



LAILAPS – An Integrated Search Engine for Life Science Data

Jinbo Chen & Uwe Scholz

Bioinformatics and Information Technology
IPK Gatersleben - Germany



Motivation

Barke ?

Motivation

Barke ?

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- ☐ [Comparative analysis of genome composition in Triticeae reveals strong variation in transposable element dynamics and nucleotide diversity.](#)
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: 23057863 [PubMed - as supplied by publisher]
[Related citations](#)
- ☐ [Quantitative RT-PCR based platform for rapid quantification of the transcripts of highly homologous multigene families and their members during grain development.](#)
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, Meiwes-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**
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Motivation



barke



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[Attention-deficit hyperactivity disorder and hyperkinetic disorder.](#)

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 ...*, 2006 - 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

barke



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[Long variation in transposable](#)

[Transcripts of highly homologous](#)

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Epub 2012 Sep 24.

[theses in German schoolchildren](#)

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[PDF] from [adhsnetz-koeln.de](#)



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



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
maze	estimated hits 2
mazie	estimated hits 0
maire	estimated hits 2
maine	estimated hits 0
faize	estimated hits 0

Indexed
Database

LAILAPS

THE LIFE SCIENCE SEARCH ENGINE



glucose-6-phosphate

Search

Your query like: germin

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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

[OptiV1S28309](#)

Database: ensembl

[ENST00000356487](#)

[ENSMUST00000038027](#)

[ENSRNOT00000032813](#)

[ENST00000415930](#)

[ENST00000392234](#)

Database: crest

[TS034F02r](#)

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[HT12K01r](#)

[HT12K01u](#)

[HW07M21u](#)

Database: metacrop

[46](#)

[5](#)

[45](#)

[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

[400](#)

[84](#)

[399](#)

[400](#)

[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

[OptiV1S32887](#)

Database: ensembl

[ENSMUST0000004327](#)

[ENST00000291567](#)

[ENST00000393562](#)

[ENST00000393564](#)

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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)	PHI1	
Organism source	Zea mays (Maize).	
Taxonomy	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogoneae; Zea.	
NCBI TaxID	4577	

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;
PubMed	7630947



ENSRNOT00000056317



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=Phosphoglucose Short=PGI; Full=Phosphohexose Short=PHI;
Gene name(s)	PHI1	
Organism source	Zea mays (Maize).	
Taxonomy	Eukaryota; Viridiplantae; Streptophyta	
NCBI TaxID	4577	

References

[1]	Lal,S.K., Sachs,M.M., Cloning and characterization of the maize gene encoding phosphoglucose isomerase (1995) <i>Plant Physiol.</i> 108 :1-6		
	Position	NUCLEOTIDE SEQUENCE	
	Comments	STRAIN=cv. B73; 1	
	Medline	95357418	
	DOI	10.1104/pp.108.3.1	
	PubMed	7630947	

MetaCrop

Conversions

- Overview
- Details
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Conversion details

phosphoglucose isomerase (pPGI)		Add To Cart
Conversion name:	phosphoglucose isomerase (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:	phosphoglucose isomerase (pPGI, PGI II)	
EC number:	5.3.1.9	

Compartment Locations

CONVERSIONNAME
phosphoglucose isomerase (pPGI)
phosphoglucose isomerase (pPGI) (amyloplast)
phosphoglucose isomerase (pPGI) (etioplast)
phosphoglucose 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: 16652944	Hordeum vulgare	PO:0009012 (plant growth and development stage)	IO:3 (etiolated leaf)	IO:1 (unknown)	IO:1 (unknown)	GO:0009513 (etioplast)

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 isomerase, cytosolic

Short=GPI;

EC=5.3.1.9;

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; 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

10.1104/108.3.1295

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Conversion details

phosphoglucose isomerase (pPGI)

Conversion name:

phosphoglucose isomerase (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:

phosphoglucose isomerase (pPGI, PGI II)

EC number:

5.3.1.9

Compartment Locations

CONVERSIONNAME

phosphoglucose isomerase (pPGI)

phosphoglucose isomerase (pPGI) (amyloplast)

phosphoglucose isomerase (pPGI) (etioplast)

phosphoglucose isomerase (pPGI) (plastid)

1 - 4

Conversion pathways

Pathway ▼

Pentose phosphate pathway

Glycolysis, Gluconeogenesis

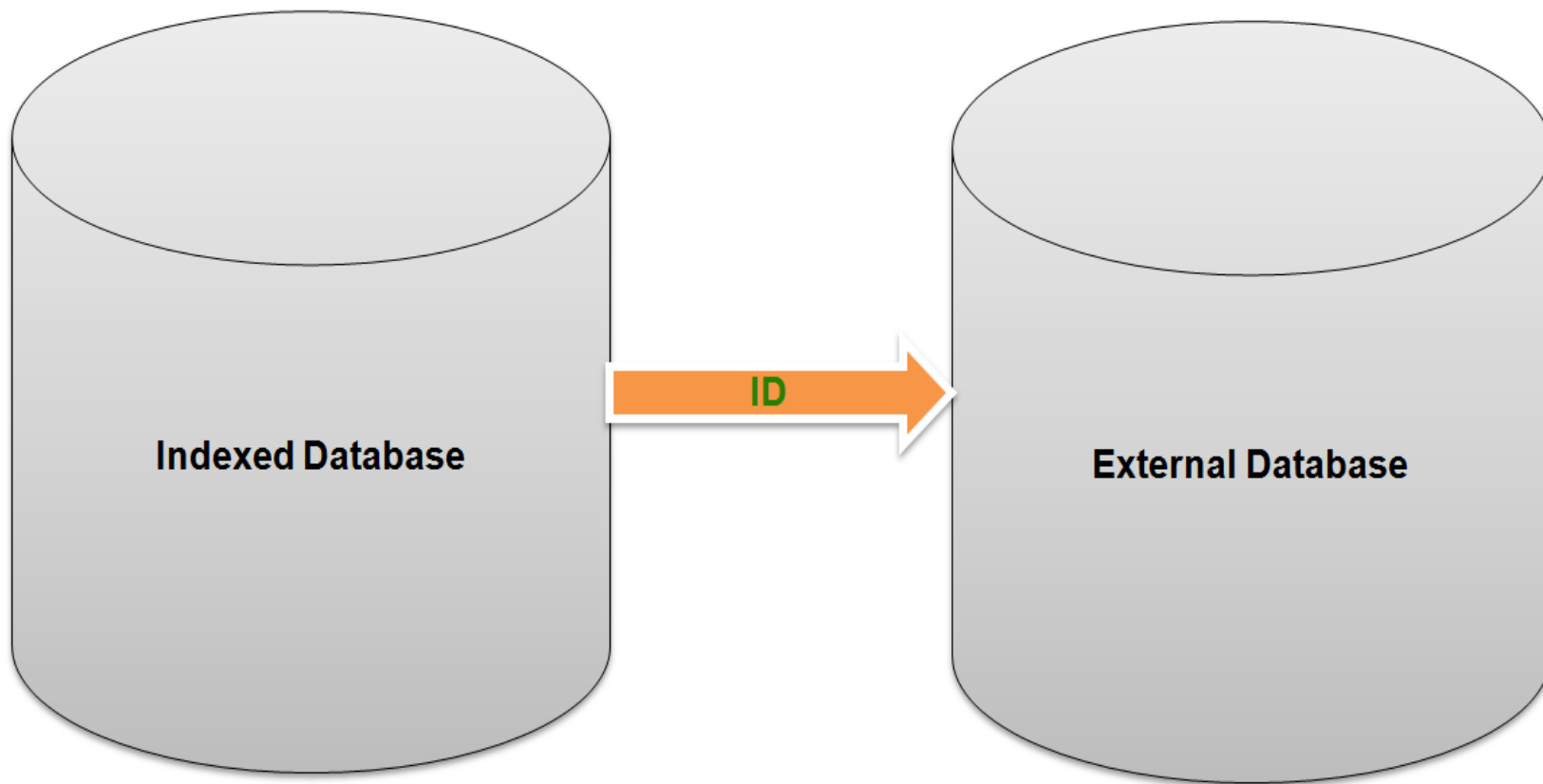
Conversion locations

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

SEVENTH FRAMEWORK PROGRAMME

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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
[OptiV1S28309](#)

Database:ensembl
[ENST00000356487](#)
[ENSMUST00000038027](#)
[ENSRNOT00000032613](#)
[ENST00000415930](#)
[ENST00000392234](#)

Database:crest
[TS034F02r](#)
[TS034F02u](#)
[HT12K01r](#)
[HT12K01u](#)
[HW07M21u](#)

Database:metacrop
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THE LIFE SCIENCE SEARCH ENGINE

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estimated hits 12

parke

estimated hits 40780

darke

estimated hits 6636

jarke

estimated hits 67

harke

estimated hits 41


estimated hits 5


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[METK4 HORVU Reviewed: 396 AA:](#) (Score: 95.1% Source: uniprot_sprot)


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


Database:ensembl 


ENST00000372213 


ENSMUST00000047286 


ENST00000306434 


ENSMUST00000059472 


ENSPPYT00000014193 


Database:crest 

HZ62F04r 


HZ65L24r 

HV07J17r 

HV10F14r 

HV11C07r 


Database:metacrop

555 

[2vm2 OXIDOREDUCTASE 21-JAN-08:](#) (Score: 95.1% Source: pdb)


SOURCE: **BARKE**;6 EXPRESSION_SYSTEM: ESCHERICHIA COLI;7 EXPRESSION_SYSTEM_TAXID;


Database:optimas


OptiV1S20255 


[2imt 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 

[METK3 HORVU Reviewed: 394 AA:](#) (Score: 95.1% Source: uniprot_sprot)

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

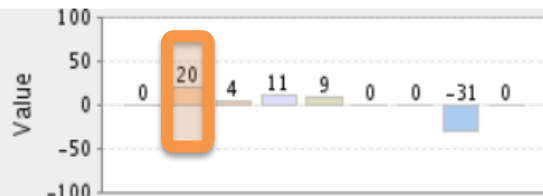
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THE LIFE SCIENCE SEARCH ENGINE

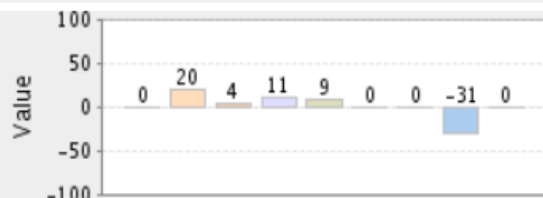


Statistics

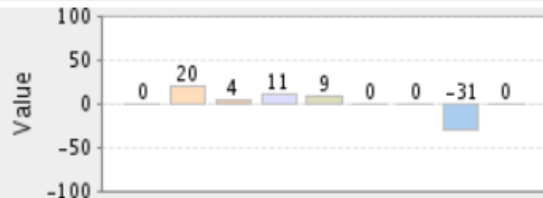
METK4_HORVU Reviewed;
396 AA.



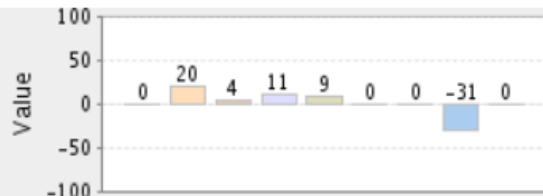
2vm2 OXIDOREDUCTASE
21-JAN-08



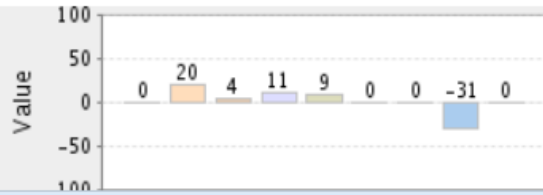
2iwt OXIDOREDUCTASE
04-JUL-06



METK3_HORVU Reviewed;
394 AA.



2vlu OXIDOREDUCTASE
16-JAN-08



Legend:

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

BarChart

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 The predicted score:
 ★★★★★★★☆☆☆ 70%

Lailaps Data Browser and Feedback System

General Description References Comments Links Keywords Featu

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= 2.5.1.6 ;
	Synonym	Full=Methionine adenosyltransferase 4; Short=MAT 4;
Gene name(s)	SAM4	

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.](#)

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=cv. Barke ; TISSUE=Seed;
DOI	10.1007/s11103-005-8881-1 ;
PubMed	16247558   CiteXplore

Comments



Barke	estimated hits 12
larke	estimated hits 46766
parke	estimated hits 6636
darke	estimated hits 67
jarke	estimated hits 41
harke	estimated hits 5

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

Query time: 0 seconds

[28081 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%

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

Accession names

Type	Name	Language	Number of similar	
cultivar name	Barke	Unknown	1	Show

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Lailaps Result Browser

LAILAPS

THE LIFE SCIENCE SEARCH ENGINE

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fructose-6-phosphate

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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

[Vw13s0064g00050.t01](#)

[Vw16s0098g00290.t01](#)

[Vw3s0038g00880.t01](#)

[Vw6s0004g06830.t01](#)

[Vw8s0007g05260.t01](#)

Database:ensembl

[ENST00000357308](#)

[ENST00000357308](#)

[ENST00000357308](#)

[ENST00000357308](#)

[ENST00000357308](#)

Database:crest

[HC03B24w](#)

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

[Vw11s0016g04080.t01](#)

[Vw12s0028g02020.t01](#)

[Vw19s0014g01260.t01](#)

[Vw13s0064g00050.t01](#)

[Vw16s0098g00290.t01](#)

Database:ensembl

[ENST00000357308](#)

[ENSMUST00000032057](#)

[ENSMUST00000113658](#)

[ENSRNOT00000025070](#)

[ENSBTAT00000002867](#)

GFPT1 MOUSE Reviewed: 697 AA.: RecName: Full=Glucosamine--fructose-6-phosphate aminotransferase [isomerizi

(Score: 95.2% Source: uniprot_sprot)

Search in Databases:

☒ uniprot_trembl

☒ uniprot_sprot

☒ pdb

☒ gene_ontology

No Synonyms found

Filter linked Database:

☒ optimas

☒ gnpis

☒ ensembl

☒ metacrop

Firefox

pggriplk-gatersleben.de/lailaps/Result,filterSelection.sdirect

Google

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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

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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](#)

[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

[ENSBTAT00000002753](#)

[ENSRNOT00000005729](#)

[ENSRNOT00000037679](#)

[ENSRNOT00000050354](#)

[ENSRNOT00000050859](#)

[GO:0003873:](#)

(Score: 95%

Source: gene_ontology)

Search in Databases:

☐ uniprot_trembl

☐ uniprot_sprot

☐ pdb

☒ gene_ontology

No Synonyms found

Filter linked Database:

☒ optimas

☒ gnpis

☒ ensembl

☒ metacrop



Rate me!
★★★★★★★★★★★★ 100%
The predicted score:
★★★★★★☆☆☆☆ 63%

Lailaps Data Browser and Feedback System



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.

Firefox

pgc:ipk-gatersleben.de/lailaps/Result,filterSelection.sdirect

Google

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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:0047334; F:diphosphate-fructose-6-phosphate; ORGANISM SPECIES:Zea mays (Maize).;

Database:optimas

OptiV1C09420

OptiV1C09420

OptiV1C09420

OptiV1C09420

OptiV1C05440

Database:ensembl

ENSBTAT00000000359

ENST00000340802

ENST00000359794

ENSMUST00000051226

ENSMUST00000163507

[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

ENSBTAT00000000359

ENST00000340802

ENST00000359794

ENSMUST00000051226

ENSMUST00000163507

[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

Search in Databases:

☒ uniprot_trembl

☒ uniprot_sprot

Filter Synonyms:

☒ ZEA MAYS

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- Transcripts
- Metabolites
- Ionomes
- Enzymes
- Phenotypes
- Experiments
- Analysis

- 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

Firefox

pgcr:ipk-gatersleben.de/lailaps/Result,filterSelection.sdirect

Google

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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

Database:ensembl

[Vv13s0064g00050.t01](#)

[Vv16s0098g00290.t01](#)

[Vv3s0038g00880.t01](#)

[Vv6s0004g06830.t01](#)

[Vv8s0007g05260.t01](#)

[ENST00000357308](#)

[ENSMUST00000032057](#)

[ENSMUST00000113658](#)

[ENSRNOT00000025070](#)

[ENSBTAT00000002867](#)

[E3Q6E5](#)

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

Database:ensembl

[Vv13s0064g00050.t01](#)

[Vv16s0098g00290.t01](#)

[Vv3s0038g00880.t01](#)

[Vv6s0004g06830.t01](#)

[Vv8s0007g05260.t01](#)

[ENST00000357308](#)

[ENSMUST00000032057](#)

[ENSMUST00000113658](#)

[ENSRNOT00000025070](#)

[ENSBTAT00000002867](#)

Search in Databases:

☒ uniprot_trembl

☒ uniprot_sprot

Filter Synonyms:

☐ ZEA MAYS

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fructose-6-phosphate maize

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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;

Search in Databases:

- ☐ uniprot_trembl
- ☒ uniprot_sprot

Database:gnpis	Database:ensembl	Database:crest	Database:metacrop
Vv0s0218g00110.t01	ENSBTAT00000036390	HV09B07r	582
Vv15s0048g00370.t01	ENST00000369915	HV09B07u	581
Vv16s0022g01440.t01	ENSMUST00000010127	HW08E10u	580
Vv5s0020g02130.t01	ENSBTAT00000011778	HW08E10V	89
Vv0s0218g00110.t01	ENST00000280605	HX05E20r	353

Filter Synonyms:

- ☒ ZEA MAYS

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MetaCrop

Conversions
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Conversion details

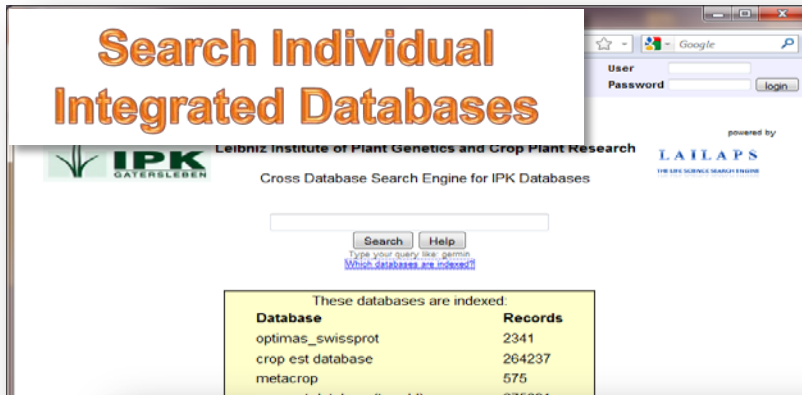
Add To Cart

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

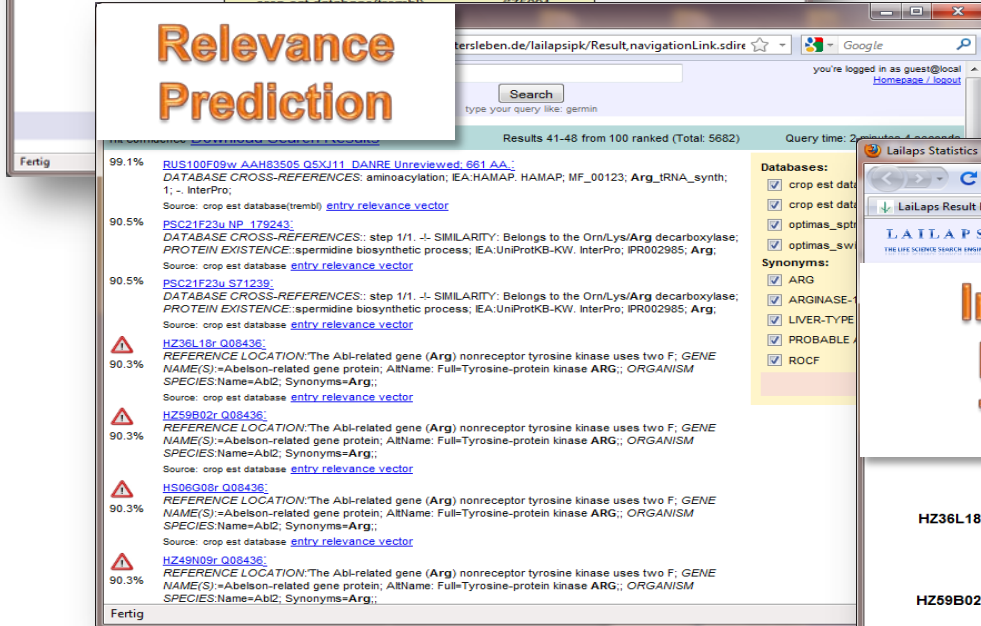
Conversion name:	transketolase (fructose 6-P - erythrose 4-P) (cTK)
Formula:	D-fructose 6-phosphate + D-glyceraldehyde 3-phosphate <=> D-erythrose 4-phosphate + D-xylulose 5-phosphate
Reversible?:	yes
Catalysed?:	yes
Substrate:	D-fructose 6-phosphate
Substrate:	D-glyceraldehyde 3-phosphate
Product:	D-xylulose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

Summary

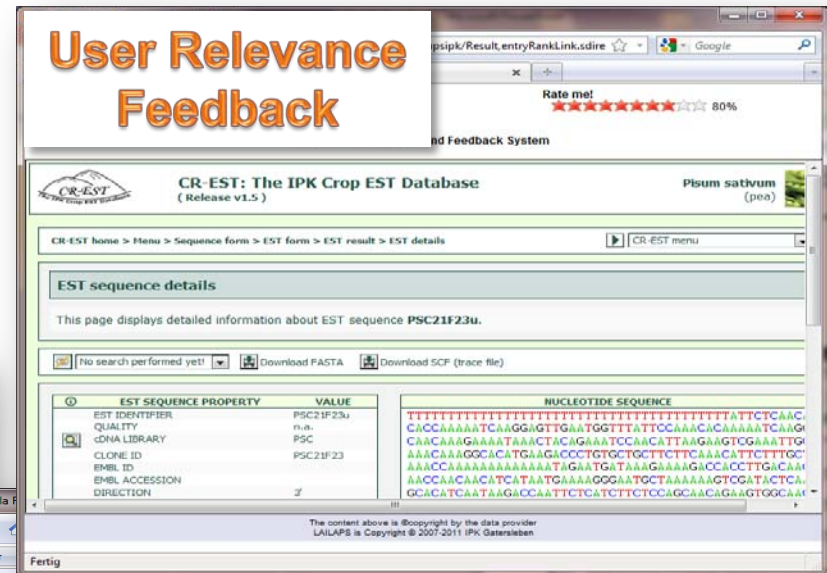
Search Individual Integrated Databases



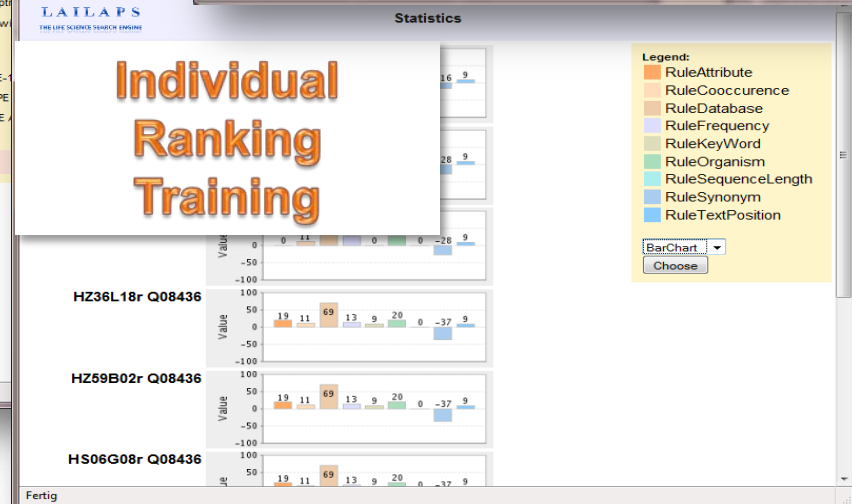
Relevance Prediction



User Relevance Feedback



Individual Ranking Training



Acknowledgements



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

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)

[LAILAPS] [Technology] [Downloads] [Literature] [Legal & Contact]

www.transplantdb.eu



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