum is used. When the enzymes are used as e |

Ligands

| Role | Ligand | Structure | inchi | chebilD | Reference |
|-----------------|----------|-----------|-------|---------|-----------|
| KM Value | D-xylose | | | | 711018 |
| Substrate | D-xylose | | | | 711018 |
| Turnover Number | D-xylose | | | | 711018 |

acetylxylan esterase

(EC 3.1.1.72) from Trichoderma reesei
 Application



BRENDA Exercises EC Explorer

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- You are looking for enzymes that transfer methyl groups
- There are several search modes which you might use for this search.
- However this time use the EC Explorer for this search
- Start with using the search mode of the EC Explorer
- try using a part-name
- try using a compound which is able to donate a methyl group
- Then use the browse mode
- Look at the various links and display the information provided there
- Now try other search modes for this tasks (your instructor will appreciate your feedback)





EC Explorer

| owse EC tree] - [search] | | | | | |
|-------------------------------|----------|-------------------------|---------|-------------------------|--|
| ease use AND or OR in combin | natio | n with NOT to re | efine y | you query | |
| EC number | v | begins with | • | | |
| Common name | √ | contains | • | | First thing you may guess that these enzymes |
| Reaction | ✓ | contains | • | | are called "methyltransferase" and enter the |
| Systematic name | | contains | • | | term into "synonyms" |
| Comment | | contains | • | | |
| CAS registry number | | contains | • | | |
| Synonyms | √ | contains | • | methyltransferase | |
| History | | contains | • | | |
| clude 🔲 class (x.) 🔲 subclass | (x.x. |) 🔲 sub-subcla | iss (x. | x.x.) 🗹 serial number (| x.x.x.x) |
| | sea | arch 10 🔻 | resu | Its | |

| EC 🔺 👻 | Common name 🔺 👻 | Reaction 🔺 🔫 | Synonyms 🔺 👻 |
|--------|---|---|--|
| | [methionine synthase] reductase | 2 [methionine synthase]-methylcob(I)alamin + 2 <i>S</i> -adenosylhomocysteine + NADP ⁺ = 2 [methionine synthase]-cob(II)alamin + NADPH + H ⁺ + 2 <i>S</i> -adenosyl-L-methionine | methionine synthase cob(II)alamin reducta synthase]-cobalamin methyltransferase (co |
| | nicotinamide <i>N</i> -methyltransferase | S-adenosyl-L-methionine + nicotinamide = S-adenosyl-L-homocysteine + 1-methylnicotinamide | nicotinamide methyltransferase |
| | guanidinoacetate | S-adenosyl-L-methionine + guanidinoacetate = S-adenosyl-L-homocysteine + creatine | GA methylpherase; guanidinoacetate meth |



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EC Explorer

[browse EC tree] - [search] back to top EC Browser 1 Oxidoreductases (7908 organisms) 🖕 2 Transferases (5546 organisms) 📑 🖬 👘 🧖 🖕 2.1 Transferring one-carbon groups (1114 organisms) 📑 📼 🧖 🖕 2.1.1 Methyltransferases (963 organisms) 📑 💷 🦻 2.1.1.1 nicotinamide N-methyltransferase (6 organisms) 🛆 📑 📾 🦻 2.1.1.2 guanidinoacetate N-methyltransferase (9 organisms) 🚡 📑 🔤 🦻 2.1.1.3 thetin-homocysteine S-methyltransferase (1 organism) A Frame Frame 2.1.1.4 acetylserotonin O-methyltransferase (15 organisms) 🛆 📑 🛲 · 2.1.1.5 betaine—homocysteine S-methyltransferase (13 organisms) 🛆 📑 🛲 📑 📼 2.1.1.6 catechol O-methyltransferase (22 organisms) 🛆 🎫 – 2.1.1.7 nicotinate N-methyltransferase (5 organisms) 🛆 📑 📼 📑 2.1.1.8 histamine N-methyltransferase (9 organisms) 🛆 📑 2.1.1.9 thiol S-methyltransferase (19 organisms) 🛆 Press - 2.1.1.10 homocysteine S-methyltransferase (13 organisms) 🛽 📑 🏧 – 2.1.1.11 magnesium protoporphyrin IX methyltransferase (14 organisms) 🛆 📑 🛲 👘 – 2.1.1.12 methionine S-methyltransferase (15 organisms) 🛆 📑 🛲 📑 🚥 2.1.1.13 methionine synthase (28 organisms) 🛆 📑 📾 🦻 2.1.1.14 5-methyltetrahydropteroyltriglutamate—homocysteine S-methyltransferase (23 organisms) 🛆 📑 🛲 2.1.1.15 fatty-acid O-methyltransferase (4 organisms) 🛆 📑 🔤 2.1.1.16 methylene-fatty-acyl-phospholipid synthase (1 organism) 🛆 📑 📾 2.1.1.17 phosphatidylethanolamine 2.1.1.18 polysaccharide O-methyltr You can systematically click through the tree 2.1.1.19 trimethylsulfonium-tetrah until you reach the desired enzyme class. 2.1.1.20 glycine N-methyltransferas Sequences, reaction, flatfils can be displayed







BRENDA Exercises Taxonomic Tree





- Search the scientific name for yeast
- How many EC numbers and amino acid sequences are stored in BRENDA for this organism?
- How many synonyms are reported for this organism?







Tax Tree Explorer

| browse taxonomy tree] - [sear | ch] - 🔓 [Example] | |
|--|--|---|
| Scientific name or synony | m: exact 🔹 yeast | (use AND, OR, AN |
| type of synonym (optiona | al): all types of synonyms 🔹 | |
| NCBI Taxonomy I | D: = • | |
| Rar | nk: all types of ranks ▼ | |
| | Search | |
| 1 different results found | | |
| 1: yeast (Saccharomyces cere | evisiae) 🔻 | |
| cerevisiae û î 1405 aa sequences of Saccharomyces cerevisiae NCBI 4932 Found 2518 enzymes for Saccharomyces cerevisiae 1.1.1.1 Show enzyme Synonyms 1. Candida robusta 2. Saccaromyces | └ cellular organisms └ Eukaryota I (superkingdom) └ Opisthokonta I └ Fungi I (kingdom) └ Dikarya I (subkingdom) └ Ascomycota I (phylum) └ saccharomyceta I └ Saccharomyceta I └ Saccharomyceta I └ Saccharomyceta └ Saccharomyceta └ Saccharomyceta └ Saccharomyceta | ፪ (class) les ፪ (order) taceae ፪ (family) |

7405 amino acid sequences2518 EC classes15 synonyms

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BRENDA Exercises BTO





- How many terms in the BTO contain "skin"?
- How many EC numbers are stored in BRENDA for skin cancer cells?
- What is the definition of this term?







Ontology explorer

| - BTO (BRENDA Tissue Or | itology) | |
|---|--|--|
| Change ontology: | BTO (BRENDA Tissue Ontology) | ✓ Version 2015-04-30 |
| Term: | contains 🔻 skin | use AND (NOT) or OR |
| Synonym: | contains 🔻 | use AND (NOT) or OR |
| Definition: | contains 🔹 | use AND (NOT) or OR |
| restrict to BRENDA links: | | |
| Tissue | | |
| | search | |
| 12 different search results foun | d | |
| 3: foreskin keratinocyte cell lin 4: foreskin melanocyte cell lin 5: skin 6: skin cancer cell Details for skin cancer cell | e - | Tree view |
| | - tissues, cell types and enzyme sources t | issues, cell types and enzyme sources |
| cell | └ animal 1 └ whole body 1 | 占 tissues, cell types and enzyme sources fmm 占 animal fmm |
| BTO (BRENDA Tissue Ontology) ID | L integument | 占 whole body 111 |
| BTO:0001286 | └ skin ⑤ └ <mark>skin cancer cell</mark> | │ |
| BTO:0001286 is linked to 150 enzymes: | | |
| 1.1.1.42 - | | │ |
| Show enzyme | | 🖶 cancer stem cell 🚱 🗂 🗂 👘 |
| Definition | | |
| The two most common forms | | |



BRENDA Exercises Ligands



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- How many enzymes are affected by promethazine?
- Which enzymes are inhibited by this compound?
- Which enzyme can metabolize this compound and what is the product?
- What happens to the enzyme after the product is formed?

Exercise 13

- How many enzymes can metabolize cellobiose in an oxidative manner?
- How many enzyme can hydrolyze this compounds?

Exercise 14

- Display the structure of cellopentaose.
- What are the products of cellopentaose hydrolysis?



| Substrates and Products (Substrate) | celloplose | contains - | show 10 - results | | | |
|--|---|--------------------|-------------------|--|--|--|
| | Don't snow organism sp | ecific information | (fast!) | | | |
| | Search organism in taxonomic tree (slow, e.g. "mammalia" for rat,human,monkey,) | | | | | |
| | (Not possible to combine with the | ne first option) | | | | |
| Refine your search | | | | | | |
| Recommended Name: 🗵 | | contains - |] | | | |
| EC Number | 1. | ber ins with 👻 |] | | | |
| Commentary Substrates: | | contains - |] | | | |
| Organism: | | contains - |] | | | |
| Products: | | contains - |] | | | |
| Commentary (Products): | | contains - | | | | |
| Reversibility: | | contains - |] | | | |
| | Search | | | | | |

Tip: unclick all options for this search EC number begins with 1. gives 45 results

EC number begins with 3. (for hydrolases) gives 65 results

Search term: cellobiose



| EC Number 🔨 | Recommended Name | |
|-------------------------|-----------------------------------|--|
| 蒙诊 🌐 1.1.1.121 | aldose 1-dehydrogenase (NAD+) | |
| 診 诊 fft 1.1.1.47 | glucose 1-dehydrogenase [NAD(P)+] | |

Exercise 14: cellooligosaccharides and D-glucose





BRENDA Exercises Pathways



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- How many enzymes are part of the BRENDA pyrimidine metabolism?
- How many enzymes are part of the KEGG pyrimidine metabolism? •

Exercise 16

- Display the BRENDA interactive benzoyl-CoA degradation pathway ٠
- What is the final metabolite in this pathway?
- Show the molecule diagram, the molecular formula and the INChI key for this metabolite.



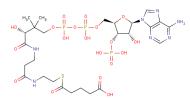


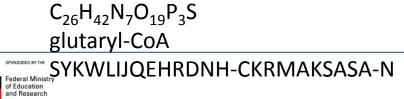
| Search Pathway | | 32 EC classes in the BRENDA |
|--|--------------------------------|-----------------------------|
| Patheav: pyrimidine meta Refine your search | bolism exact how 100 - results | pyrimidine metabolism |
| Recommended Name: Z | contains | 61 EC classes in the KEGG |
| KEGG Link: 🗵 | contains ▼ | pyrimidine metabolism |
| Source Data ase: V BRENDA | contains | |

Search term: pyrimidine metabolism

| end download all results as CSV | | | | | | | |
|---------------------------------|---|-----------------------|-----------|------------------|-----------------|--|--|
| EC Number VA | Recommended Name | Pathway 🔨 | KEGG Link | MetaCyc Link 🔨 📥 | Source Database | | |
| ≇ு் நி 1.3.1.2 | dihydropyrimidine dehydrogenase (NADP+) | pyrimidine metabolism | - | - | BRENDA | | |
| 診 合 fft 1.3.1.14 | dihvdroorotate dehvdrogenase (NAD+) | pvrimidine metabolism | - | - | BRENDA | | |

Results 1 - 32 of 32
 N





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BRENDA Exercises Sequences, Genomes





- Search for amino acid sequences of RUBISCO from soybean (if you can't remember the EC number or the recommened name for RUBISCO or the scientific name for the soybean you might try to find it in BRENDA by yourself. Of course your instructor can give valuable tips)
- Perform a BLAST with entry P00865 and find out how many other sequences can be matched with 100% identity.
- Find out the molecular weight and a literature reference for P00865.

Exercise 18

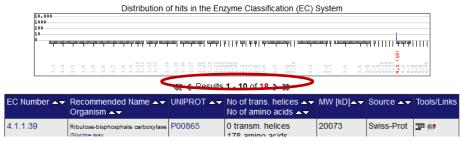
- Search for transferases in the genomes of the genus Solanum.
- Select 5 entries for visualization and look for enzyme details





Amino acid sequence search

| Amino acid Sequence: | contains • |
|----------------------------------|-------------------------|
| | |
| | |
| No. of results: | 10 🗸 |
| Recommended name: (of enzyme) | contains - |
| EC Number: | exact 🗸 4.1.1.39 |
| 1st Accession Code: (UniProt) | contains - |
| Organism: | colitains - glycine max |
| Number of amino acids: | |
| Molecular weight [Da]: | |
| Transmembrane helices: | |
| N-terminus: | inside outside |
| Source: | SwissProt TREMBL |
| | search reset |

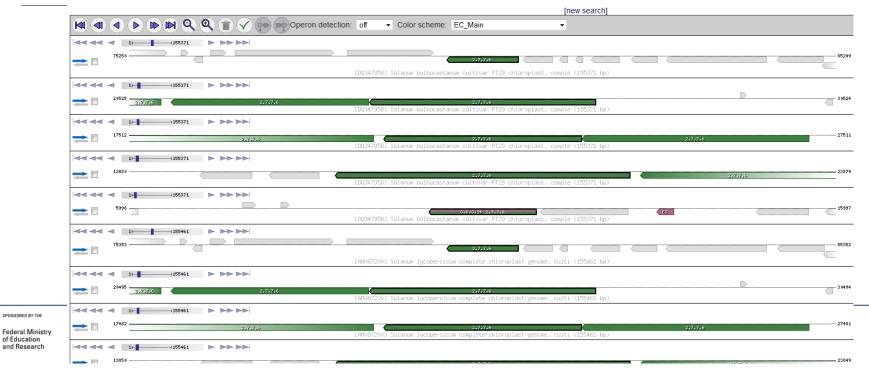








| | | honeive Fre | une a bufe see able a | e | the set | | |
|---|--|---|-----------------------|-------|--|-----------------------------------|--------|
| Available genomes: down CTRL or SHIFT to select multiple genomes) | Elkaryota Solanum bulbocastanum cultivar PT29 chloroplast Solanum lycopersicum chromosome ch01 Solanum lycopersicum chromosome ch02 Solanum lycopersicum chromosome ch04 Solanum lycopersicum chromosome ch04 Solanum lycopersicum chromosome ch05 | Please select one or more genomes from below for vis Visualize selected Visualize selecte | | | e or more genomes from below for visualization. isualize selected Visualize i Results r - 20 of 85 C | alization. EC Number Accession | |
| Organism: | Solanum lycopersicum chromosome ch06 | | Solanum bulbocastanum | rpoA | RNA polymerase alpha subunit DNA-directed RNA polymerase subunit alpha Plastid-encoded RNA polymerase subunit alpha | 2.7.7.6 | Q2MIF6 |
| Taxonomy: | begins with | | Solanum bulbocastanum | rpoB | RNA polymerase beta subunit DNA-directed RNA polymerase subunit beta PEP Plastid-encoded RNA polymerase subunit beta | <mark>2.</mark> 7.7.6 | Q2MIJ5 |
| EC Number- UniProt Accession: | exact | | Solanum bulbocastanum | rpoC1 | RNA polymerase beta subunit DNA-directed RNA polymerase subunit beta' PEP Plastid-encoded RNA polymerase subunit beta' | <mark>2.</mark> 7.7.6 | Q2MIJ6 |
| Protein Name: Max. number of results: | exact | | Solanum bulbocastanum | rpoC2 | RNA polymerase beta' subunit DNA-directed RNA polymerase subunit beta'' PEP Plastid-encoded RNA polymerase subunit beta'' | <mark>2.</mark> 7.7.6 | Q2MIJ7 |
| | □ Display homolog proteins with min. ○ 50% ○ 90% ○ | 10 | Solanum bulbocastanum | atpA | | 3.6.3.14 <mark>2.</mark> 7.7.6 | Q2MIK2 |
| Genome | Explorer | | | | | | |





BRENDA Exercises Exploring more Features



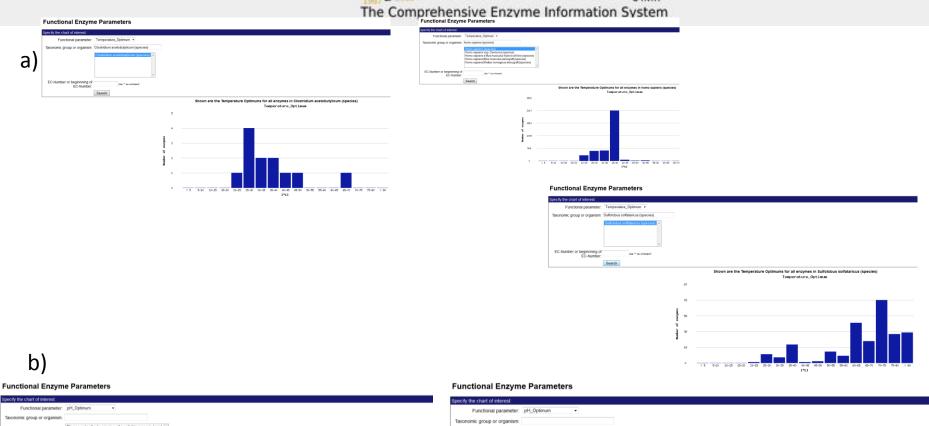


Extra Exercises

- a) Organisms and their enzymes are adapted to the environment in which they live. Use the search option **Functional Parameters** to display the temperature optimum for the enzymes of Clostridium acetobutylicum, Homo sapiens, and Sulfolobus solfataricus to display the optimal temperatures. Can you detect differences?
- b) The pH optima of enzyme-catalyzed reactions often depends on the type of reaction. Redox reactions are catalyzed best at neutral pH-values. Hydrolytic reactions require different conditions. Display the pH optima for oxidoreductases acting on C-OH bond with NAD(P)+ as cofactors. Then display the pH optima for serine endopeptidases. (Note: you may have to consult the EC Explorer to find out the EC subclasses for these enzymes)



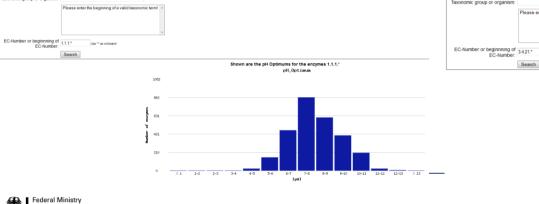




Please enter the beginning of a valid taxonomic term! -

Use ** as wildcard!

Search



of Education and Research

Shown are the pH Optimums for the enzymes 3.4.21.* pH_Optimum 377 302 226 Ja Ja 151 < 1 1-2 2-3 0 11-12 12-13 > 13 3-4 4-5 7-8 8-9 9-10 5-6 6-7

[pH]