

Module 7

Enzymatic Function

Verifying enzymatic function of your gene product if working with an enzyme

Question to Answer:

Can you verify if your gene has enzymatic function?

Is your protein a part of a pathway or a system

Objectives

1. Document pathways or processes in which the protein functions
2. If your protein is an enzyme
 - Determine Enzyme Commission (EC) Number

Notebook

Enzymatic Function Module

Module Instructions

KEGG

go to <http://www.genome.jp/kegg/pathway.html>

KEGG pathway ID

Pathway map

MetaCyc

go to <http://metacyc.org/>

Pathway map

E.C. Number

<http://www.expasy.ch/enzyme/enzyme-search-ec.html>

EC Number

EC Name

EC Number

Summarize the results of the enzymatic function module in the box below.

What are Enzymes??

Enzymes: proteins that act as catalysts for reaction in cells and organisms

1. A catalyst speeds up the rate of a chemical reaction (no change)
2. Enzymes can be
 1. intracellular (speed up reactions) and
 2. extracellular enzymes (let out to work in systems like digestive)
3. Enzymes are highly specific and takes part in metabolic reactions from the digestion of food to the synthesis of DNA, to clotting of blood.
 1. Enzymes can build UP (**anabolic**)
 2. break down substances (**catabolic**)
4. Most enzymes are proteins, although some catalytic RNA molecules have been identified.

Does the protein of interest have enzymatic function?

GENI-ACT

Select Team

Selected Team: Instructor Demonstration Genes - Rama

Switch to Hrithik Bagga

Switch to Stephen Vasquez

Switch to Dhruv Prasad

Switch to Yvette Rodriguez

Switch to Emily Brooks

Switch to Jillian O'Shaughnessy

Switch to Syed Adnan Uddin

Switch to Erica Wicher

Switch to Matthew Spink

Switch to Aparna Viswanathan

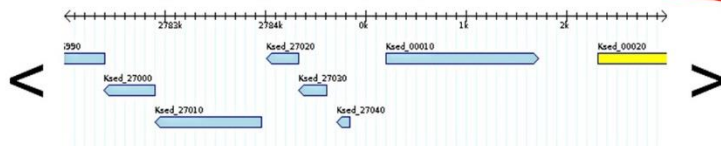
Team Overview

Select Team Assignment

Selected Locus: KSED_RS00010

Change Selection

click



Locus Ksed_00020

Coordinates 2317..3453

Length 1137/378

Gene Name

Gene Products DNA polymerase III, beta subunit

Note

PFAM: DNA polymerase III beta subunit, C-terminal domain; DNA polymerase III beta subunit, central domain; DNA polymerase III beta subunit, N-terminal domain; TIGRFAM: DNA polymerase III, beta subunit

Go to the [gene details](#) page in GENI-ACT and look at the product name.

If your gene ends in “**ase**” it is probably an enzyme and further investigation is required!

A Word of Caution...

Gene Information	
Gene Object ID	2500607918
Gene Symbol	
Locus Tag	PlimDRAFT_27940
Product Name	ABC-type branched-chain amino acid transport system, permease component
IMG Product Source	COG4177

A permease is **NOT** an enzyme...just a membrane transport protein facilitating the diffusion of a specific molecule in or out of the cell by passive transport.

KEGG

Kyoto Encyclopedia of Genes and Genomes

- KEGG is a database of biological information compiled from published material.
- Includes information on genes, proteins and metabolic pathways for specific organisms and how these components are organized in the cell.

The Good: Information is reliable!

The Bad: Information is not available for many organisms, for e.g. *Kytococcus*. We may have to rely on information from other organisms.



SOP – KEGG PATHWAY


- First choose the name of your protein of interest from Notebook.
- Decide whether to start with nr or SP database results
- Click on link: <https://www.genome.jp/kegg/pathway.html>
- Select Menu on left panel – click on KEGG2 in drop-down menu
- Add short name in Search window (you have to try all names that you see associated with BLAST results.) Hit Go.
- It returns an interface which users can examine for KEGG Orthology
- Click on the first ortholog. This orthology interface allows one to examine EC Number, Pathways ko #, BRITE hierarchy, Reaction (RN#) as well as the different gene from different organisms. Get familiar with EC #.
- Copy and paste any information into notebook. The more information you keep about your gene of interest in your notebook the better to understand your gene.
- Once you find the generic pathway the gene of interest is in red surrounded by a red box. Next, you can check if the gene has been called in *Kytococcus*
- For that go to top of page and in the search window labeled Reference pathway (KO) start typing *Kytococcus sedentarius*, select and Hit Go.
- You should check to see if the EC # is in a green box =called in K.sed. If in white box uncalled. Keep both Pathway maps in notebook.

GENI-ACT

Gene Details page

Microbial Genomics / *Kytococcus sedentarius* DSM 20547 / NC_013169 / KSED_RS02105 ★

Gene Browser (reset)



425k 426k 427k 428k 429k 430k

KSED_RS02100 KSED_RS02105 KSED_RS02110

Genome
Kytococcus sedentarius DSM 20547

Replicon
NC_013169

Locus
KSED_RS02105

Coordinates
complement(427153..428313)

Old Locus Tag
Ksed_04340

Products
sarcosine oxidase subunit beta

Length
1161 / 386

>KSED_RS02105-Ksed_04340-aa sequence

```
MSDQNFPTRRARVVVIGGGVMGLSTAYHLAKQGVQDVVLVERGELGAGSTCKAAGGVRAQFSDAV
NIELGMRSLEVFNRNPELFDQDIDLDECYGLFLLEREEDLRTFERNVELQRSMGLESRITSVEE
AKELSPLISTEGLIAGVWSPEAGHCTPESVVQGYARAARALGVRIIRHCEVTDVVREGDTITSV
ETAQGSIATD'TVCCAGAWSRALGDMVGVLDLPVDPVRRRELLVTEPMPDL PANVPFTIDFST'TMY
FHREGPGLLVGMSNQDEE PGFSLEHTDEWLEQVVEAAGRVPVLEEVGMASRWAGLYEVTDPHNALIGEAEVSRFLYATGFSGHGFLQGPVAVGQVMAELYLGQTP
SVDVTALHGRRFEGAGLRPEFN IV
```

BLAST – Best Choice

nr database



FAD-binding oxidoreductase
[Propionibacteriaceae bacterium]
sarcosine oxidase subunit beta
[Propionibacteriaceae bacterium NML 030167]

SP database



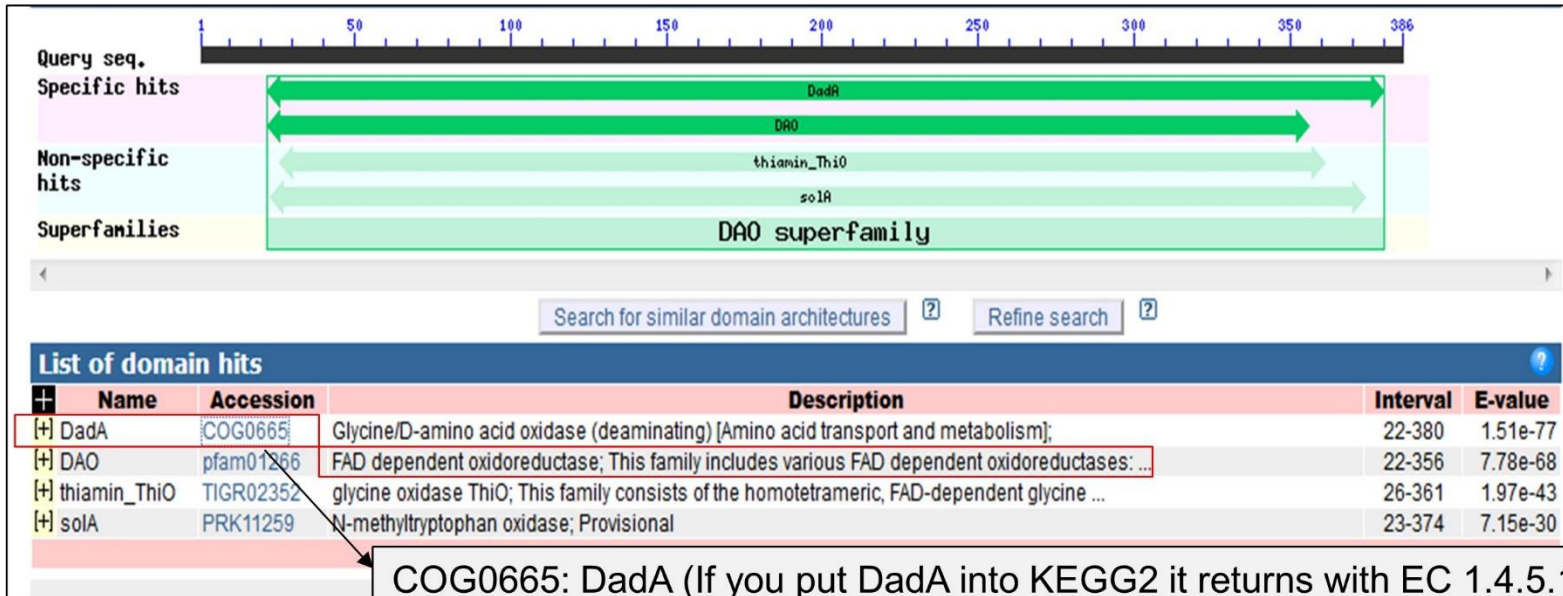
Sarcosine dehydrogenase, mitochondrial; Short=SarDH; (oxidoreductase)
Rattus norvegicus

BLAST:

- 1) FAD-binding oxidoreductase (Propionibacteriaceae)
- 2) Sarcosine oxidase subunit beta (Propionibacteriaceae)

Best choice

CDD Search



COG0665: DadA (If you put DadA into KEGG2 it returns with EC 1.4.5.1 D-amino-acid dehydrogenase which is not called in K Sed. And incl in phenylalanine metabolism

COG0665 is a member of the DAO superfamily **CI26293**.

CI26293 : FAD dependent oxidoreductase (Flavin adenine dinucleotide= FAD)

This family includes various **FAD dependent oxidoreductases**: **Glycerol-3-phosphate dehydrogenase** EC:1.1.99.5, **Sarcosine oxidase beta subunit** EC:1.5.3.1, **D-alanine oxidase** EC:1.4.99.1, **D-aspartate oxidase** EC:1.4.3.1.

BLAST:

- 1) FAD-binding oxidoreductase (Propionibacteriaceae)
- 2) Sarcosine oxidase subunit beta (Propionibacteriaceae)

KEGG Pathway Database

<https://www.genome.jp/kegg/pathway.html>

CLICK Menu



KEGG PATHWAY Database

Wiring diagrams of molecular interactions, reactions and relations

Menu PATHWAY BRITE MODULE KO GENES LIGAND NETWORK DISEASE DRUG DBGET

KEGG Select prefix

Enter keywords

KEGG2

Organism

Go

Help

PATHWAY

BRITE

MODULE **Maps**

KO

GENOME

GENES

SSDB

Annotation

SeqData

Pathogen

Virus

Plant

LIGAND

COMPOUND

CLICK KEGG2

[[New pathway maps](#) | [Update history](#)]

KEGG PATHWAY is a collection of manually drawn pathway maps representing our knowledge on the molecular interaction, reaction and relation networks for:

1. Metabolism

[Global/overview](#) [Carbohydrate](#) [Energy](#) [Lipid](#) [Nucleotide](#) [Amino acid](#) [Other amino](#) [Glycan](#)
[Cofactor/vitamin](#) [Terpenoid/PK](#) [Other secondary metabolite](#) [Xenobiotics](#) [Chemical structure](#)

Genetic Information Processing

Environmental Information Processing

4. Cellular Processes

5. Organismal Systems

6. Human Diseases

Drug Development



KEGG - Table of Contents

Put in the name of the protein in search window

Menu **PATHWAY** BRITE MODULE KO GENOME GENES LIGAND DISEASES

Search for


Data-oriented entry points

Category	Entry Point	Content	DBGET Search
Systems information	KEGG PATHWAY	KEGG pathway maps	PATHWAY
	KEGG BRITE	BRITE hierarchies and tables	BRITE
	KEGG MODULE	KEGG modules	MODULE
Genomic information	KO (KEGG Orthology)	Functional orthologs	ORTHOLOGY
	KEGG GENOME	KEGG organisms (complete genomes)	GENOME
	KEGG GENES KEGG SSDB	Genes and proteins GENES sequence similarity	GENES
Chemical information (KEGG LIGAND)	KEGG COMPOUND	Small molecules	COMPOUND
	KEGG GLYCAN	Glycans	GLYCAN
	KEGG REACTION	Reactions and reaction classes	REACTION RCLASS
	KEGG ENZYME	Enzyme nomenclature	ENZYME
Health information	KEGG DISEASE	Human diseases	DISEASE
	KEGG DRUG	Drugs and drug groups	DRUG DGROUP
	KEGG ENVIRON	Health related substances	ENVIRON
	KEGG MEDICUS	Japanese drug labels (JAPIC) FDA drug labels (DailyMed)	

KEGG is developed by Kanehisa Laboratories. See Kanehisa et al. (2017) for updates of KEGG.

Subject-oriented entry points

SEARCH Term : sarcosine oxidase

 Search for

Database: KEGG - Search term: sarcosine oxidase

KEGG BRITE

ko00001
KO; KEGG Orthology (KO)
ko01000
Enzyme; Enzymes

KEGG ORTHOLOGY

K00301
E1.5.3.1; sarcosine oxidase [EC:1.5.3.1]
K00302
soxA; sarcosine oxidase, subunit alpha [EC:1.5.3.1]
K00303
soxB; sarcosine oxidase, subunit beta [EC:1.5.3.1]
K00304
soxD; sarcosine oxidase, subunit delta [EC:1.5.3.1]
K00305
soxG; sarcosine oxidase, subunit gamma [EC:1.5.3.1]
... » display all

KEGG GENES

hsa:51268
PIPOX, LPIPOX; pipecolic acid oxidase (EC:1.5.3.1 1.5.3.7); K00306 sarcosine oxidase / L-pipecolate oxidase [EC:1.5.3.1 1.5.3.7]
ptr:454541
PIPOX; pipecolic acid oxidase; K00306 sarcosine oxidase / L-pipecolate oxidase [EC:1.5.3.1 1.5.3.7]
pps:100992747
PIPOX; pipecolic acid oxidase; K00306 sarcosine oxidase / L-pipecolate oxidase [EC:1.5.3.1 1.5.3.7]
ggo:101145672
PIPOX; peroxisomal sarcosine oxidase; K00306 sarcosine oxidase / L-pipecolate oxidase [EC:1.5.3.1 1.5.3.7]
pon:100172798
PIPOX; pipecolic acid oxidase; K00306 sarcosine oxidase / L-pipecolate oxidase [EC:1.5.3.1 1.5.3.7]
... » display all

KEGG DGENES

T10005:8761
K00306 sarcosine oxidase / L-pipecolate oxidase [EC:1.5.3.1 1.5.3.7]
T10016:PHUM240800
monomeric sarcosine oxidase, putative; K18166 FAD-dependent oxidoreductase domain-containing protein 1

Entry	K00301	KO
Name	E1.5.3.1	
Definition	sarcosine oxidase [EC:1.5.3.1]	
Pathway	ko00260 Glycine, serine and threonine metabolism ko01100 Metabolic pathways	
Brite	KEGG Orthology (KO) [BR:ko00001] 09100 Metabolism 09105 Amino acid metabolism 00260 Glycine, serine and threonine metabolism K00301 E1.5.3.1; sarcosine oxidase Enzymes [BR:ko01000] 1. Oxidoreductases 1.5 Acting on the CH-NH group of donors 1.5.3 With oxygen as acceptor 1.5.3.1 sarcosine oxidase K00301 E1.5.3.1; sarcosine oxidase BRITE hierarchy	
Other DBs	RN: R00610 COG: COG0665 GO: 0008115	
Genes	HAA: A5892_09805 BMQ: BMQ_1540 BMD: BMD_1521 BMH: BMWSH_3689(solA) BMEG: BG04_3832(soxA) PBJ: VN24_07410 TMR: Tmar_0598 MAV: MAV_0142 MMC: Mmcs_2460 MKM: Mkms_2505 » show all Taxonomy KOALA UniProt	
Reference	PMID:10220347 Authors Wagner MA, Khanna P, Jorns MS Title Structure of the flavocoenzyme of two homologous amine oxidases: monomeric sarcosine oxidase and N-methyltryptophan oxidase. Journal Biochemistry 38:5588-95 (1999) DOI:10.1021/bi9829550	

1. EC NUMBER 1.5.3.1

3. Click for pathways

2. Click for reaction

Reaction



REACTION: R00610

[Help](#)

Entry	R00610	Reaction
Name	sarcosine:oxygen oxidoreductase (demethylating)	
Definition	Sarcosine + H ₂ O + Oxygen \rightleftharpoons Glycine + Formaldehyde + Hydrogen peroxide	
Equation	C00213 + C00001 + C00007 \rightleftharpoons C00037 + C00067 + C00027	
RPair	RP00006 C00007_C00027 cofac [RC:RC02755] RP00161 C00037_C00213 main [RC:RC00060] RP05693 C00001_C00067 leave RP05940 C00067_C00213 main [RC:RC00557]	
Enzyme	1.5.3.1	
Pathway	rn00260 Glycine, serine and threonine metabolism rn01100 Metabolic pathways	
Orthology	K00301 sarcosine oxidase [EC:1.5.3.1] K00302 sarcosine oxidase, subunit alpha [EC:1.5.3.1] K00303 sarcosine oxidase, subunit beta [EC:1.5.3.1] K00304 sarcosine oxidase, subunit delta [EC:1.5.3.1] K00305 sarcosine oxidase, subunit gamma [EC:1.5.3.1] K00306 sarcosine oxidase / L-pipecolate oxidase [EC:1.5.3.1 1.5.3.7]	



Substrate

Product

Sarcosine oxidase is the enzyme (EC1.5.3.1) that catalyzes the oxidative demethylation of sarcosine to yield formaldehyde, H₂O₂, and glycine,

Entry	K00301	KO
Name	E1.5.3.1	
Definition	sarcosine oxidase [EC:1.5.3.1]	
Pathway	ko00260 Glycine, serine and threonine metabolism ko01100 Metabolic pathways	
Brite	KEGG Orthology (KO) [BR:ko00001] 09100 Metabolism 09105 Amino acid metabolism 00260 Glycine, serine and threonine metabolism K00301 E1.5.3.1; sarcosine oxidase Enzymes [BR:ko01000] 1. Oxidoreductases 1.5 Acting on the CH-NH group of donors 1.5.3 With oxygen as acceptor 1.5.3.1 sarcosine oxidase K00301 E1.5.3.1; sarcosine oxidase BRITE hierarchy	
Other DBs	RN: R00610 COG: COG0665 GO: 0008115	
Genes	HAA: A5892_09805 BMQ: BMQ_1540 BMD: BMD_1521 BMH: BMWSH_3689(solA) BMEG: BG04_3832(soxA) PBJ: VN24_07410 TMR: Tmar_0598 MAV: MAV_0142 MMC: Mmcs_2460 MKM: Mkms_2505 » show all Taxonomy KOALA UniProt	
Reference	PMID: 10220347 Authors Wagner MA, Khanna P, Jorns MS Title Structure of the flavocoenzyme of two homologous amine oxidases: monomeric sarcosine oxidase and N-methyltryptophan oxidase. Journal <i>Biochemistry</i> 38:5588-95 (1999) DOI: 10.1021/bi9829550	

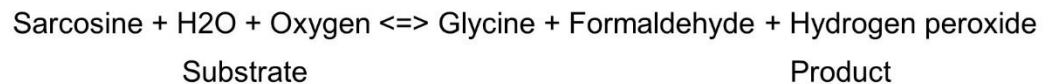
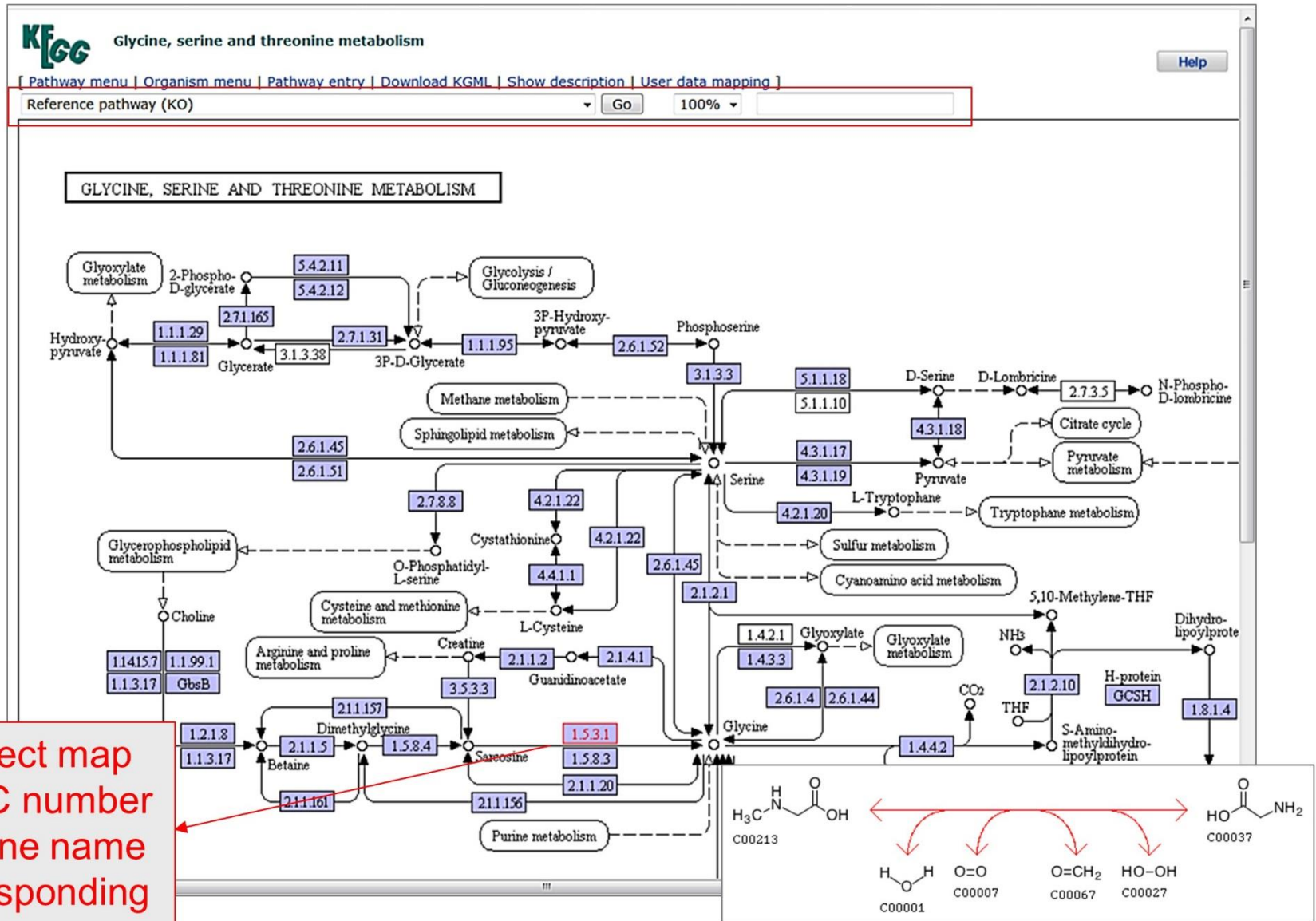
1. EC NUMBER 1.5.3.1

2. Click for reaction

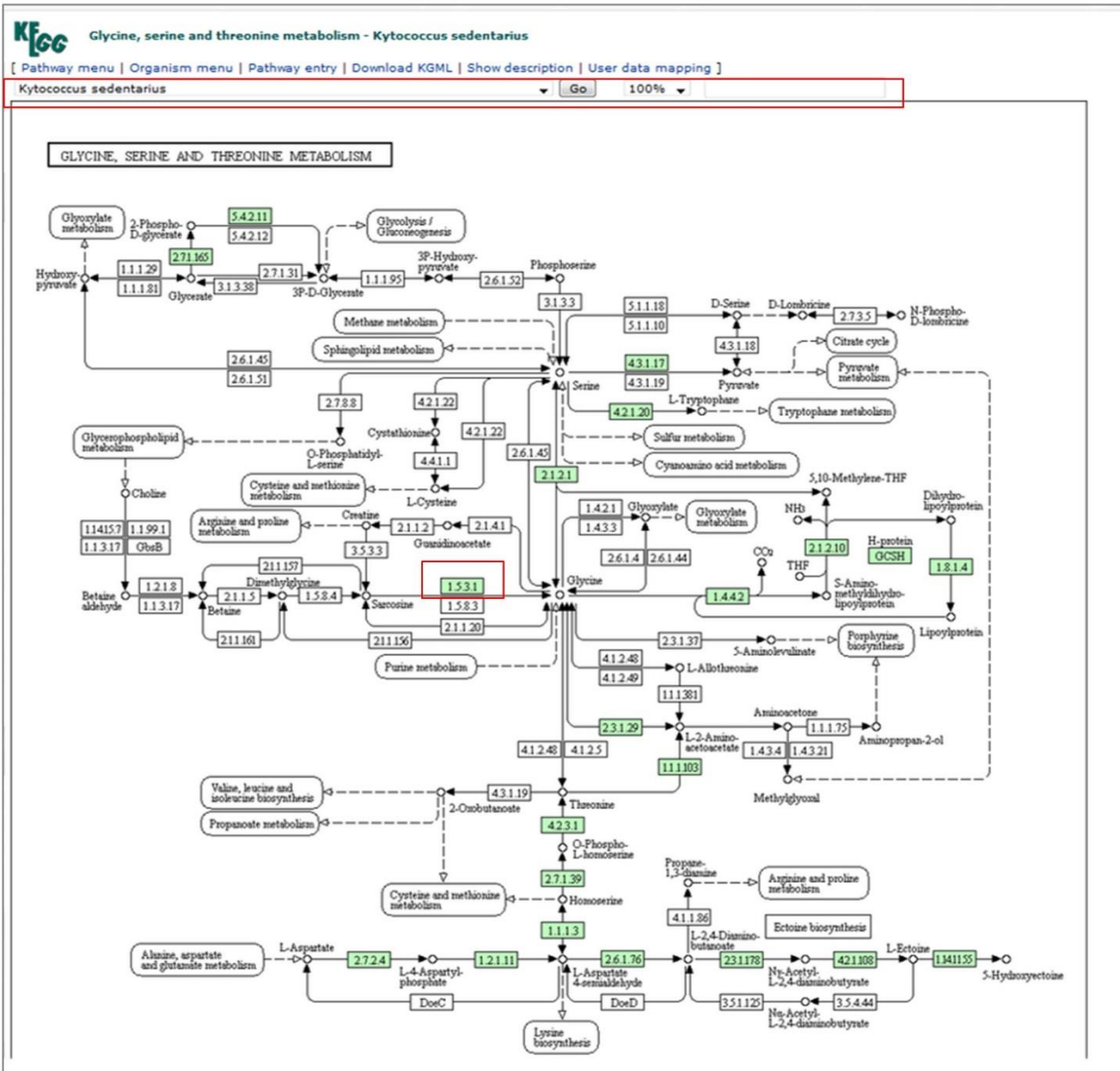
3. Click for pathways

Ko 00260: Amino acid metabolism

Glycine, Serine, and Threonine Metabolism



In *Kytococcus sedentarius*



If you start typing *Kytococcus sedentarius* in the search window and hit Go

you will be taken to the same pathway which will be annotated and color coded specifically for the genes in the pathway that have been called in *Kytococcus sedentarius*

IMPORTANT

1. Even if the gene does not appear to be an enzyme by name, still perform the KEGG search and report any pathway information, but make a note that the gene has “no enzymatic function”
2. Your gene may function in more than one pathway in the cell

E.g. Ksed_00010_RS00005

>Ksed_00010

```
MSQTPDDHATAIWQEAMVHLQGAGLAPRDIGVLRRLATLVGLLEGTALLAVKYDHVKDAVEGHLR
EDVSTALAEVLDRDIRLAVSVDPAVSAAQEEAAPPAPSPADEDDPATGEGPLSTAVDGAVEKH
EGSSPARAGESVAPATTASLTATNSSPGVERDYSALNHKYTFDTFVLGSSNRFAHAAATAVAEA
PARAYNPLFIYGGSGLGKTHLLHAIGHYARTLDSSVRVKYVNSEEFNQNQFINAVSAGQANAFQR
QYRDVDVLLIDDIQFLQGKEQTMEEFFHTFNTLHNSEKQIVITSDQPPKKLSGFAERMRSRFEW
GLLTDVQPPDLETRIAILRRKAAADKLDIPDDVLHLIASKISSNIRELEGALTRVTAFASLSGS
PLDEYLARTVLKDVMPGGDSGQITPTMILEETAGYFVISVEEIQGASRSRNLTRARQIAMYLRCR
ELTDLSLPKIGKEFGGRDHTTVMHAERKIKQLLGEDRRVYDEVSELTSIIRKKAARGR
```

Example 1 : Gene : Ksed_00010

Chromosomal replication initiator protein



KEGG - Table of Contents

[COG0593: DnaA](#)

Chromosomal replication initiation ATPase DnaA

KEGG2 PATHWAY BRITE MODULE KO GENOME GENES LIGAND DISEASE DRUG DBGET

Search for

Category	Entry Point	Search & Compute	DBGET Search
Systems information	KEGG PATHWAY	Search Pathway	PATHWAY
	KEGG BRITE	Search Brite	BRITE
	KEGG MODULE	Reconstruct Module	MODULE
	KEGG Mapper	Map Taxonomy	
	KEGG Atlas		
Genomic information	KEGG ORTHOLOGY	BlastKOALA <i>New!</i>	ORTHOLOGY
	KEGG Annotation	KO system	
	KEGG GENOME	SSDB search	GENOME
	KEGG GENES	OC viewer†	GENES DGENES
	KEGG Organisms [Species Genus]	BLAST† / FASTA† KAAS†	MGENOME† MGENES†
	KEGG LIGAND	SIMCOMP† / SUBCOMP†	

Example 1 : Gene : Ksed_00010 or RS 00005

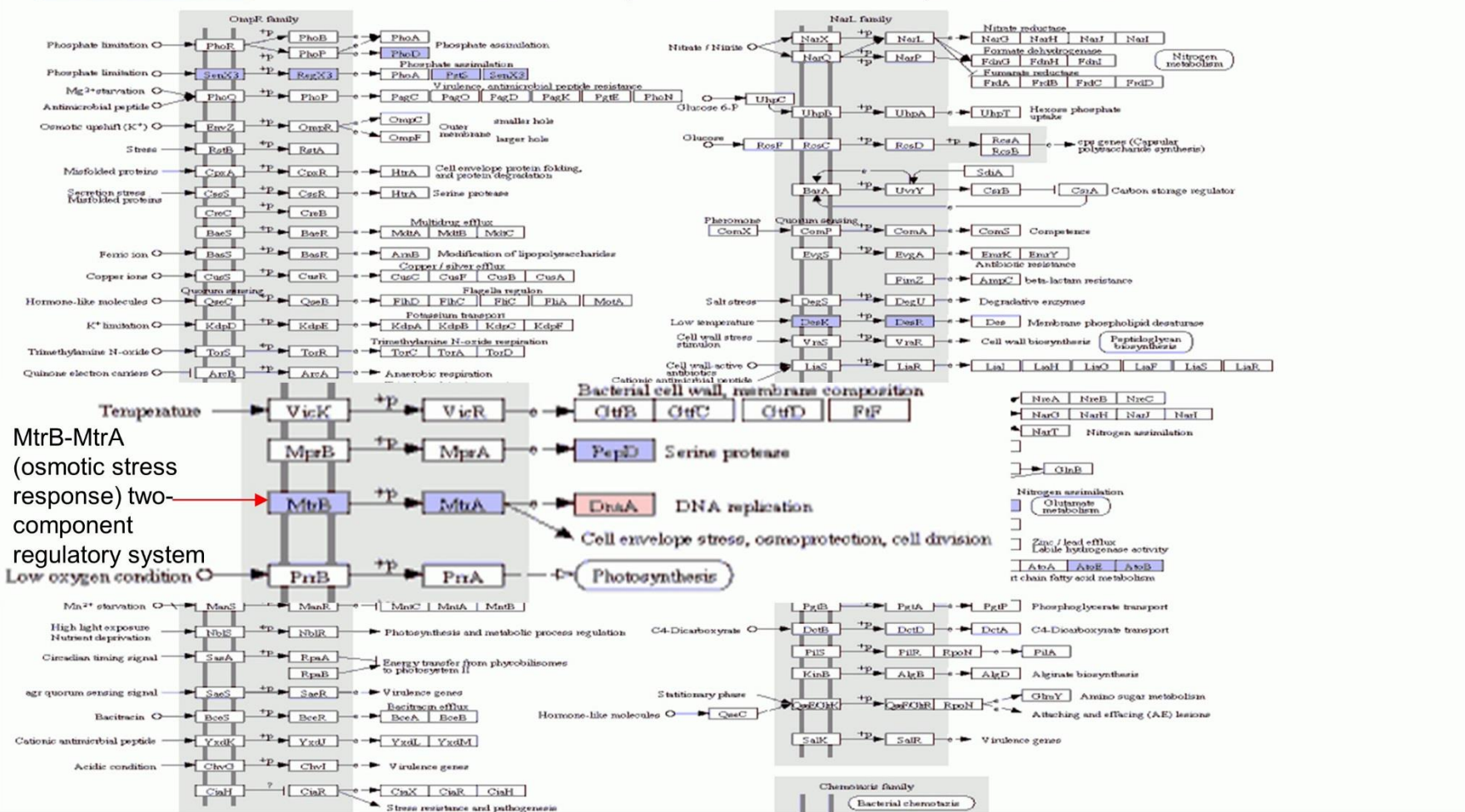
KEGG ORTHOLOGY: K02313 [Help](#)

Entry	K02313 KO
Name	dnaA
Definition	chromosomal replication initiator protein
Pathway	ko02020 Two-component system ko04112 Cell cycle - Caulobacter
Brite	KEGG Orthology (KO) [BR:ko00001] Environmental Information Processing Signal transduction 02020 Two-component system K02313 dnaA; chromosomal replication initiator pro Cellular Processes Cell growth and death 04112 Cell cycle - Caulobacter K02313 dnaA; chromosomal replication initiator pro DNA replication proteins [BR:ko03032] Prokaryotic Type DNA Replication Initiation Factors Initiation factors (bacterial) K02313 dnaA; chromosomal replication initiator pro Chromosome [BR:ko03036] Prokaryotic Type Nucleoid associated proteins Other nucleoid associated proteins K02313 dnaA; chromosomal replication initiator pro BRITE hierarchy
Genes	ECO: b3702 (dnaA) ECJ: Y75_p3471 (dnaA) EBW: BWG_3392 (dnaA) ECOK: ECMDS42_3138 (dnaA) ECE: Z5193 (dnaA) ECS: ECs4637 (dnaA) ECF: ECH74115_5130 (dnaA) ETW: ECSP_4748 (dnaA) ELX: CDCO157_4373 (dnaA) EOJ: ECO26_4880 (dnaA) » show all Taxonomy KOALA UniProt
Reference	DMTD-10551881

Ko-02020- 2 Component System: Environment information processing

Signal transduction

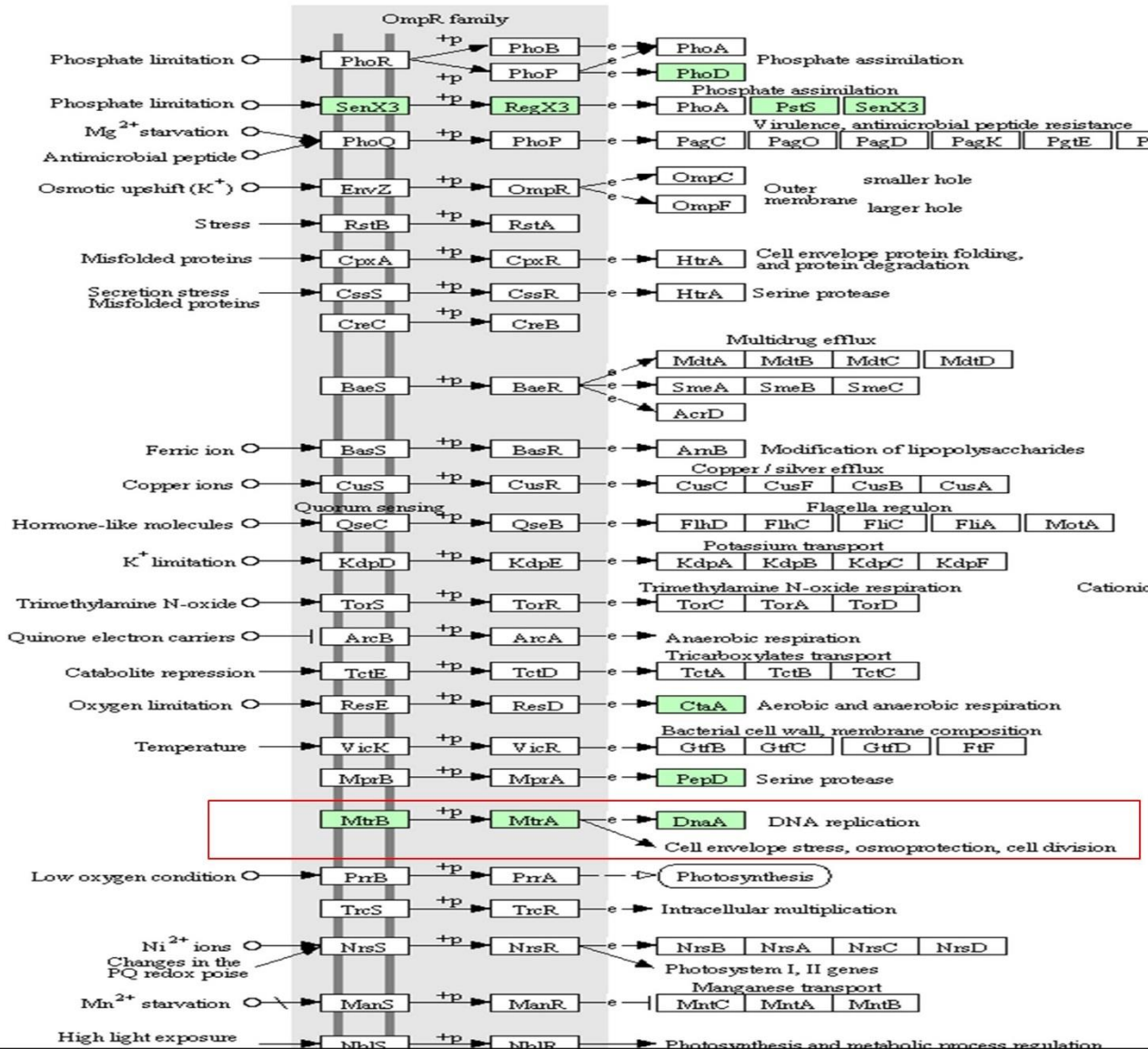
chromosomal replication initiator protein DnaA



Two-component signal transduction systems enable bacteria to sense, respond, and adapt to changes in their environment or in their intracellular state. Two-component pathways thus often enable cells to sense and respond to stimuli by inducing changes in transcription. In this case it is osmotic stress.

Your current gene is highlighted
in pink.
Scroll down to find it.

TWO-COMPONENT SYSTEM



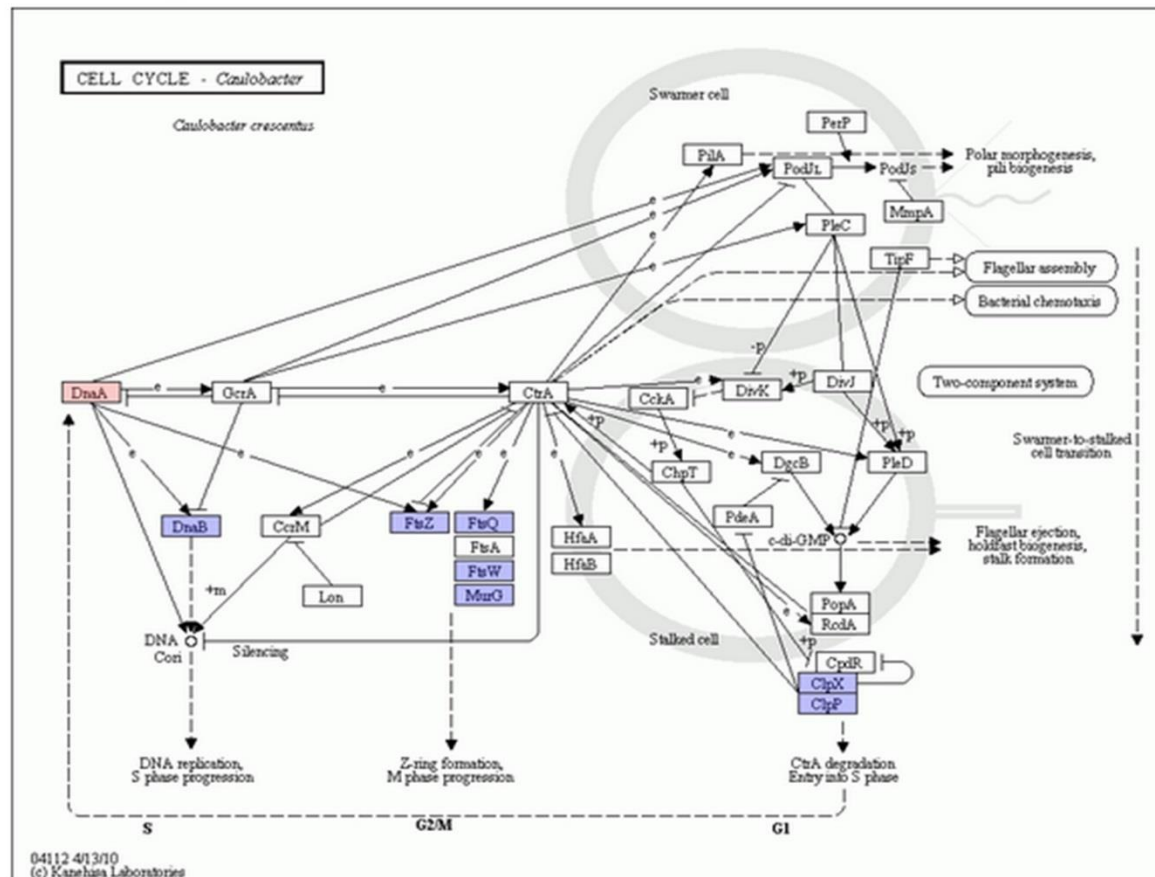
If you start typing *Kytococcus sedentarius* in the search window and hit Go you will be taken to the same pathway which will be annotated and color coded specifically for the genes in the pathway that have been called in *Kytococcus sedentarius*

Ksed_00010 : Cellular Processes : Cell growth and death

KEGG Map

Current Genome: [Kytococcus sedentarius 541, DSM 20547](#)
Current Gene: [644990317 \[Ksed_00010\]](#)

■ Current Gene
■ Positional Cluster Gene
■ Other genes in *Kytococcus sedentarius* 541, DSM 20547
■ Genes found in other genomes



[Pathway Details](#)

The division process is centered around three master regulator proteins, DnaA, GcrA, and CtrA. DnaA and GcrA together drive the synthesis of proteins needed to complete DNA replication.

DnaA is highlighted in pink.

In this case the cell cycle from *Caulobacter* has been shown

MetaCyc



-MetaCyc is a curated database of nonredundant, experimentally elucidated metabolic pathways

-The goal of MetaCyc is to catalog the universe of metabolism by storing a representative sample of each experimentally elucidated pathway

SOP MetaCyc

- Go to <http://metacyc.org/>
- Enter the EC # Quick Search
- Results 3 proteins, 1 Reaction and 1 EC #
- Click on the actual reaction
- Look for “In Pathway”
- In this case creatinine degradation II, creatinine degradation I, glycine betaine degradation I
- Look at descriptions below and copy whatever is necessary to understand the function of the gene under study
- Select each and read up and keep as much information in notebook as helps you.
- Look at schematic gene reaction

1.5.3.1 in Quick Search window

metacyc.org/META/substring-search?type=NIL&object=1.5.3.1&quickSearch=Quick+Search

Getting Started Most Visited Google Facebook Pubmed Blackboard Learn SID UB Lib geni-act mgan WNY-NSF COE sharepoint HGNC database of hu... GeneCards - Human G... Twitter STELAR - STEM Learn...

META CYC A member of the BioCyc database collection

Metabolic Modeling Tutorial registration ends Sat Mar 7th, 2015

1.5.3.1 Searching MetaCyc change organism database

Sites Search Genome Metabolism Analysis SmartTables Help

Search Results for 1.5.3.1

using database MetaCyc [what is this?](#)

Proteins (3) | Reactions (1) | EC Numbers (1)

Proteins Gene/Gene Product pages contain: chromosomal location of gene; depiction of its operon; link to genome browser; detailed summaries and citations; subunit structure (for protein complexes); cofactors, activators, and inhibitors (for enzymes), depiction of regulon (for transcriptional regulators), protein features.

- sarcosine oxidase - *Achromobacter denitrificans*
- sarcosine oxidase - *Arthrobacter sp. TE1826*
- sarcosine oxidase - *Corynebacterium sp.*

Turn into a temporary SmartTable or log in to turn into a permanent SmartTable.

Reactions Reaction pages contain: reaction equation with chemical structures, links to all enzymes that catalyze the reaction, and all pathways in which the reaction participates.

- sarcosine + oxygen + H₂O → glycine + formaldehyde + hydrogen peroxide

Click

Turn into a temporary SmartTable or log in to turn into a permanent SmartTable.

EC Numbers EC Number pages contain: links to reaction and enzymes associated with the EC number in this database, names, description, citations, etc. from the Enzyme Commission ontology.

- 1.5.3.1 -- sarcosine oxidase

Turn into a temporary SmartTable or log in to turn into a permanent SmartTable.

Report Errors or Provide Feedback
Page generated by SRI International Pathway Tools version 18.5 on Tue Mar 10, 2015, BIOCYC148.
MetaCyc version 18.5.

Alternative searches:

- Full text search for 1.5.3.1 on all pages in this database using Google
- Full text search for 1.5.3.1 on all pages of this website using Google

Reaction Schematic + Pathways

metacyc.org/META/NEW-IMAGE?type=REACTION&object=SARCOX-RXN

Reactions Classified By Substrate → Small-Molecule Reactions

EC Number: 1.5.3.1

Enzymes and Genes:
sarcosine oxidase (Achromacter denitrificans)
sarcosine oxidase : soxA (Arthrobacter sp. TE1826)
sarcosine oxidase : soxA, soxB, soxG, soxD (Corynebacterium sp.)

In Pathway: creatinine degradation II, creatinine degradation I, glycine betaine degradation

Show Atom Mapping: Coloring? Atom Numbering?

CC(N)C(=O)C(=O)[O-] + O=O + O → CC(N)C(=O)C(=O)[O-] + C=O + OO
sarcosine + oxygen + H₂O → glycine + formaldehyde + hydrogen peroxide

Can Keep in Notebook

The reaction direction shown, that is, A + B ↔ C + D versus C + D ↔ A + B, is in accordance with the Enzyme Commission system.

Mass balance status: Balanced.

Enzyme Commission Primary Name: sarcosine oxidase

Standard Gibbs Free Energy ($\Delta_r G^\circ$ in kcal/mol): -19.853012 [Latendresse13]

Enzyme Commission Summary:
A flavoprotein (FAD). The flavin is both covalently and non-covalently bound in a molar ratio of 1:

Citations: [Suzuki81, Hayashi80]

Gene-Reaction Schematic: ?

1.5.3.1 → Cs-soxA, Cs-soxB, Cs-soxG, Cs-soxD (Corynebacterium sp.)
1.5.3.1 → 1, 2 → Arthrobacter sp. TE1826 (soxA)

Unification Links: KEGG:R00610, Rhea:13313

Relationship Links: BRENDA:EC:1.5.3.1, ENZYME:EC:1.5.3.1, IUBMB-ExplorEnz:EC:1.5.3.1, UniProt:RELATED-TO:P23342, UniProt:RELATED-TO:P40859, UniProt:RELATED-TO:P40875

References
Hayashi80: Hayashi S, Nakamura S, Suzuki M (1980). "Corynebacterium sarcosine oxidase: a unique enzyme having covalently-bound and noncovalently-bound flavins." Biochem Biophys Res Commun 96(2):924-30. PMID: 6158947

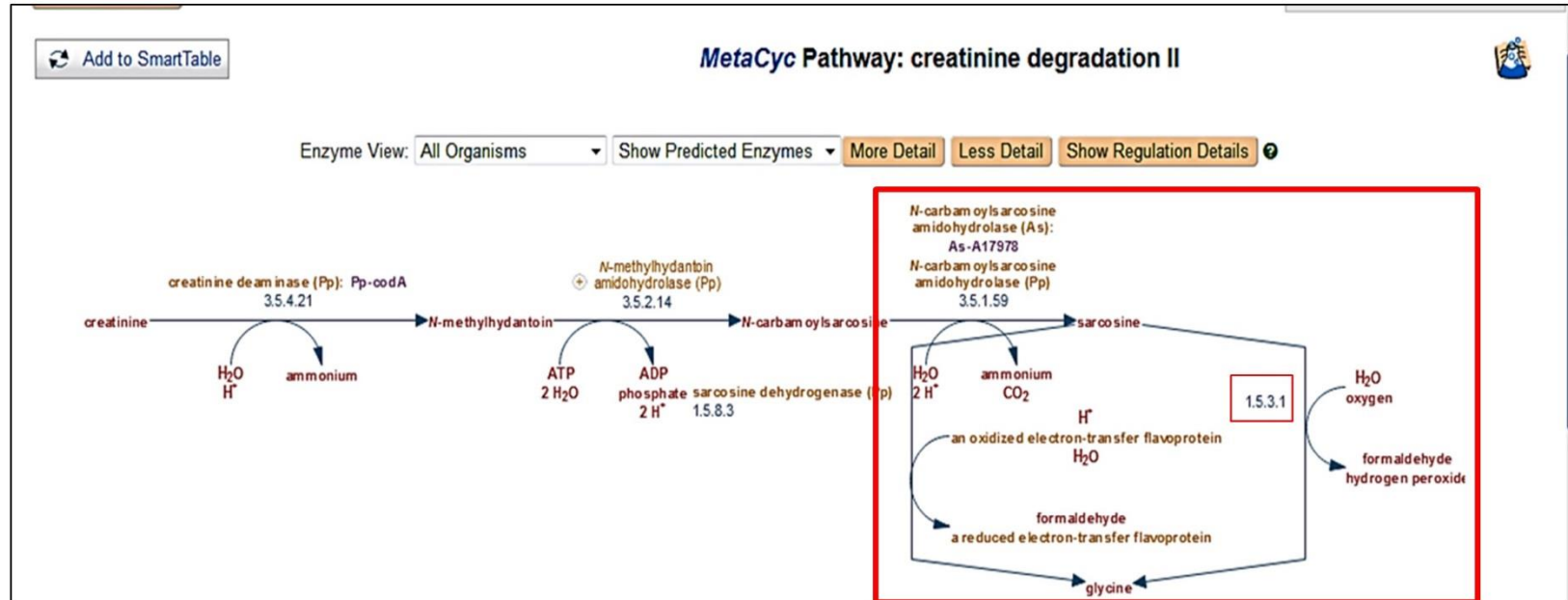
MetaCyc
Reaction: 1.5.3.1
OPERATIONS
Download atom mapping(s) for this reaction
Comparison Operations
Show this reaction in another database
Change organisms/databases for comparison operations
Search for this reaction in other databases
Species Comparison

Look at Pathways

Can Keep in Notebook

Look at gene Reaction schematic

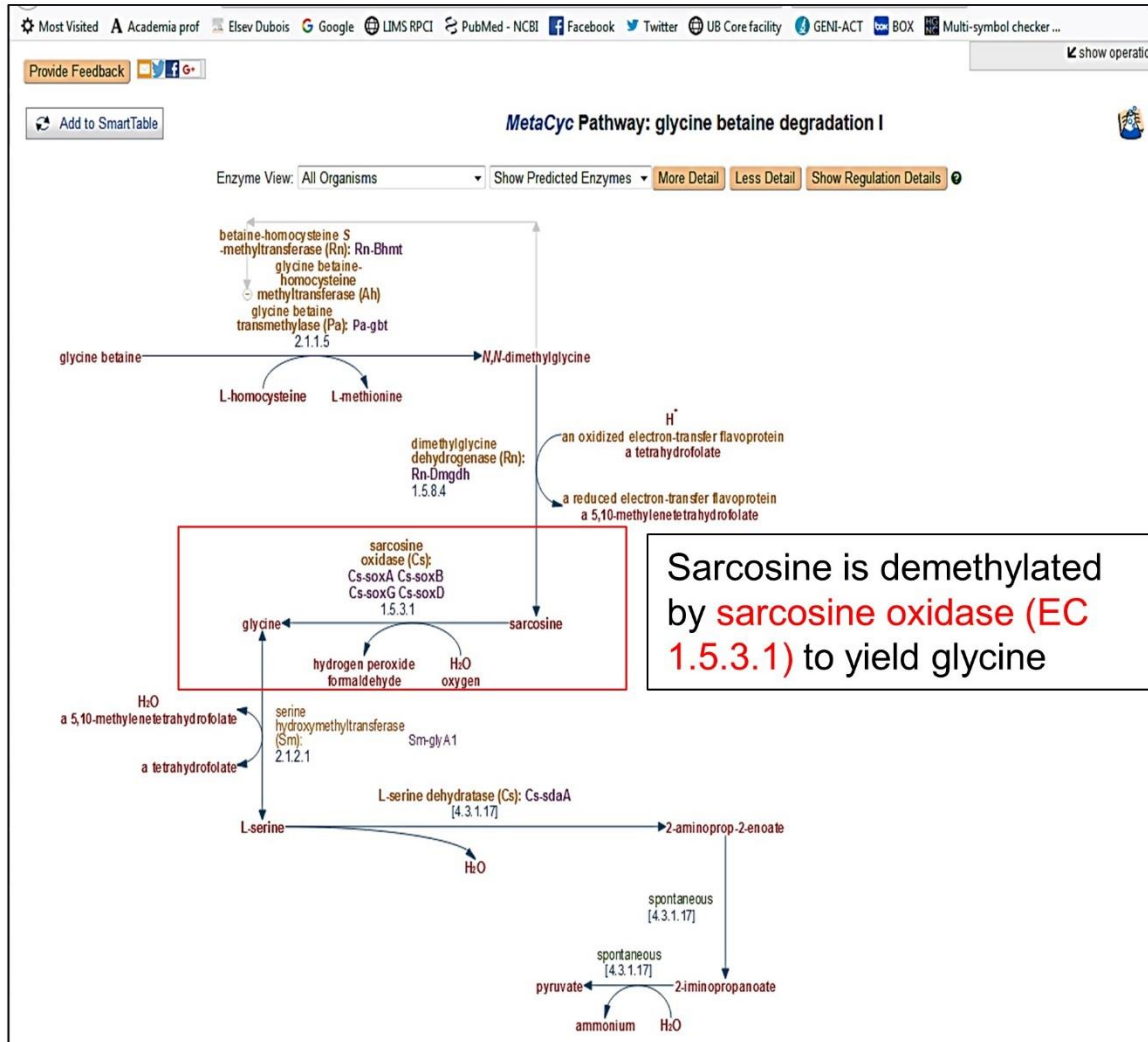
MetaCyc Pathway 1: creatinine degradation II



In this pathway, creatinine is not hydrolyzed back to creatine. Instead, it is deaminated to *N*-methylhydantoin, releasing an ammonia molecule, by the action of creatinine deaminase (also known as creatinine iminohydrolase). In all organisms studied so far, a single enzyme shares both creatinine deaminase and cytosine deaminase [Wyss00]. *N*-methylhydantoin is then hydrolyzed to *N*-carbamoylsarcosine, by the action of *N*-methylhydantoin amidohydrolase, at the expense of one ATP molecule [Kim87a]. *N*-carbamoylsarcosine is deaminated further to sarcosine by *N*-carbamoylsarcosine amidohydrolase, releasing a second ammonia molecule. **In the last step of this pathway, which is shared with creatinine degradation I, sarcosine is hydrolyzed to glycine and formaldehyde, by either sarcosine dehydrogenase or sarcosine oxidase.**

All of the enzyme involved in this pathway are highly inducible when the bacteria grow on creatinine as the main source of nitrogen, and in some cases, carbon.

Pathway 3: Glycine betaine degradation 1.5.3.1



- Glycine betaine (*N,N,N*-trimethylglycine) is a very efficient osmolyte found in a wide range of bacteria and plants, where it is accumulated at high cytoplasmic concentrations in response to osmotic stress, to act as an osmoprotectant.
- Many organisms are also able to catabolize glycine betaine, using it as a sole source for both carbon and nitrogen [Smith88, Lisa83].
- **Sarcosine oxidase is a complex enzyme, containing four cofactors, one of which is tetrahydrofolate (THF).**

Pathways + Reaction schematics

MetaCyc EC 1.5.3.1

Reactions Classified By Substrate → Small-Molecule Reactions

EC Number: 1.5.3.1

Enzymes and Genes:

- sarcosine oxidase (*Achromacter denitrificans*)
- sarcosine oxidase : soxA (*Arthrobacter* sp. TE1826)
- sarcosine oxidase : soxA, soxB, soxG, soxD (*Corynebacterium* sp.)

In Pathway: creatinine degradation II, creatinine degradation I, glycine betaine degradation I

Show Atom Mapping: Coloring? Atom Numbering?

sarcosine + oxygen + H₂O → glycine + formaldehyde + hydrogen peroxide

The reaction direction shown, that is, A + B → C + D versus C + D → A + B, is in accordance with the Enzyme Commission system.

Mass balance status: Balanced.

Enzyme Commission Primary Name: sarcosine oxidase

Standard Gibbs Free Energy ($\Delta_r G^\circ$ in kcal/mol): -19.853012 [Latendresse13]

Enzyme Commission Summary:
A flavoprotein (FAD). The flavin is both covalently and non-covalently bound in a molar ratio of 1:1.

Citations: [Suzuki81, Hayashi80]

Gene-Reaction Schematic:

1.5.3.1

Achromacter denitrificans

1.5.3.1

Arthrobacter sp. TE1826

1.5.3.1

Look at Pathways

Look at gene Reaction schematic

MetaCyc
Reaction: 1.5.3.1
OPERATIONS
Download atom mapping(s) for this reaction
Comparison Operations
Show this reaction in another database
Change organisms/databases for comparison operations
Search for this reaction in other databases
Species Comparison

Unification Links: KEGG:R00610, Rhea:13313

Relationship Links: BRENDA:EC:1.5.3.1, ENZYME:EC:1.5.3.1, IUBMB-ExplorEnz:EC:1.5.3.1, UniProt:RELATED-TO:P23342, UniProt:RELATED-TO:P40859, UniProt:RELATED-TO:P40875

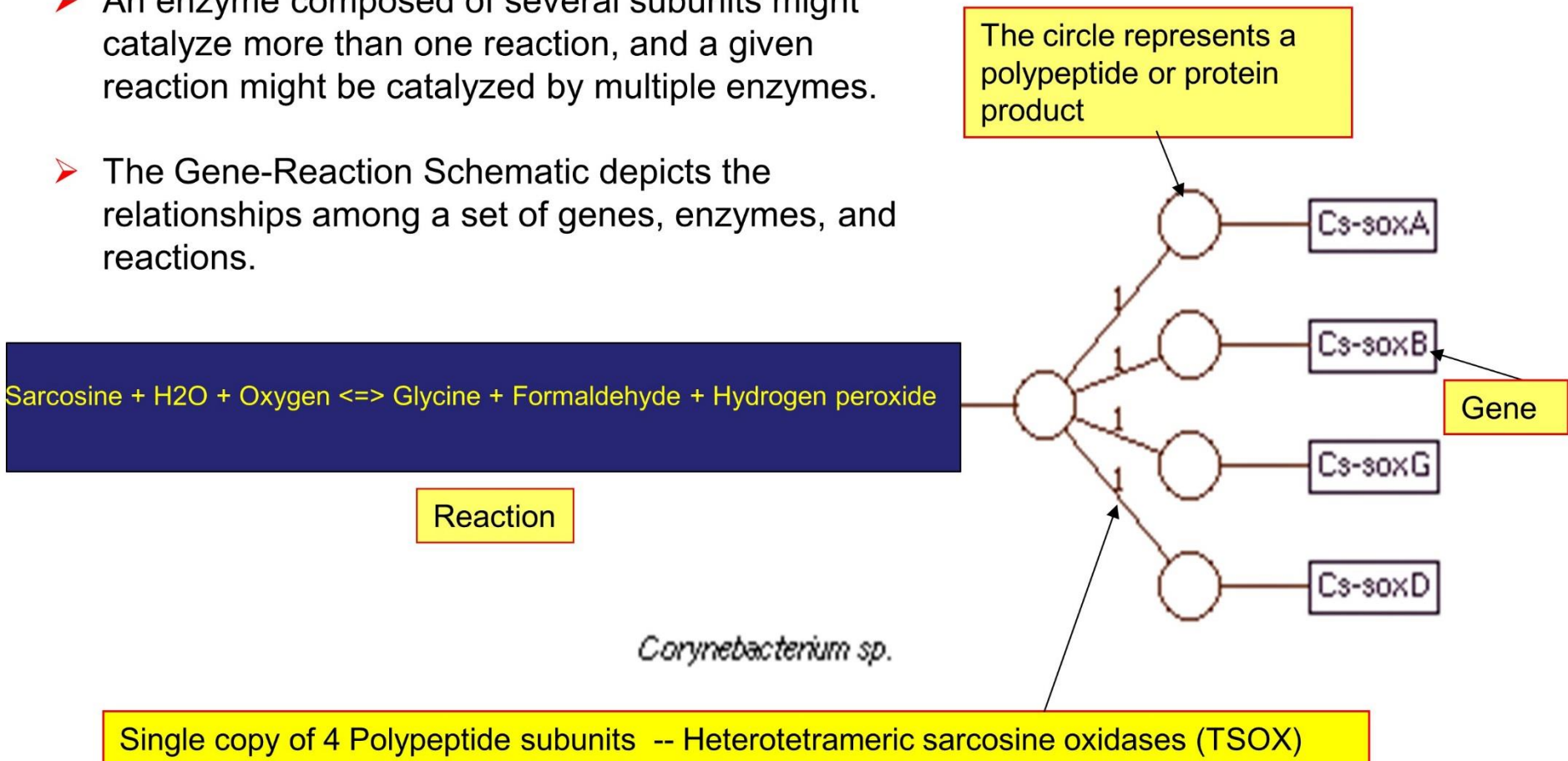
References
Hayashi80: Hayashi S, Nakamura S, Suzuki M (1980). "Corynebacterium sarcosine oxidase: a unique enzyme having covalently-bound and noncovalently-bound flavins." *Biochem Biophys Res Commun* 96(2):924-30. PMID: 6158947

YOU CAN ADD THIS TO YOUR NOTEBOOK

“Gene-Reaction Schematic”

- The many-to-many relationships among genes, enzymes, and reactions can be complex.
- An enzyme composed of several subunits might catalyze more than one reaction, and a given reaction might be catalyzed by multiple enzymes.
- The Gene-Reaction Schematic depicts the relationships among a set of genes, enzymes, and reactions.

Citations: [Suzuki81, Hayashi80]



Remember

- Both KEGG database and Metacyc can give pathway information as well as reaction schematics
- It is good to look at both databases to get as much information about pathways and structural processes and reaction schematics as is necessary to make it easier for you to understand the gene under investigation and its function.

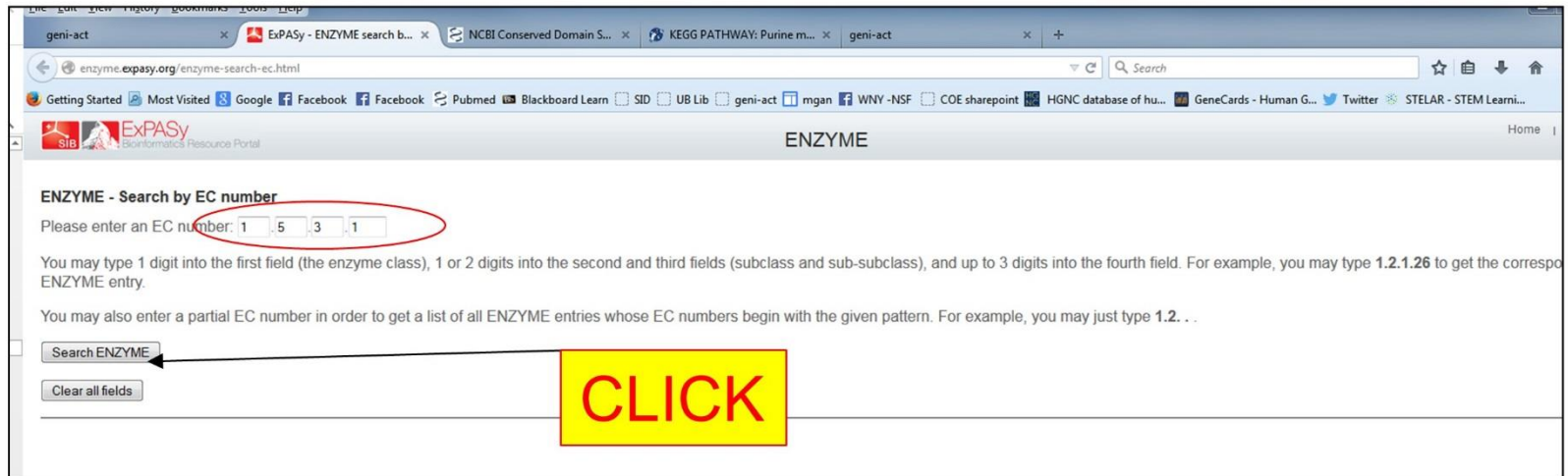
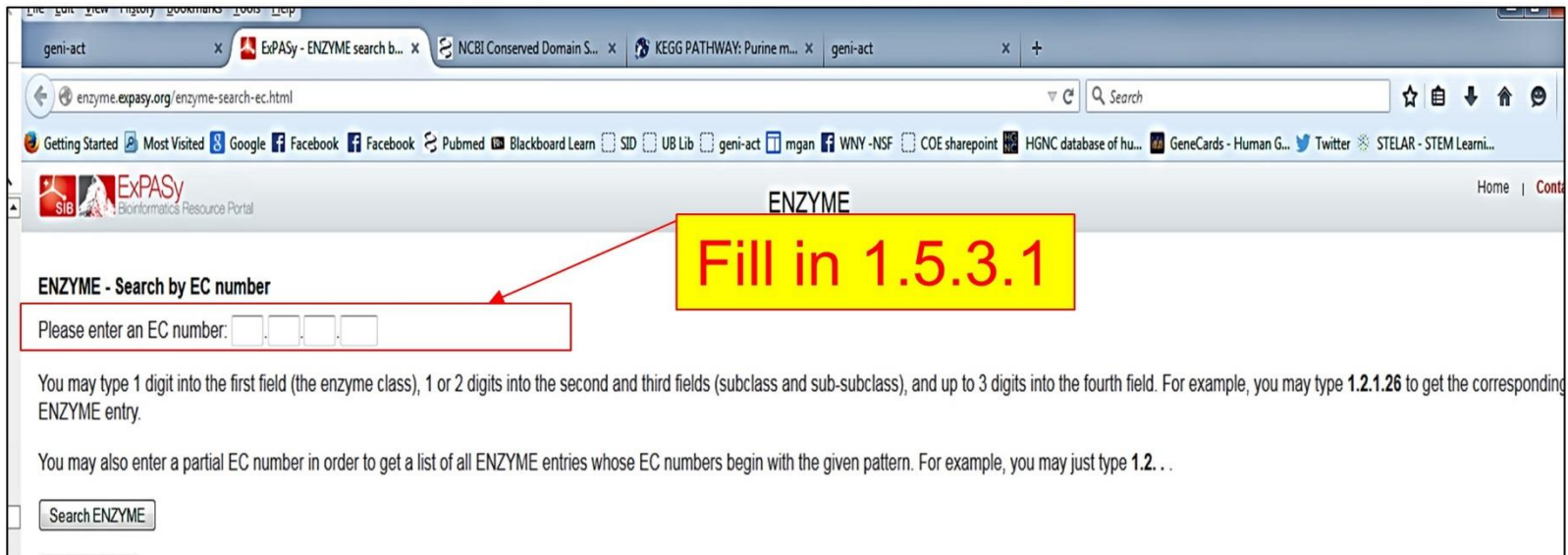
Remember

- Not all genes will have an EC number.
- Only genes with enzyme function are assigned an EC number.
- If your gene ends with 'ase', it could be an enzyme.
- Remember, enzymes have catalytic function.

SOP ExPASy

- Go to <http://www.expasy.ch/enzyme/enzyme-search-ec.html>
- Enter the EC # in appropriate boxes
- Hit Search enzyme
- Results
- Keep Accepted name of enzyme in notebook with EC #
- Select each active link and read up and keep as much information in notebook as helps you.

go to ExPASy ENZYME at <http://www.expasy.ch/enzyme/enzyme-search-ec.html>



Details of the Enzyme

Getting Started Most Visited Google Facebook Facebook Pubmed Blackboard Learn SID UB Lib geni-act mgan WNY -NSF COE sharepoint HGNC database of hu... GeneCards - Human G... Twitter STELAR - STEM Learn...

SIB ExpASy Bioinformatics Resource Portal ENZYME Home | Contact

ENZYME entry: EC 1.5.3.1

Accepted Name			
Sarcosine oxidase.			
Reaction catalysed			
Sarcosine + H(2)O + O(2) <=> glycine + formaldehyde + H(2)O(2)			
Cofactor(s)			
FAD.			
Comment(s)			
The flavin is both covalently and non-covalently bound in a molar ratio of 1:1.			
Cross-references			
BRENDA	1.5.3.1		
EC2PDB	1.5.3.1		
ExplorEnz	1.5.3.1		
PRIAM enzyme-specific profiles	1.5.3.1		
KEGG Ligand Database for Enzyme Nomenclature	1.5.3.1		
IUBMB Enzyme Nomenclature	1.5.3.1		
IntEnz	1.5.3.1		
MEDLINE	Find literature relating to 1.5.3.1		
MetaCyc	1.5.3.1		
	P40873, MSOX_ARTST;	P40859, MSOX_BACB0;	P23342, MSOX_BACSN;
	Q827H4, MSOX_STRAW;	P40854, MSOX_STRSB;	Q9AGP1, SOXA_ARTSP;
	Q46337, SOXA_CORS1;	O87386, SOXA_RHIME;	Q9AGP3, SOXB_ARTSP;
	P40875, SOXB_CORS1;	O87388, SOXB_RHIME;	Q52671, SOXB_RHOCSB;
	Q9AGP2, SOXD_ARTSP;	Q46336, SOXD_CORS1;	O87387, SOXD_RHIME;
	Q9AGP0, SOXG_ARTSP;	Q46338, SOXG_CORS1;	Q9SJA7, SOX_ARATH;
	Q29RU9, SOX_BOVIN;	Q18006, SOX_CAEEL;	Q9P0Z9, SOX_HUMAN;
	Q9D826, SOX_MOUSE;	P79371, SOX_RABIT;	Q54EW2, Y9130_DICDI;
UniProtKB/Swiss-Prot			

View entry in original ENZYME format
View entry in raw text format (no links)

All UniProtKB/Swiss-Prot entries referenced in this entry, with possibility to download in different formats, align etc.
All ENZYME / UniProtKB/Swiss-Prot entries corresponding to 1.5.3.-
All ENZYME / UniProtKB/Swiss-Prot entries corresponding to 1.5.-.-

EC Number

<http://www.expasy.ch/enzyme/enzyme-search-ec.html>

A series of 4 numbers describing enzymatic function:

1: Shows to which of the 6 main categories the enzyme belongs (oxidoreductase, transferase, hydrolase, lyase, isomerase, ligase)

2 and 3: Depends on the enzyme class
(for example, in oxidoreductases: 2 describes the substrate, and 3 describes the acceptor)

4: Gives the specific enzyme activity

Example

Enzyme Commission Number

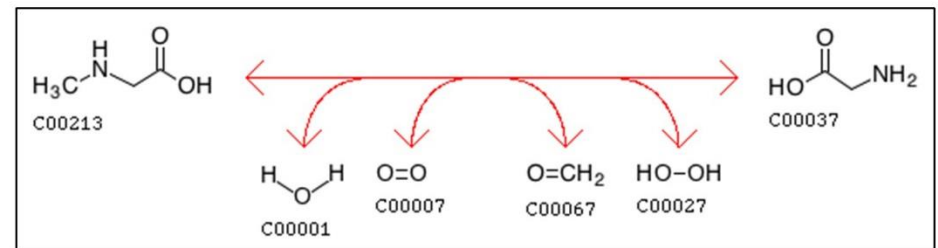
- For example, the **tripeptide aminopeptidases** have the code "EC 3.4.11.4", whose components indicate the following groups of enzymes:
 1. *EC 3* enzymes are **hydrolases** (enzymes that use **water** to break up some other molecule)
 2. *EC 3.4* are **hydrolases** that act on **peptide bonds**
 3. *EC 3.4.11* are those **hydrolases** that cleave off the **amino-terminal amino acid** from a **polypeptide**
 4. *EC 3.4.11.4* are those that cleave off the **amino-terminal end from a tripeptide**

Example

Ksed_04340 - soxB

- For example, sarcosine oxidase has the code "EC 1.5.3.1", whose components indicate the following groups of enzymes:

- EC 1* enzymes are oxidoreductases (enzymes that transfer electrons from reductant to the oxidant)
- EC 1.5* Acting on CH-NH group of donors
- 1.5.3* With oxygen as acceptor
- 1.5.3.1* sarcosine oxidase



Sarcosine + H₂O + Oxygen \rightleftharpoons Glycine + Formaldehyde + Hydrogen peroxide

Substrate

Product

QUESTIONS?



Rama Dey-Rao, PhD

Department of Microbiology /Immunology

&

Biotechnical and Clinical Laboratory Sciences

University at Buffalo School of Medicine and Biomedical Sciences

Buffalo, NY

dey@buffalo.edu