

Acknowledging contributions to online expert assistance

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*OPS.gpml - PathVisio 2.0.11

File Edit Data View Help

Zoom: 115.7%

Title: New Pathway

7410:BDH2

TP53INP2

P00196

acetyl-L-carnitine

Objects Properties Backpage

Data Nodes

Basic Shapes

Basic interactions

MIM interactions

Cellular compartments

Annotations

Templates

Gene database: ...s_Derby_20100601.bridge | Metabolite database: ...metabolites_081205.pgdb

Title: New Pathway

7410:BDH2

TP53INP2

P00196

- Delete
- Select
- Copy ⌘C
- Paste ⌘V
- Add State...
- Order
- Literature
- Properties
- Pathway Loom

- Local Interaction data
- Interaction data (Remote webservices)
- Interaction data (Semantic web)
- Preferences...

- WikiPathways Suggestions
- HMDB Suggestions
- Whatizit Suggestions
- KEGG
- Pathway Commons

Data Nodes

Basic Shapes

Basic interactions

MIM interactions

Cellular compartments

Annotations

Templates

Nature Precedings : doi:10.1038/npre.2011.6043.1 : Posted 21 Jun 2011

Title: New Pathway

7410:BDH2

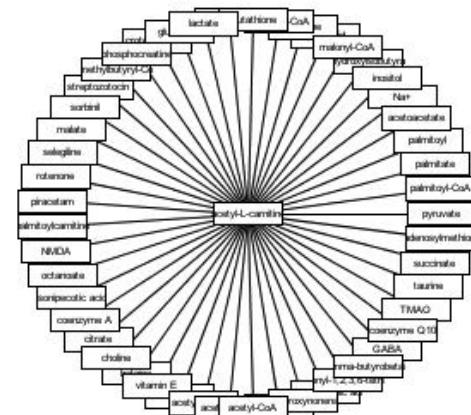
TP53INP2

P00196

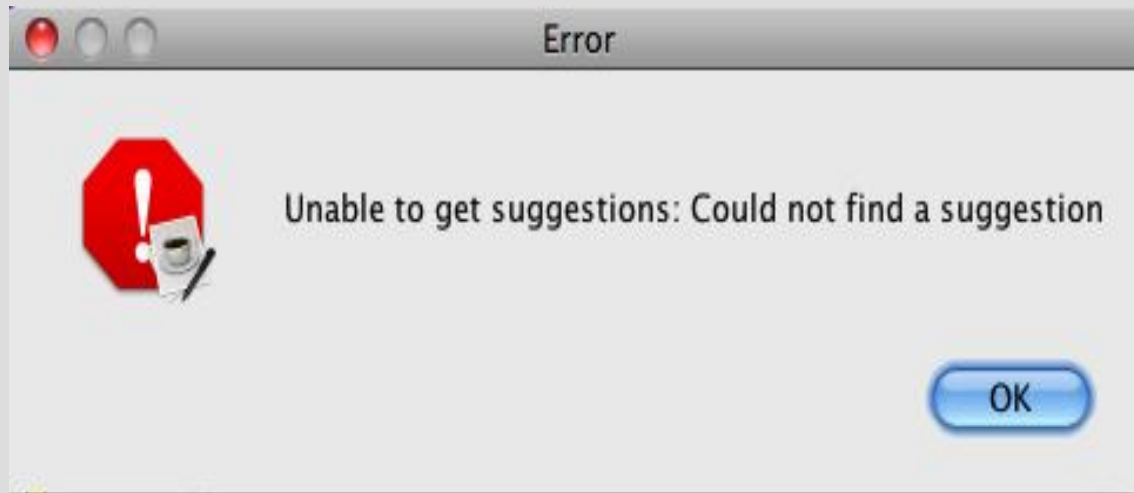
acetyl-L-carnitine

Putative pathway part: STITCH

Title: untitled



Error!



Which are stable text mining solution for biologists.

6

I am working on integrating pathway relations into a pathway diagram. I have two text mining solutions that I use to find interactions. I am looking for new suggestions. The idea is that I provide a pathway entity (ie. gene/protein, metabolite) and all relations based on the literature are returned.

text-mining interaction pathway

☆
2

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edited Mar 1 at 7:28
Lars Juhl Jensen ♦
5,260 ● 1 ● 7 ● 17

asked Feb 26 at 21:08
Andra Waagmeester
1,709 ● 1 ● 13

Could you please tell us which are the two text mining solutions that you already have? –

Lars Juhl Jensen ♦ Feb 27 at 7:57

I am using Whatizit: ebi.ac.uk/webservices/whatizit/info.jsf and Phasar: phasar.cs.ru.nl. The first works decently, the second has issues with performance and accessibility. – Andra Waagmeester
Feb 27 at 9:41

add comment

5 Answers

oldest newest votes

5

You might want to take a look at [STITCH](#). It is a database that allows you to query with a gene/protein or a small molecule (e.g. a metabolite) and retrieve the interaction partners. A very large part of the evidence in STITCH comes from text mining, and if you really want to, you can turn off all the other evidence types to *exclusively* get the results obtained through text mining.

Edit:

If you are using Whatizit, I would suggest that you take a look at the [REST API](#) of [Reflect](#). It is designed for speed, so you do not need to worry about hammering the API. If you send too many requests at the same time, some of them will simply be rejected and you will get an error code back.

tagged

pathway × 25

interaction × 17

text-mining × 13

asked
3 months ago

viewed
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Nature Precedings . doi:10.1038/npre.2011.6043.1 . Posted 24 Jun 2011

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4 votes	6 answers	93 views	What is your favorite wiki use case in bioinformatics?	29m ago	Pierre Lindenbaum	7,274 4 13
3 votes	4 answers	75 views	downloading fasta files	2h ago	Lee Katz	225 6
1 vote	0 answers	11 views	Velvet: retain read names in afg file	4h ago	Lee Katz	225 6
8 votes	4 answers	206 views	What NGS read simulators are available for paired-end data?	6h ago	jordjal	1
16 votes	12 answers	734 views	What tools/libraries do you use to visualize genomic feature data?	8h ago	Pierre Lindenbaum	7,274 4 13
4 votes	1 answer	37 views	How to transform microarray data to adjust for batch effects	8h ago	Daniel Swan	2,669 1 3 14
1 vote	2 answers	25 views	Oligo design from ESTs	9h ago	darked89	1,337 8

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Genomic coordinates from UCSC

I have a list of gene symbols.

2 APOB, TTC39B, ATF3, RGS1, LIPG,

I am trying to get the genomic coordinates (as in bp) with +/-5KB position of these genes via UCSC TableBrowser / MySQL server using NCBI 36/hg18 build. I have tried to get this information via TableBrowser, but I can't find the chromStart and chromEnd field in the given table. Am I missing something?

Also, please share your favorite tutorial / docs that explain the schema/tables in UCSC MySQL server.

Thanks in advance.

data-mining human-genome genome-analysis ucsc

retag | flag

add comment

asked 1 hour ago

Khader Shameer 4,381 1 4 15

2 Answers

oldest newest votes

3 from the table browser <http://genome.ucsc.edu/cgi-bin/hgTables?command=start>, select group= Genes, track= UCSC gene, table=knownGene and then 'describe table schema'

You'll see that knownGene is linked to kgXref:

hg18.kgXref.kgID (via knownGene.name)

Add Another Answer

answer questions

Not the answer you're looking for? Browse other questions tagged data-mining

human-genome genome-analysis ucsc or ask your own question.

Exponentially increasing genomes slide

10 I always see a slide in talks what shows an increasing number of genomes available in GenBank or other database. Where is this slide from? I have seen an outdated one from Genomes Online but nothing recent.

How can I find this graph and cite it for my own talk?

genome graph slides

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add comment

edited Oct 19 at 10:06
giovanni 3,422 1 2 15

asked Oct 18 at 16:02
Lee Katz 225 6

5 Answers

oldest newest votes

8 You might want to have a look at the statistics from GOLD the 'Genomes OnLine Database' here as this has statistics at the genome, not basepair level.

link | flag

answered Oct 18 at 16:26
Daniel Swan 2,694 1 3 14

question has accepted answer

tags help identify topics

rate question and answers

highlight/store "favorite" questions

accepted answer

OpenHelix
www.openhelix.com
1-888-861-5051

OpenHelix offers outreach for BioStar, but does not own or maintain this resource

OpenHelix, LLC, 12600 SE 38th Street, Suite 230 Bellevue, WA 98006; (425) 401-1400, version 11-10, Quick Reference Card Copyright © 2010, OpenHelix is a trademark of OpenHelix, LLC

How do you acknowledge Biostar and its contributors in your research output?

17

I am really impressed with Biostar. The quality of the answers here is often so good that it surely will have an influence. In a way Biostar extends the informal helping among peers of which gratitude is often expressed in the acknowledgments.

How does this work with Biostar. Should we acknowledge the system, all contributors, or both? Do you acknowledge Biostar in your output and if so, how?



biostar alt-metrics acknowledgments

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edited Apr 5 at 21:10



Chris Evelo
3,794 ● 3 ● 16

asked Mar 3 at 12:57

Andra Waagmeester
1,709 ● 1 ● 13

add comment

tagged

biostar × 19

alt-metrics × 2

acknowledgments

asked

3 months ago

viewed

378 times

latest activity

1 month ago

9 Answers

oldest

newest

votes

13

Perhaps the founders and moderators of BioStar could get together and put together a publication on BioStar and their experiences in managing it, get it published. This would provide a publication to be referenced by those who want to acknowledge the site, and would provide some direct academic benefit (a publication and citations) for at least some of those who contribute.

link

answered Mar 3 at 13:57



gawp
712 ● 1 ● 8

4 How about giving a DOI to outstanding questions? You would then have a founding paper published by the founders/moderators and a DOI to cite a specific question. This would also be an additional incentive to the biostar community. – [Andra Waagmeester](#) Mar 3 at 15:03

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Answers

1. Examples
- 2. NLM citation standard for citing blogs
 - 3. A Document Object Identifier
-
- <http://biostar.stackexchange.com/questions/6062/>

NLM citation standard for Blogs

Author
Bernstein M.

Title
Bioethics Discussion Blog [Internet].

Type of Medium
[Internet].

Place of Publication
Los Angeles: Maurice Bernstein.

Publisher
Maurice Bernstein.

Date of Publication
2004 Jul -

Date of Citation
[cited 2007 May 16].

Availability
Available from: <http://bioethicsdiscussion.blogspot.com/>.

Acknowledgements

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- Jahn Saito
- Martijn van Iersel

USC - SF

- Alexander Pico

BIOSTAR <http://biostar.stackexchange.com>

- Lars Juhl Jensen
- Casey Bergman
- Egon Willighagen
- Dominique Noel



Acknowledgements distributed over twitter

@egonwillighagen, @larsjuhljensen You've been thanked by Andra Waagmeester at #ib2011 for responding to BioStar query <http://bit.ly/hyWCBu>
3:05 AM Mar 22nd via web