



# **LAILAPS – An Integrated Search Engine for Life Science Data**

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Bioinformatics and Information Technology  
IPK Gatersleben - Germany



[www.transplantdb.eu](http://www.transplantdb.eu)

The transPLANT project is funded by the European Commission within its 7<sup>th</sup> Framework Programme under the thematic area "Infrastructures". Contract number 283496.



# Motivation

Barke ?



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# Motivation

## Barke ?

NCBI Resources How To

PubMed barke

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Text availability

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Publication dates

5 years

10 years

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Species

Humans

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Clinical Trial

Randomized Controlled Trial

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Results: 1 to 20 of 210 << First < Prev Page 1 of 11 Next >> Last >>

[Comparative analysis of genome composition in Triticeae reveals strong variation in transposable element dynamics and nucleotide diversity.](#)  
1. Middleton CP, Stein N, Keller B, Kilian B, Wicker T.  
Plant J. 2012 Oct 12. doi: 10.1111/tpj.12048. [Epub ahead of print]  
PMID: 23057663 [PubMed - as supplied by publisher] [Free Article](#)  
[Related citations](#)

[Quantitative RT-PCR based platform for rapid quantification of the transcripts of highly homologous multigene families and their members during grain development.](#)  
2. Kaczmarczyk A, Bowra S, Elek Z, Vincze E.  
BMC Plant Biol. 2012 Oct 9;12(1):184. [Epub ahead of print]  
PMID: 23043496 [PubMed - as supplied by publisher] [Free Article](#)  
[Related citations](#)

[Confined doping on a metallic atomic chain structure.](#)  
3. Barke I, Polei S, V Oeynhausen V, Meiwas-Broer KH.  
Phys Rev Lett. 2012 Aug 10;109(6):066801. Epub 2012 Aug 7.  
PMID: 23006291 [PubMed - in process] [Related citations](#)

[The german version of the internet addiction test: a validation study.](#)  
4. Barke A, Nyenhuis N, Kröner-Herwig B.  
Cyberpsychol Behav Soc Netw. 2012 Oct;15(10):534-42. doi: 10.1089/cyber.2011.0616. Epub 2012 Sep 24.  
PMID: 23002984 [PubMed - in process] [Related citations](#)

[Sex-specific predictor analyses for the incidence of recurrent headaches in German schoolchildren.](#)  
5. Gaßmann J, Barke A, van Gessel H, Kröner-Herwig B.  
Psychosoc Med. 2012;9:Doc03. Epub 2012 Aug 7.  
PMID: 22879857 [PubMed] [Free PMC Article](#)  
[Related citations](#)

# Motivation

NCBI Resources How To

PubMed barke

RSS Save search Advanced

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Page 1 of 11 Next > Last >>

Google Scholar barke

About 25,500 results (0.02 sec)

Articles JM Swanson, JA Sergeant, E Taylor, EJ Sonuga-Barke... - Lancet, 1998 - ncbi.nlm.nih.gov

Attention-deficit hyperactivity disorder and hyperkinetic disorder. ... Swanson JM, Sergeant JA, Taylor E, Sonuga-Barke EJ, Jensen PS, Cantwell DP, ... UCI Child Development Center, University of California, Irvine 92715, USA. ... Comment in Lancet. 1998 May 9;351(9113): ... Cited by 624 Related articles BL Direct All 13 versions Cite

Psychological heterogeneity in AD/HD—a dual pathway model of behaviour and cognition EJS Sonuga-Barke - Behavioural brain research, 2002 - Elsevier

Psychological accounts have characterised attention-deficit/hyperactivity disorder (AD/HD) as either a neuro-cognitive disorder of regulation or a motivational style. Poor inhibitory control is thought to underpin AD/HD children's dysregulation while delay aversion is a ... Cited by 461 Related articles All 13 versions Cite

Causal models of attention-deficit/hyperactivity disorder: from common simple deficits to multiple developmental pathways EJS Sonuga-Barke - Biological psychiatry, 2005 - Elsevier

Until recently, causal models of attention-deficit/hyperactivity disorder (ADHD) have tended to focus on the role of common, simple, core deficits. One such model highlights the role of executive dysfunction due to deficient inhibitory control resulting from disturbances in the ... Cited by 387 Related articles All 12 versions Cite

Characterizing cognition in ADHD: beyond executive dysfunction FX Castellanos, EJS Sonuga-Barke, MP Milham... - Trends in cognitive ..., 2006 - Elsevier

The hypothesis that Attention-Deficit/Hyperactivity Disorder (ADHD) reflects a primary inhibitory executive function deficit has spurred a substantial literature. However, empirical findings and methodological issues challenge the etiologic primacy of inhibitory and ... Cited by 383 Related articles All 14 versions Cite

Hyperactivity and delay aversion—I. The effect of delay on choice EJS Sonuga-Barke, E Taylor, S Sembi... - Journal of Child ..., 2008 - Wiley Online Library

Abstract Two experiments are reported in which hyperactive and control children repeatedly chose between small immediate and large delayed rewards. In experiment 1, the best choice option was manipulated by varying levels of delay after reward delivery. In ... Cited by 341 Related articles All 6 versions Cite

The ecological validity of delay aversion and response inhibition as measures of impulsivity in AD/HD: a supplement to the NIMH multimodal treatment study of AD/HD MV Solanto, H Abikoff, E Sonuga-Barke... - Journal of abnormal ..., 2001 - Springer

Impulsivity is a primary symptom of the combined type of Attention Deficit/Hyperactivity Disorder (AD/HD). The Stop Signal Paradigm is premised upon a primary deficit in inhibitory control in AD/HD, whereas the Delay Aversion Hypothesis, by contrast, conceptualizes ... Cited by 334 Related articles BL Direct All 14 versions Cite

European clinical guidelines for hyperkinetic disorder—first upgrade .... A Rothenberger, E Sonuga-Barke... - European child & ..., 2004 - Springer

Background The validity of clinical guidelines changes over time, because new evidence-based knowledge and experience develop. Objective Hence, the European clinical guidelines on hyperkinetic disorder from 1998 had to be evaluated and modified. Method ... Cited by 332 Related articles BL Direct All 33 versions Cite

[PDF] from ucsd.edu

Epub 2012 Sep 24.

[PDF] from vanderbilt.edu

[PDF] from adhsnetz-koeln.de

ong variation in transposable transcripts of highly homologous genes in German schoolchildren.



# Features

- + user specific relevance profiles
  - + order of the hit's based on relevance ranking
  - + self learning by user tracking
  - + built-in recommender system
  - + multiple link types
- LAILAPS: Integrated Search Engine

## Integrated Search in Genomics Resources

trans-National Infrastructure for Plant Genomic Science

glucose-6-phosphate maize	estimated hits 21
maize	estimated hits 2
mazie	estimated hits 0
maire	estimated hits 2
maine	estimated hits 0
faize	estimated hits 0



Indexed  
Database



glucose-6-phosphate

Search

our query like: germin

Download Search Results

Results 1-8 from 20 ranked (Total: 20 )

G6PI\_MAIZE Reviewed: 567 AA; RecName: Full=Glucose-6-phosphate isomerase, cytosolic; Short=GPI; EC=5.3.1. (Score: 91.2% Source: uniprot\_sprot)  
FEATURE TABLE DATA:CHAIN 1 567 Glucose-6-phosphate isomerase, cytosolic; REFERENCE TITLE: encoding glucose-6-phosphate isomerase from maize.; DESCRIPTION:RecName: Full=Glucose-6-phosphate isomerase, cytosolic; Short=GPI; EC;

Database:optimas	Database:ensembl	Database:crest
<a href="#">OptiV1S28309</a>	<a href="#">ENST00000356487</a>	<a href="#">TS034F02r</a>
	<a href="#">ENSMUST00000038027</a>	<a href="#">TS034F02u</a>
	<a href="#">ENSRNOT0000032613</a>	<a href="#">HT12K01r</a>
	<a href="#">ENST00000415930</a>	<a href="#">HT12K01u</a>
	<a href="#">ENST00000392234</a>	<a href="#">HW07M21u</a>

Database:metacrop
<a href="#">46</a>
<a href="#">5</a>
<a href="#">45</a>

G6PD\_MAIZE Reviewed: 15 AA; RecName: Full=Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform; Sho (Score: 90.5% Source: uniprot\_sprot)  
FEATURE TABLE DATA:CHAIN <1 15 Glucose-6-phosphate; REFERENCE TITLE: The maize two dimensional gel protein database: towards; DESCRIPTION:RecName: Full=Glucose-6-phosphate 1-dehydrogenase, cytoplasmic; DATABASE CROSS-REFERENCES: glucose-6-phosphate dehydrogenase activity; IEA:EC. GO; GO:0006006; P:glucose;

Database:metacrop
<a href="#">400</a>
<a href="#">84</a>
<a href="#">399</a>
<a href="#">400</a>

C0HEF0\_MAIZE Unreviewed: 384 AA; RecName: Full=Glucose-6-phosphate 1-dehydrogenase; EC=1.1.1.49. (Score: 90% Source: uniprot\_trembl)  
REFERENCE TITLE: Maize Full-length cDNA Project.; DESCRIPTION:RecName: Full=Glucose-6-phosphate 1-dehydrogenase; EC=1.1.1.49.; DATABASE CROSS-REFERENCES: glucose-6-phosphate dehydrogenase activity; IEA:EC. GO; GO:0050661; F:NADP binding;

Database:optimas	Database:ensembl	Database:metacrop
<a href="#">OptiV1S32887</a>	<a href="#">ENSMUST0000004327</a>	<a href="#">400</a>
	<a href="#">ENST00000291587</a>	<a href="#">84</a>
	<a href="#">ENST00000393562</a>	<a href="#">399</a>
	<a href="#">ENST00000393564</a>	<a href="#">400</a>
	<a href="#">ENSRNOT0000056317</a>	

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## General information

Entry name	G6PI_MAIZE
Accession number	P49105
Integrated	01-FEB-1996, UniProtKB/Swiss-Prot.
Sequence update	01-FEB-1996, sequence version 1
Annotation update	03-OCT-2012, entry version 65
UniSave	P49105
UniRef100	UniRef100_P49105
UniParc	UPI0000036BD3

## Description and origin of the Protein

Description	Recommended Full=Glucose-6-phosphate isomerase, cytosolic; Short=GPI; EC= <a href="#">5.3.1.9</a> ;
	Synonym Full=Phosphoglucose isomerase; Short=PGI; Full=Phosphohexose isomerase; Short=PHI;

Gene name(s)	PHI1
Organism source	Zea mays (Maize).
Taxonomy	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogoneae; Zea.
NCBI TaxID	<a href="#">4577</a>

## References

- [1] Lal,S.K., Sachs,M.M.,  
**Cloning and characterization of an anaerobically induced cDNA encoding glucose-6-phosphate isomerase from maize**  
(1995) *Plant Physiol.* **108**:1295-1296

Position NUCLEOTIDE SEQUENCE [MRNA].

Comments STRAIN=cv. B73; TISSUE=Root;

Medline [95357418](#)

DOI [10.1104/pp.108.3.1295](https://doi.org/10.1104/pp.108.3.1295);

PubMed [7630947](#)

[CiteXplore](#)

ENSRNOT00000056317



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## General information

Entry name **G6PI\_MAIZE**

Accession number **P49105**

Integrated 01-FEB-1996, UniProtKB/Swiss-Prot

Sequence update 01-FEB-1996, sequence version 1

Annotation update 03-OCT-2012, entry version 65

UniSave **P49105**

UniRef100 **UniRef100\_P49105**

UniParc **UPI0000036BD3**

## Description and origin of the Protein

Description Recommended Full=Glucose-6-phosphate  
Short=GPI;  
EC=**5.3.1.9**;

Synonym Full=Phosphoglucomutase  
Short=PGI;  
Full=Phosphohexose-6-phosphate  
Short=PHI;

Gene name(s) PHI1

Organism source Zea mays (Maize).

Taxonomy Eukaryota; Viridiplantae; Streptophytina

NCBI TaxID **4577**

## References

- [1] Lal,S.K., Sachs,M.M.,  
**Cloning and characterization of the maize phosphoglucomutase gene**  
(1995) *Plant Physiol.* **108**:1

Position NUCLEOTIDE SEQUENCES

Comments STRAIN=cv. B73; Tissue=L

Medline [95357418](#)

DOI [10.1104/pp.108.3.1](#)

PubMed [7630947](#)

ENSRNOT00000056317

# MetaCrop

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### Conversions

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### Conversion details

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phosphoglucomutase (pPGI)

Conversion name: phosphoglucomutase (pPGI)

Formula: D-fructose 6-phosphate <=> D-glucose 6-phosphate

Reversible?: yes

Catalysed?: yes

Substrate: D-fructose 6-phosphate

Product: D-glucose 6-phosphate

Catalyst: phosphoglucomutase (pPGI, PGI II)

EC number: **5.3.1.9**

### Compartment Locations

#### CONVERSIONNAME

phosphoglucomutase (pPGI)

phosphoglucomutase (pPGI) (amyloplast)

phosphoglucomutase (pPGI) (etioplast)

phosphoglucomutase (pPGI) (plastid)

1 - 4

### Conversion pathways

#### Pathway ▾

Pentose phosphate pathway

Glycolysis, Gluconeogenesis

### Conversion locations

Publication	Species	State Of Plant	Organ	Tissue	Cell	Compartment
PubMed ID: <a href="#">16652944</a>	Hordeum vulgare	PO:0009012 (plant growth and development stage)	IO:3 (etiolated leaf)	IO:1 (unknown)	IO:1 (unknown)	GO:0009513 (etioplast)



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## General information

Entry name **G6PI\_MAIZE**Accession number **P49105**

Integrated 01-FEB-1996, UniProtKB/Swiss-Prot.

Sequence update 01-FEB-1996, sequence version 1

Annotation update 03-OCT-2012, entry version 65

UniSave **P49105**UniRef100 **UniRef100\_P49105**UniParc **UPI0000036BD3**

## Description and origin of the Protein

Description Recommended Full=Glucose-6-phosphate isomerase, cytosolic

Short=GPI;

EC=**5.3.1.9**Synonym Full=Phosphoglucose isomerase;  
Short=PGI;  
Full=Phosphohexose isomerase;  
Short=PHI;

Gene name(s) PH11

Organism source Zea mays (Maize).

Taxonomy Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoph

NCBI TaxID **4577**

## References

- [1] Lal,S.K., Sachs,M.M.,  
**Cloning and characterization of an anaerobic**  
(1995) *Plant Physiol.* **108**:1295-1296

Position NUCLEOTIDE SEQUENCE [mRNA].

Comments STRAIN=cv. B73; TISSUE=Root;

Medline **95357418**DOI [10.1104/108.2.1295](https://doi.org/10.1104/108.2.1295)The transPLANT project is funded by the European Commission within its 7<sup>th</sup> Framework Programme under the thematic area "Infrastructures". Contract number 283496.

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## Conversions

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## Conversion details

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phosphoglucone isomerase (pPGI)

Conversion name: phosphoglucone isomerase (pPGI)

Formula: D-fructose 6-phosphate &lt;=&gt; D-glucose 6-phosphate

Reversible?: yes

Catalysed?: yes

Substrate: D-fructose 6-phosphate

Product: D-glucose 6-phosphate

Catalyst: phosphoglucone isomerase (pPGI, PGI II)

EC number: **5.3.1.9**

## Compartment Locations

### CONVERSIONNAME

phosphoglucone isomerase (pPGI)

phosphoglucone isomerase (pPGI) (amyloplast)

phosphoglucone isomerase (pPGI) (etioplast)

phosphoglucone isomerase (pPGI) (plastid)

1 - 4

## Conversion pathways

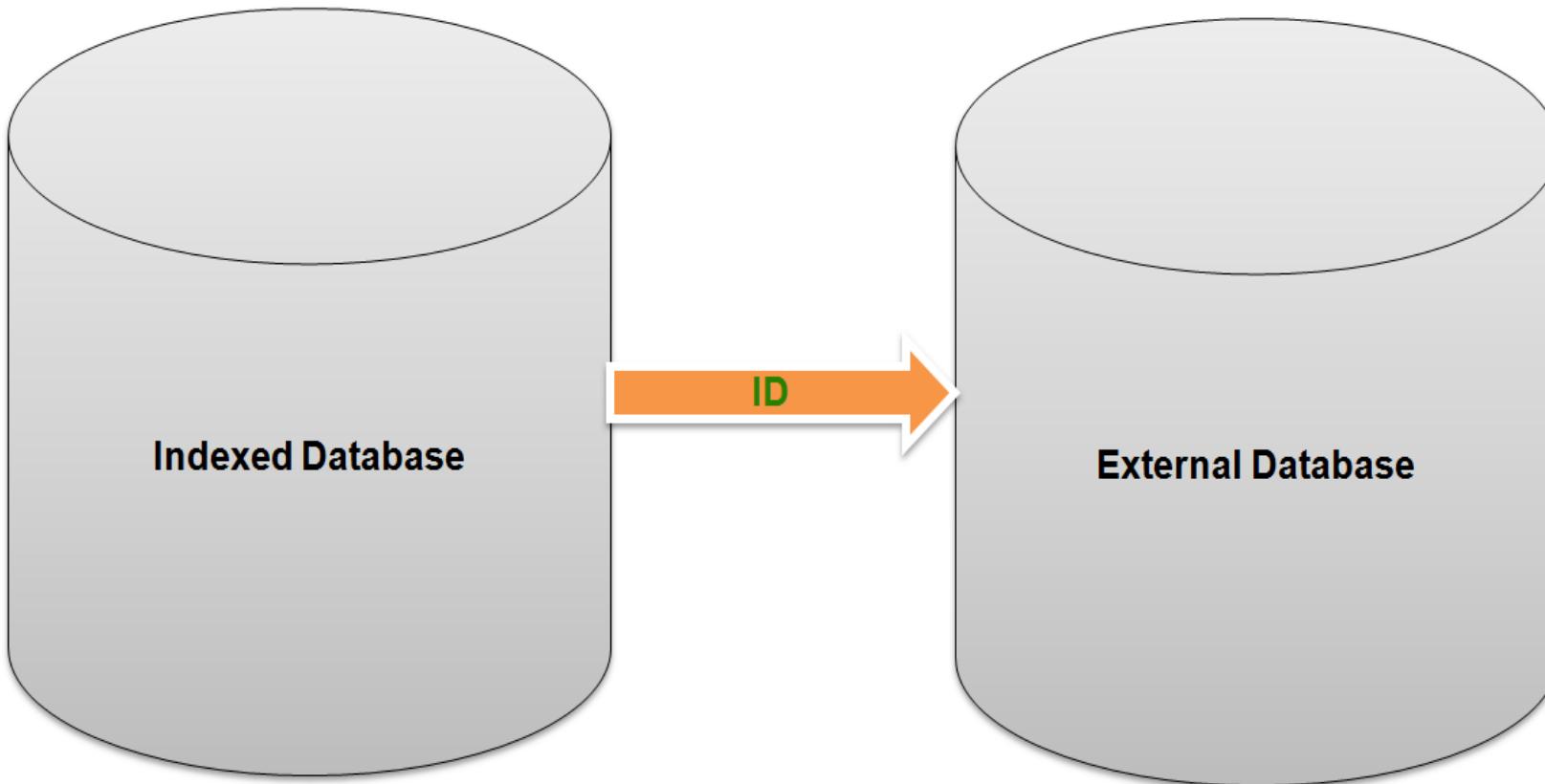
### Pathway ▾

[Pentose phosphate pathway](#)[Glycolysis, Gluconeogenesis](#)

## Conversion locations

Publication	Species	State Of Plant	Organ	Tissue	Cell	Compartment
PubMed ID: <a href="https://pubmed.ncbi.nlm.nih.gov/16652944/">16652944</a>	Hordeum vulgare	PO:0009012 (plant growth and development stage)	IO:3 (etiolated leaf)	IO:1 (unknown)	IO:1 (unknown)	GO:0009513 (etioplast)





[G6PI\\_MAIZE](#) Reviewed: 567 AA; RecName: Full=Glucose-6-phosphate isomerase, cytosolic; Short=GPI; EC=5.3.1 (Score: 91.2% Source: uniprot\_sprot)  
 FEATURE TABLE DATA: CHAIN 1 567 Glucose-6-phosphate isomerase, cytosolic; REFERENCE TITLE: encoding glucose-6-phosphate isomerase from maize.; DESCRIPTION: RecName: Full=Glucose-6-phosphate isomerase, cytosolic; Short=GPI; EC;

Database:optimas	Database:ensembl	Database:crest
<a href="#">OptiV1S28309</a>	<a href="#">ENST00000356487</a>	<a href="#">TS034F02r</a>
	<a href="#">ENSMUST0000038027</a>	<a href="#">TS034F02u</a>
	<a href="#">ENSRNOT0000032613</a>	<a href="#">HT12K01r</a>
	<a href="#">ENST00000415930</a>	<a href="#">HT12K01u</a>
	<a href="#">ENST00000392234</a>	<a href="#">HW07M21u</a>
		<a href="#">ENSNOT0000056317</a>

Database:metacrop
46
5
45

# Online Demo

Firefox pgc.ipk-gatersleben.de/lailaps/app Lailaps + you're logged in as guest@local Homepage / logout

LAILAPS THE LIFE SCIENCE SEARCH ENGINE THE FILE SYSTEM SEARCH ENGINE  
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Integrated Search in Genomics Resources trans-National Infrastructure for Plant Genomic Science

Search Help Type your query like: germin [Which databases are indexed?](#)

These databases are indexed:

Database	Records
trait ontology	1172
pfam	230
gramene taxonomy ontology	6737
plant_ontology	1585
taxonomic allium reference collection	3871
uniprot_sprot	531473
gene_ontology	36803
uniprot_trembl	15325220
garlic shallot core collection	176
pdb	85195
genebank information system of the ipk gatersleben	146420

<http://lailaps.ipk-gatersleben.de>



[www.transplantdb.eu](http://www.transplantdb.eu)

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User

Password

# LAILAPS

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THE LIFE SCIENCE SEARCH ENGINE



## Integrated Search in Genomics Resources

trans-National Infrastructure for Plant Genomic Science

powered by

# LAILAPS

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THE LIFE SCIENCE SEARCH ENGINE

Type your query like: germin

[Which databases are indexed?](#)

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BuildID: LAILAPS-Frontend: Ver. 1.0 Rev. 2012-02-14 11:33:34 LAILAPS: ver. 1.0-SNAPSHOT rev. 2012-11-09 09:43:21 time 09:43:21

**http://lailaps.ipk-gatersleben.de**



you're logged in as guest@local  
[Homepage](#) / [logout](#)



# LAILAPS

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THE LIFE SCIENCE SEARCH ENGINE



Barke|

estimated hits 12

- barke estimated hits 40730
- parke estimated hits 6636
- darke estimated hits 67
- jarke estimated hits 41
- harke estimated hits 5

Hit confidence [Download Search Results](#)

Query time: 0 seconds

[METK4\\_HORVU Reviewed; 396 AA.:](#) (Score: **95.1%** Source: uniprot\_sprot)

REFERENCE COMMENT(S): STRAIN=cv. **Barke**; ISSUE=Seed;;

Database:ensembl

[ENST00000372213](#)

[ENSMUST00000047286](#)

[ENST00000306434](#)

[ENSMUST00000059472](#)

[ENSPPYT0000014193](#)

Database:crest

[HZ62F04r](#)

[HZ65L24r](#)

[HV07J17r](#)

[HV10F14r](#)

[HV11C07r](#)

Database:metacrop

[555](#)

Results 1-8 from 12 ranked (Total: 12 )

## Search in Databases:

- uniprot\_trembl
- uniprot\_sprot
- genebank information
- system of the ipk gatersleben
- pdb

[2vm2\\_OXIDOREDUCTASE\\_21-JAN-08:](#) (Score: **95.1%** Source: pdb)

SOURCE:: **BARKE**;6 EXPRESSION\_SYSTEM: ESCHERICHIA COLI;7 EXPRESSION\_SYSTEM\_TAXID;

Database:optimas

[OptiV1S20255](#)

[2iwt\\_OXIDOREDUCTASE\\_04-JUL-06:](#) (Score: **95.1%** Source: pdb)

SOURCE:: BARLEY;4 ORGANISM\_TAXID: 4513;5 VARIANT: **BARKE**;6 EXPRESSION\_SYSTEM;

Database:crest

[RUS34H10w](#)

[HT12H20r](#)

[HX10L17w](#)

[HB03N10r](#)

[HB19I01r](#)

No Synonyms found

## Type of Data Link:

- all hits
- direct data links
- indirect data links

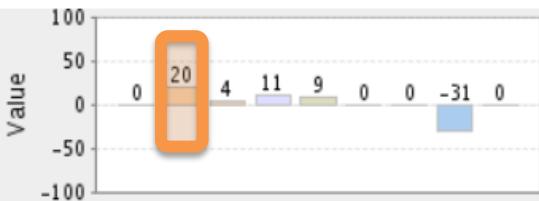
[METK3\\_HORVU Reviewed; 394 AA.:](#) (Score: **95.1%** Source: uniprot\_sprot)

# LAILAPS

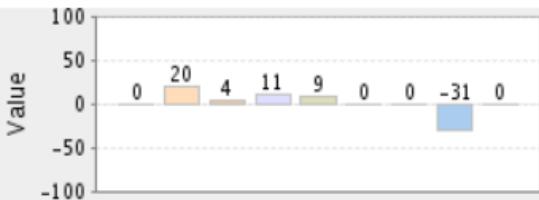
THE LIFE SCIENCE SEARCH ENGINE  
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## Statistics

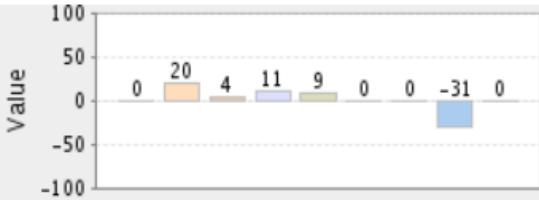
**METK4\_HORVU** Reviewed;  
396 AA.



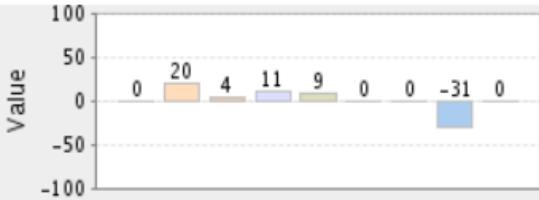
**2vm2 OXIDOREDUCTASE**  
21-JAN-08



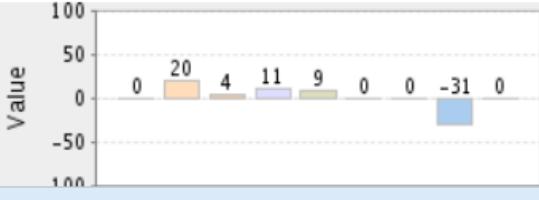
**2iwt OXIDOREDUCTASE**  
04-JUL-06



**METK3\_HORVU** Reviewed;  
394 AA.



**2vlu OXIDOREDUCTASE**  
16-JAN-08

**Legend:**

- █ RuleAttribute
- RuleDatabase **Selected**
- █ RuleFrequency
- █ RuleCooccurrence
- █ RuleTextPosition
- █ RuleSynonym
- █ RuleOrganism
- █ RuleSequenceLength
- █ RuleKeyWord

BarChart ▾

Choose



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Rate me!



100%

The predicted score:



70%

## Lailaps Data Browser and Feedback System

[General](#) [Description](#) [References](#) [Comments](#) [Links](#) [Keywords](#) [Features](#)

## General information

Entry name **METK4\_HORVU**Accession number [Q4LB21](#)

Integrated 10-FEB-2009, UniProtKB/Swiss-Prot.

Sequence update 02-AUG-2005, sequence version 1

Annotation update 03-OCT-2012, entry version 47

UniSave [Q4LB21](#)UniRef100 [UniRef100\\_Q4LB21](#)UniParc [UPI000054B592](#)

## Description and origin of the Protein

Description	Recommended	Full=S-adenosylmethionine synthase 4; Short=AdoMet synthase 4; EC= <a href="#">2.5.1.6</a> ;
	Synonym	Full=Methionine adenosyltransferase 4; Short=MAT 4;

Gene name(s)

SAM1

## Text View

top 5 related entries:

- [uniprot\\_trembl](#),similarity:0.66  
[Q6J9X6\\_MEDSA](#) Unreviewed; 391 AA.
- [uniprot\\_trembl](#),similarity:0.65  
[B0YIL2\\_9ASCO](#) Unreviewed; 381 AA.
- [uniprot\\_trembl](#),similarity:0.63  
[F4HGA5\\_MYCHR](#) Unreviewed; 380 AA.
- [uniprot\\_trembl](#),similarity:0.63  
[F4MMQ7\\_9BACT](#) Unreviewed; 420 AA.
- [uniprot\\_trembl](#),similarity:0.6  
[F3YQU0\\_LISMO](#) Unreviewed; 412 AA.



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100%

The predicted score:



70%

## Lailaps Data Browser and Feedback System

EC=2.5.1.6;

## Synonym

Full=Methionine adenosyltransferase 4;  
Short=MAT 4;

## Gene name(s)

SAM4

## Organism source

Hordeum vulgare (Barley).

## Taxonomy

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Pooideae; Triticeae; Hordeum.

## NCBI TaxID

[4513](#)

## References

- [1] Radchuk,V.V., Sreenivasulu,N., Radchuk,R.I., Wobus,U., Weschke,W.,  
**The methylation cycle and its possible functions in barley endosperm development.**  
(2005) *Plant Mol. Biol.* **59**:289-307

Position NUCLEOTIDE SEQUENCE [MRNA].

Comments STRAIN=:v. Barke; T ISSUE=Seed;

DOI [10.1007/s11103-005-8881-1](https://doi.org/10.1007/s11103-005-8881-1);PubMed [16247558](#) [CiteXplore](#)

## Comments

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LaiLaps Result Browser



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Barke	estimated hits 12
larke	estimated hits 46766
parke	estimated hits 6636
darke	estimated hits 67
jarke	estimated hits 41
harke	estimated hits 0

Hit confidence [Download Search Results](#)

Results 1-1 from 1 ranked (Total: 1 )

Query time: 0 seconds

98081 *Hordeum vulgare* convar. *distichon* var. *nutans*: (Score: 95.1%      Source: genebank information system of the ipk gatersleben)  
ACCESSION NAME Barke

**Search in Databases:**

- uniprot\_trembl
- uniprot\_sprot
- genebank information system of the ipk gatersleben
- pdb

No Synonyms found

**Type of Data Link:**

- all hits
- direct data links
- indirect data links

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100%

The predicted score:

66%

## Lailaps Data Browser and Feedback System



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### Detailed information

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Previous/next accession

#### + Passport data

Accession number: HOR 13170  
Life form: winter type  
Availability: available

#### Accession names

Type	Name	Language	Number of similar	
cultivar name	Barke	Unknown	1	<a href="#">Show</a>



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type your query like: germin

 Hit confidence [Download Search Results](#)

Results 1-8 from 100 ranked (Total: 5154 )

Query time: 29 seconds

[GFPT1\\_HUMAN Reviewed; 699 AA.: RecName: Full=Glucosamine--fructose-6-phosphate aminotransferase \[isomerizi\]](#)

 (Score: [95.2%](#) Source: uniprot\_sprot)

FEATURE TABLE DATA: 699 Glucosamine--**fructose-6-phosphate** aminotransferase; REFERENCE TITLE: glutamine:**fructose-6-phosphate** amidotransferase.; 'Generation; DESCRIPTION:RecName: Full=Glucosamine--**fructose-6-phosphate** aminotransferase;

Database:gnpis

[W13s0064g00050.t01](#)
[W16s0098g00290.t01](#)
[W3s0038g00880.t01](#)
[W6s0004g06830.t01](#)
[W8s0007g05260.t01](#)

Database:ensembl

[ENST00000357308](#)
[ENST00000357308](#)
[ENST00000357308](#)
[ENST00000357308](#)
[ENST00000357308](#)

Database:crest

[HC03B24w](#)
**Search in Databases:**
 uniprot\_trembl

 uniprot\_sprot

 pdb

 gene\_ontology

[GLMS\\_METJA Reviewed; 1099 AA.: RecName: Full=Glucosamine--fructose-6-phosphate aminotransferase \[isomerizi\]](#)

 (Score: [95.2%](#) Source: uniprot\_sprot)

FEATURE TABLE DATA: 71 Glucosamine--**fructose-6-phosphate** aminotransferase; DESCRIPTION:RecName: Full=Glucosamine--**fructose-6-phosphate** aminotransferase; DATABASE CROSS-REFERENCES: IEA:InterPro. GO; GO:0004360; F:glutamine:**fructose-6-phosphate**;

Database:gnpis

[W11s0016g04080.t01](#)
[W12s0028g02020.t01](#)
[W19s0014g01260.t01](#)
[W13s0064g00050.t01](#)
[W16s0098g00290.t01](#)

Database:ensembl

[ENST00000357308](#)
[ENSMUST0000032057](#)
[ENSMUST00000113658](#)
[ENSRNOT00000025070](#)
[ENSBTAT00000002867](#)
**No Synonyms found**
**Filter linked Database:**
 optimas

 gnpis

 ensembl

 metacrop

[GFPT1\\_MOUSE Reviewed; 697 AA.: RecName: Full=Glucosamine--fructose-6-phosphate aminotransferase \[isomerizi\]](#)

 (Score: [95.2%](#) Source: uniprot\_sprot)

**LAILAPS**THE LIFE SCIENCE SEARCH ENGINE  
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fructose-6-phosphate	estimated hits 5,487
fructose-1-phosphate	estimated hits 295
fructose-6-phosphate1	estimated hits 16
fructose-6-phosphate2	estimated hits 14
fructose-6-phosphate3	estimated hits 11
fructose-6-phosphate9	estimated hits 3

Hit confidence [Download](#) [Search Results](#)

Results 1-7 from 7 ranked (Total: 7 )

Query time: 29 seconds

[GO:0004360:](#) (Score: 95.1% Source: gene\_ontology)

SYNONYM: 'D-fructose-6-phosphate amidotransferase activity' EXACT [EC:2.6.1.16; NAME:glutamine-fructose-6-phosphate transaminase (isomerizing;

Database:ensembl

[ENST00000357308](#) [ENSMUST00000032057](#) [ENSMUST00000113658](#) [ENSRNOT00000025070](#) [ENSBTAT00000002867](#) **Search in Databases:**

- uniprot\_trembl
- uniprot\_sprot
- pdb
- gene\_ontology

[GO:0046524:](#) (Score: 95% Source: gene\_ontology)

SYNONYM: '-fructose-6-phosphate 2-alpha-D-glucosyltransferase activity' EXACT [EC:2.4.1.14;

Database:metacrop

[8](#) [GO:0003873:](#) (Score: 95% Source: gene\_ontology)

SYNONYM: '-fructose-6-phosphate 2-phosphotransferase activity' EXACT [EC:2.7.1.105;

Database:ensembl

Database:metacrop

[ENSBTAT0000002753](#) [302](#) [ENSRNOT0000005729](#) [ENSRNOT00000037679](#) [ENSRNOT00000050354](#) [ENSRNOT00000050859](#) **No Synonyms found****Filter linked Database:**

- optimas
- gnpis
- ensembl
- metacrop

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## the Gene Ontology

Search

Browse

BLAST

Homolog Annotations

Search GO  terms  genes or proteins

# glutamine-fructose-6-phosphate transaminase activity

[Term information](#)[Term neighborhood](#)[External references](#)

## Term Information

**Accession** GO:0004360**Ontology** Molecular Function**Synonyms** exact: D-fructose-6-phosphate amidotransferase activity

## Text View

top 4 related entries:

- gene\_ontology,similarity:0.44  
GO:0047905
- gene\_ontology,similarity:0.39  
GO:0047334
- gene\_ontology,similarity:0.27  
GO:0070095
- uniprot\_sprot,similarity:0.22  
NODM\_RHILT Reviewed; 102 AA.



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fructose-6-phosphate maize

Search

type your query like: germin

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Results 1-8 from 11 ranked (Total: 11 )

Query time: 0 seconds

B7ZYR6 MAIZE Unreviewed; 618 AA.: (Score: 94.9% Source: uniprot\_trembl)

REFERENCE TITLE: 'Maize Full-length cDNA Project.'; 'Maize Full-length cDNA Project.'; DATABASE CROSS-REFERENCES:; IEA:InterPro. GO: GO:0047334; F:diphosphate-fructose-6-phosphate; ORGANISM SPECIES:Zea mays (Maize);

Database:optimas

[OptiV1C09420](#)

[OptiV1C09420](#)

[OptiV1C09420](#)

[OptiV1C09420](#)

[OptiV1C05440](#)

Database:ensembl

[ENSBTAT000000000359](#)

[ENST00000340802](#)

[ENST00000359794](#)

[ENSMUST00000051226](#)

[ENSMUST00000163507](#)

## Search in Databases:

uniprot\_trembl

uniprot\_sprot

B4FQM2 MAIZE Unreviewed; 564 AA.: (Score: 94.8% Source: uniprot\_trembl)

REFERENCE TITLE: 'Maize Full-length cDNA Project.'; 'Insights into corn genes derived'; DATABASE CROSS-REFERENCES::diphosphate-fructose-6-phosphate 1-phosphotransferase activity; IEA; ORGANISM SPECIES:Zea mays (Maize);

Database:optimas

[OptiV1S29292](#)

[OptiV1C02296](#)

[OptiV1C14408](#)

[OptiV1C14408](#)

[OptiV1C14408](#)

Database:ensembl

[ENSBTAT000000000359](#)

[ENST00000340802](#)

[ENST00000359794](#)

[ENSMUST00000051226](#)

[ENSMUST00000163507](#)

## Filter Synonyms:

ZEA MAYS

B6SGB6 MAIZE Unreviewed; 616 AA.: (Score: 94.8% Source: uniprot\_trembl)

REFERENCE TITLE: 'Maize Full-length cDNA Project.'; DATABASE CROSS-REFERENCES:; GO:0047334; F:diphosphate-fructose-6-phosphate 1-phosphotransferase; ORGANISM SPECIES:Zea mays (Maize);

Database:optimas

Database:ensembl



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70%

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### Annotations

NCBI NRPEP  
NCBI Maize Unigene  
EMBL Fungi EST  
Blast2Go  
Uniref Blast  
Mapping Optimas ID to 4a.53  
Mapping 4a.53 to Optimas ID

ID

OptiV1C09420

UnirefBlast

OPTIMAS_ID	UNIREF_ID	IDENTITY	ALIGNMENT_LENGTH	MISMATCHES	GAPS	QUERY_START	QUERY_END
P_OptiV1C09420	UniRef100_C5X8X6	94.74	19	1	0	3	59

4a.53 to OPTIMAS Mapping

PARENT_GENE	CODING_SEQUENCE	OPTIMAS_ID	GO Molecular Func. ID	GO Molecular Func. Descr.	GO Biological Process

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fructose-6-phosphate maize

Search

type your query like: germin

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Results 1-2 from 2 ranked (Total: 2 )

Query time: 0 seconds

E7A287 SPORE Unreviewed; 699 AA.: SubName: Full=Probable GFA1-glucosamine--fructose-6-phosphate**transaminase:** (Score: 88.3% Source: uniprot\_trembl)DESCRIPTION:SubName: Full=Probable GFA1-glucosamine--**fructose-6-phosphate**; DATABASE CROSS-REFERENCES:cytoplasm; IEA:InterPro. GO; GO:0004360; F:glutamine-**fructose-6-phosphate**; ORGANISM SPECIES:Sporisorium reilianum (strain SRZ2) (**Maize** head smut fungus);

Database:gnpis

[W13s0064g00050.t01](#)

Database:ensembl

[ENST00000357308](#)[W16s0098g00290.t01](#)[ENSMUST00000032057](#)[W3s0038g00880.t01](#)[ENSMUST00000113658](#)[W6s0004g06830.t01](#)[ENSRNOT00000025070](#)[W8s0007g05260.t01](#)[ENSBTAT00000002867](#)

## Search in Databases:

 uniprot\_trembl uniprot\_sprotE3Q6E5 COLGM Unreviewed; 699 AA.: SubName: Full=Glutamine-fructose-6-phosphate transaminase; (Score: 88.3%)

Source: uniprot\_trembl)

DESCRIPTION:SubName: Full=Glutamine-**fructose-6-phosphate** transaminase;; DATABASE CROSS-REFERENCES:cytoplasm; IEA:InterPro. GO; GO:0004360; F:glutamine-**fructose-6-phosphate**; ORGANISM SPECIES:Colletotrichum graminicola (strain M1.001 / M2 / FGSC 10212) (**Maize**;

Database:gnpis

[W13s0064g00050.t01](#)

Database:ensembl

[ENST00000357308](#)[W16s0098g00290.t01](#)[ENSMUST00000032057](#)[W3s0038g00880.t01](#)[ENSMUST00000113658](#)[W6s0004g06830.t01](#)[ENSRNOT00000025070](#)[W8s0007g05260.t01](#)[ENSBTAT00000002867](#)

## Filter Synonyms:

 ZEA MAYS

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fructose-6-phosphate maize

Search

type your query like: germin

Hit confidence [Download Search Results](#)

Results 1-1 from 1 ranked (Total: 1 )

Query time: 0 seconds

TKTC\_MAIZE Reviewed; 675 AA.: (Score: 79.4% Source: uniprot\_sprot)

REFERENCE TITLE: Structure and properties of an engineered transketolase from maize.; IDENTIFICATION: TKTC\_MAIZE Reviewed; 675 AA.;

COMMENTS OR NOTES: group from fructose-6-phosphate or sedoheptulose-7-phosphate;

Database:gnpis

- [Wv0s0218g00110.t01](#)
- [W15s0048g00370.t01](#)
- [W16s0022g01440.t01](#)
- [W5s0020g02130.t01](#)
- [Wv0s0218g00110.t01](#)

Database:ensembl

- [ENSBTAT00000036390](#)
- [ENST00000369915](#)
- [ENSMUST00000010127](#)
- [ENSBTAT00000011778](#)
- [ENST00000280605](#)

Database:crest

- [HV09B07r](#)
- [HV09B07u](#)
- [HW08E10u](#)
- [HW08E10V](#)
- [HX05E20r](#)

Database:metacrop

- [582](#)
- [581](#)
- [580](#)
- [89](#)
- [353](#)

## Search in Databases:

- uniprot\_trembl
- uniprot\_sprot

## Filter Synonyms:

- ZEA MAYS

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The predicted score:



## Lailaps Data Browser and Feedback System

### MetaCrop

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### Conversions

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> Details

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#### Conversion details

Add To Cart

transketolase (fructose 6-P - erythrose 4-P) (cTK)

Conversion name:	transketolase (fructose 6-P - erythrose 4-P) (cTK)
Formula:	D-fructose 6-phosphate + D-glyceraldehyde 3-phosphate $\leftrightarrow$ D-erythrose 4-phosphate + D-xylulose 5-phosphate
Reversible?:	yes
Catalysed?:	yes
Substrate:	D-fructose 6-phosphate
Substrate:	D-glyceraldehyde 3-phosphate
Product:	D-xylulose 5-phosphate
Product:	D-erythrose 4-phosphate

# Summary

**Search Individual Integrated Databases**

Leibniz INSTITUTE OF PLANT GENETICS and CROP PLANT RESEARCH

Cross Database Search Engine for IPK Databases

IPK Gatersleben

These databases are indexed:

Database	Records
optimas_swissprot	2341
crop est database	264237
metacrop	575
optimas_swissprot	2341

**Relevance Prediction**

Fertig

Results 41-48 from 100 ranked (Total: 5682)

Query time: 2 seconds

Lailaps Statistics - Mozilla Firefox

Databases:

- crop est database
- optimas\_swissprot
- optimas\_spt
- optimas\_sw

Synonyms:

- ARG
- ARGINASE-1
- LIVER-TYPE
- PROBABLE
- ROOF

RUS100F9w AAH83505 Q5XJ11 DANRE Unreviewed; 661 AA.; DATABASE CROSS-REFERENCES: aminoacylation; IEA:HAMAP; HAMAP; MF\_00123; Arg\_tRNA\_synth; 1; InterPro; Source: crop est database;trembl; entry relevance vector

PSC21F23u NP\_179243; DATABASE CROSS-REFERENCES: step 1/1. -- SIMILARITY: Belongs to the Orn/Lys/Arg decarboxylase; PROTEIN EXISTENCE: spermidine biosynthetic process; IEA:UniProtKB-KW; InterPro; IPR002985; Arg; Source: crop est database; entry relevance vector

PSC21F23u S71239; DATABASE CROSS-REFERENCES: step 1/1. -- SIMILARITY: Belongs to the Orn/Lys/Arg decarboxylase; PROTEIN EXISTENCE: spermidine biosynthetic process; IEA:UniProtKB-KW; InterPro; IPR002985; Arg; Source: crop est database; entry relevance vector

H230\_L12\_D05\_39; REFERENCE LOCATION: The Abl-related gene (Arg) nonreceptor tyrosine kinase uses two F; GENE NAME(S)=Abelson-related gene protein; AltName: Full-Tyrosine-protein kinase ARG.; ORGANISM SPECIES:Name=Ab2; Synonyms=Arg; Source: crop est database; entry relevance vector

H259B02r\_Q08436; REFERENCE LOCATION: The Abl-related gene (Arg) nonreceptor tyrosine kinase uses two F; GENE NAME(S)=Abelson-related gene protein; AltName: Full-Tyrosine-protein kinase ARG.; ORGANISM SPECIES:Name=Ab2; Synonyms=Arg; Source: crop est database; entry relevance vector

HS06G08r\_Q08436; REFERENCE LOCATION: The Abl-related gene (Arg) nonreceptor tyrosine kinase uses two F; GENE NAME(S)=Abelson-related gene protein; AltName: Full-Tyrosine-protein kinase ARG.; ORGANISM SPECIES:Name=Ab2; Synonyms=Arg; Source: crop est database; entry relevance vector

Fertig

**User Relevance Feedback**

Rate me! ★★★★★ 80%

Feedback System

CR-EST: The IPK Crop EST Database (Release v1.5)

Pisum sativum (pea)

EST sequence details

This page displays detailed information about EST sequence PSC21F23u.

No search performed yet! Download FASTA Download SCF (trace file)

EST SEQUENCE PROPERTY VALUE

EST IDENTIFIER	PSC21F23u
cDNA LIBRARY	PSC
CLONE ID	PSC21F23
EMBL ID	
EMBL ACCESSION	
DIRECTION	3'

NUCLEOTIDE SEQUENCE

TATTCACAC  
CAGCAAAAGATCAGAGTGTGATGGTTATTCCAAAACGAGAAAATTCAGAGTGCAGAATTTG  
CAACAAAGAAGAAAATAACTACAGAGAACCTCAAATTAAGAGTGCAGAATTTG  
AAACCAAGGACATGAGAACCCCTGTGCTGCTTCTTCACAAATTCATTTTG  
AAACCLAAAAGAAAAGAAAATGAGATGATAGAAGAAAGCCATGTCAGAATTTG  
AAACCAACACATCAATATGAAAAAGGGAGATGCTAAAAAAAGTGCATGACTCA  
GCGCATCAATAGAGACCAATTCTCATCTCTCCAGCAACAGAAAGTGGCAAC

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Fertig

Statistics

Legend:

- RuleAttribute
- RuleCooccurrence
- RuleDatabase
- RuleFrequency
- RuleKeyWord
- RuleOrganism
- RuleSequenceLength
- RuleSynonym
- RuleTextPosition

BarChart Choose

**Individual Ranking Training**

Individual Ranking Training

BarChart Choose

HZ36L18r Q08436

HZ59B02r Q08436

HS06G08r Q08436

Fertig

# Acknowledgements

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German Research Center for Environmental Health



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LAILAPS Project: <http://lailaps.ipk-gatersleben.de>



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LAILAPS

LAILAPS search engine for life science data

LAILAPS combines a keyword driven search engine for an integrative access to life science databases, machine learning for a content driven relevance ranking, recommender systems for suggestion of related data records and query refinements with a user feedback tracking system for an self learning relevance training.

Features:

- ultra fast keyword based search
- non-static relevance ranking
- user specific relevance profiles
- suggestion of related entries
- suggestion of related query terms
- self learning by user tracking
- deployable at standard desktop PC
- 100% JAVA
- installer for in-house deployment



Demo Installations

Feel free to test pre-installed LAILAPS portals:

- [LAILAPS to map gene functions, traits, phenotypes or ontologies to genomic data](#) (developed in the frame of the transPlant consortium)
- [LAILAPS for in-house data of IPK-Gatersleben](#) (content copyright by IPK-Gatersleben)



[www.transplantdb.eu](http://www.transplantdb.eu)

The transPLANT project is funded by the European Commission within its 7<sup>th</sup> Framework Programme under the thematic area "Infrastructures". Contract number 283496.

