

TableEdit

A Mediawiki Extension

overview



- Goals
 - Merge free-form wiki's with tabular biological data
 - Make tables useful in MediaWiki
 - Make it easy to add data (for the uninitiated)
 - Get data in/out *en masse*
- Some examples:
 - Gene Ontology terms & community annotation
 - A list of participants at a GMOD 2010 meeting
 - Protein interaction data

example

pcnB:Gene Product(s)

[Quickview](#) | [Gene](#) | **[Gene Product\(s\)](#)** | [Expression](#) | [Evolution](#) | [On One Page](#)
[Nomenclature](#) | [Function](#) | [Interactions](#) | [Localization](#) | [Sequence](#) | [Domains](#) | [Structure](#) | [Resources](#) | [Accessions](#)

Nomenclature

Standard name	PcnB
Synonyms	poly(A) polymerase I ^[1] , B0143 ^{[2][1]} , PcnB ^{[2][1]} , PAP I ^{[2][1]}
Product description	poly(A) polymerase I ^{[2][3]}
EC number (for enzymes)	■ 2.7.7.19 ↗ ^[1]
edit table ↗	

See [Help:Product_nomenclature](#) for help entering or editing information in this section of EcoliWiki.

example

pcnB:Gene Product(s)

[TableEdit Help](#)

Standard name	PcnB
Synonyms	poly(A) polymerase I ^[1] , B0143 ^{[2][1]} , PcnB ^{[2][1]} , PAP I ^{[2][1]}
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	<input type="button" value="Edit"/> <input type="button" value="Copy"/> <input type="button" value="Delete"/> public

Table style

(e.g. align='right')

Heading style

(e.g. 'bgcolor = #ccccff' to make the heading background light blue)

[Cancel](#)

Extra for admins:

example

Standard name	<u>PcnB</u>
Synonyms	<pre>poly(A) polymerase I<ref name='LIB:Riley_2006' />, B0143<ref name='LIB:EcoCyc10.6' /><ref name='LIB:Riley_2006' />, <u>PcnB</u><ref name='LIB:EcoCyc10.6' /><ref</pre>
Product description	<pre>poly(A) polymerase I<ref name='LIB:EcoCyc10.6' /><ref name='LIB:EcoCyc11.1' /></pre>
EC number (for enzymes)	<pre>* [http://www.brenda-enzymes.info /php/result_flat.php4?ecno=2.7.7.19 2.7.7.19]<ref name='LIB:Riley_2006' /></pre>
<input type="text" value="Public"/> <input type="button" value="Update"/> <input type="button" value="Save"/> <input type="button" value="Cancel"/>	

creating tables

Editing CLUSTALW



```
{ {Pagetop} }
== Short Description ==
{ {UserContentHelp} }
CLUSTALW is a widely used tool for multiple sequence alignments. It is a
alignment programs, which includes CLUSTALX, a graphical version that runs
a command line program, it is often accessed via a web interface, such as
/index.html EBI] and [http://www.ch.embnet.org/software/ClustalW.html Swis

== Links ==
*[http://www.clustal.org/ clustal.org]
*[http://www.ebi.ac.uk/Tools/clustalw2/index.html CLUSTALW2 web interface
*[http://www.ch.embnet.org/software/ClustalW.html CLUSTAL at the Swiss Ins

== Requirements ==
```

creating tables

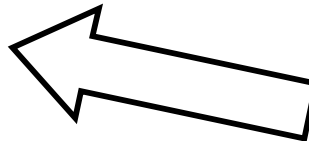
Editing CLUSTALW



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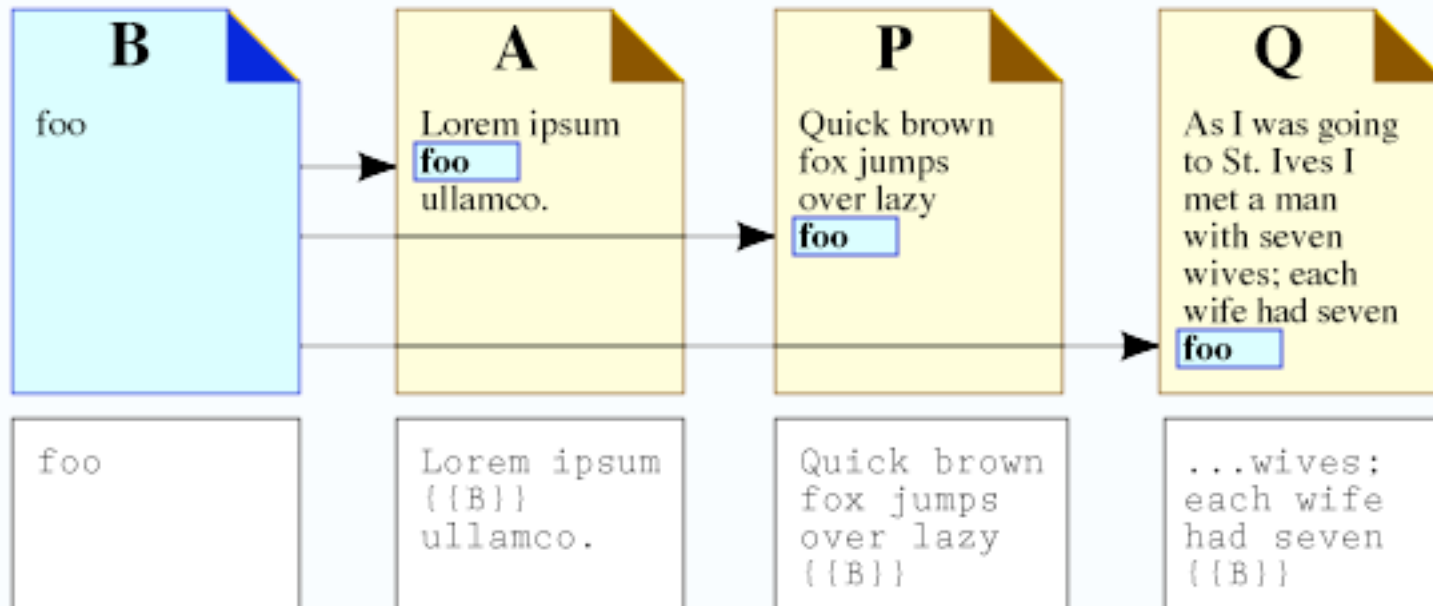
<newTableEdit>
Replace these lines
with Headings and Save
to see a table
</newTableEdit>

== Links ==
*[http://www.clustal.org/ clustal.org]
```



creating tables

- template based system
 - transclusion allows for abstraction



creating (templated) tables

Editing Template:Gene nomenclature table




```
<headings>
Standard name
Mnemonic
Synonyms
</headings>
<heading_style>{{table_heading_style}}</heading_style>
<type>1</type>

[[Category:Table templates|Gene nomenclature table]]
```

```
<newTableEdit>
Template:Gene_Nomenclature_table
</newTableEdit>
```



Standard name
Mnemonic
Synonyms
edit table 

test the demo gods

the good stuff

- really big tables & [jQuery / DataTables](#)
- conflict detector
- help links - 100% user editable
- the loader - for mass imports / edits
- documentation / specs (in progress)
- modules/plugin-ins
- "foreign tables" & mirroring

jQuery / DataTables

Showing 1 to 13 of 13 entries

Filter Rows: Evidence: Any/All

Qualifier	GO ID	GO term name	Reference(s)	Evidence Code	with/from	Aspect	Notes	Status
	GO:0003677	DNA binding	GO_REF:0000004	IEA: Inferred from Electronic Annotation				complete
	GO:0003700	transcription factor activity	GO_REF:0000002	IEA: Inferred from Electronic Annotation				te
	GO:0006350	transcription	GO_REF:0000004	IEA: Inferred from Electronic Annotation				te
	GO:0006355	regulation of transcription, DNA-dependent	GO_REF:0000002 GO_REF:0000004	IEA: Inferred from Electronic Annotation				ete
							[5]	Seeded

Evidence: Any/All

- Any/All
- not IEAs
- None
- IEA
- IMP
- NR
- RCA

Notes

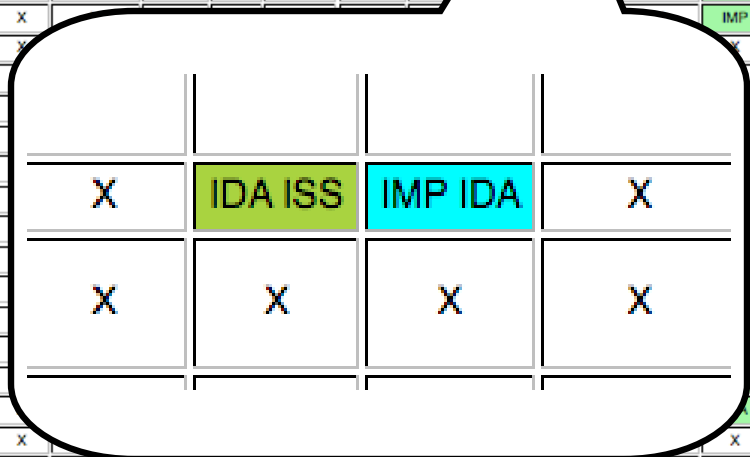
Seeded from EcoCyc [5]

summary tables

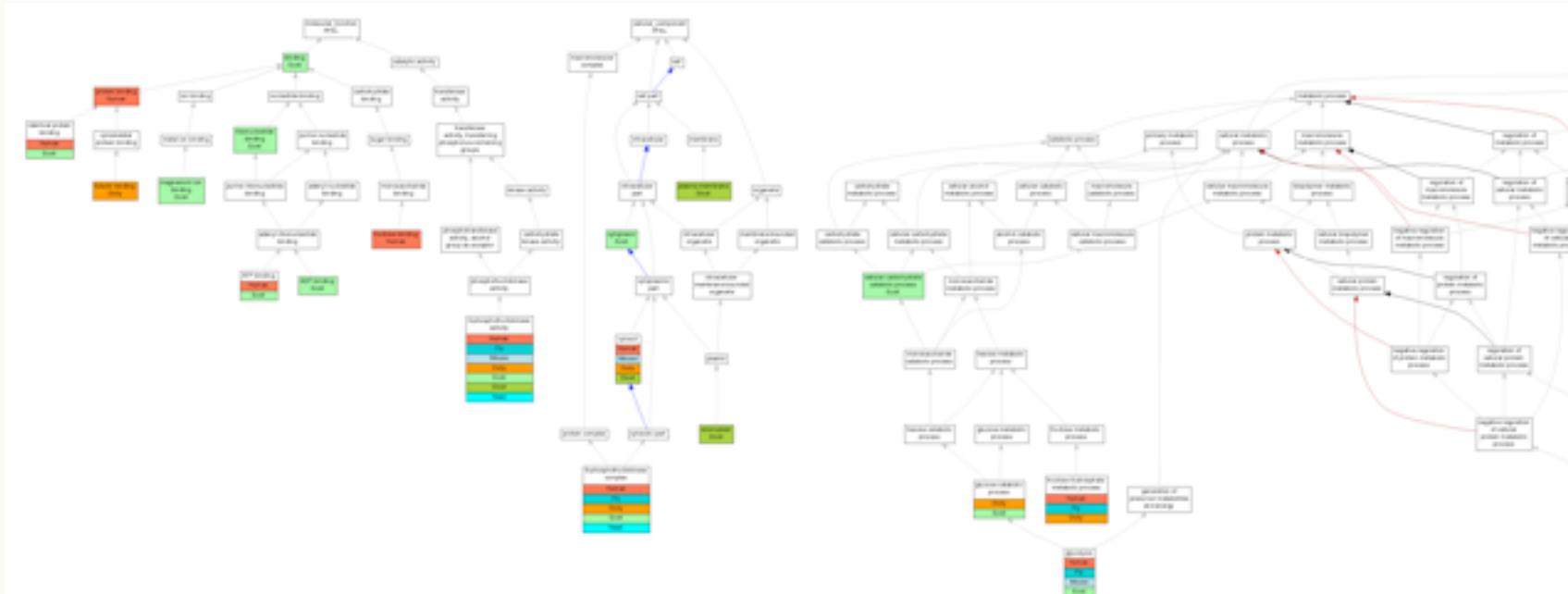
Category	ID	Term	Human	Mouse	Rat	Chicken	Zfish	Fly	Worm	Dicty	Dicot	Dicot	Yeast	Pombe	Ecoli
Biological Process	GO:0040018	positive regulation of multicellular organism growth	X	X	X	X	X	X	IMP	X	X	X	X	X	X
Biological Process	GO:0006096	glycolysis	IDA	IDA	X	X	X	IC	X	X	X	IDA ISS	IMP IDA	X	IDA
Biological Process	GO:0006002	fructose 6-phosphate metabolic process	IDA IMP	X	X	X	X	IMP	X	IDA	X	X	X	X	X
Biological Process	GO:0031115	negative regulation of microtubule polymerization	X	X	X	X	X	X	X	IDA	X	X	X	X	X
Biological Process	GO:0006007	glucose catabolic process	X	X	X	X	X	X	X	IGI	X	X	X	X	IMP
Biological Process	GO:0009792	embryonic development ending in birth or egg hatching	X	X	X	X	X	X	IMP	X	X	X	X	X	X
Biological Process	GO:0000003	reproduction	X	X	X	X	X	X	IMP	X	X	X	X	X	X
Biological Process	GO:0044275	cellular carbohydrate catabolic process	X	X	X	X	X	X	X	X	X	X	X	X	IMP
Biological Process	GO:0016052	carbohydrate catabolic process	X	X	X	X	X	X	X	X	X	X	X	X	IMP
Biological Process	GO:0046676	negative regulation of insulin secretion	X	IDA	X	X	X	X	X	X	X	X	X	X	X
Biological Process	GO:0009749	response to glucose stimulus	X	IDA	X	X	X	X	X	X	X	X	X	X	X
Molecular Function	GO:0003872	6-phosphofructokinase activity	IDA IMP	IDA	X	X	X	IMP	X	IDA IGI	X	IDA ISS	IMP	X	IMP
Molecular Function	GO:0015631	tubulin binding	X	X	X	X	X	X	X	IPI	X	X	X	X	X
Molecular Function	GO:0005524	ATP binding	IDA	X	X	X	X	X	X	X	X	X	X	X	IMP
Molecular Function	GO:0042802	identical protein binding	IPI	X	X	X	X	X	X	X	X	X	X	X	IDA
Molecular Function	GO:0005515	protein binding	IPI	X	X	X	X	X	X	X	X	X	X	X	X
Molecular Function	GO:0070061	fructose binding	IDA IC	X	X	X	X	X	X	X	X	X	X	X	X
Molecular Function	GO:0005488	binding	X	X	X	X	X	X	X	X	X	X	X	X	IDA
Molecular Function	GO:0000267	magnesium ion binding	X	X	X	X	X	X	X	X	X	X	X	X	IDA
Molecular Function	GO:0032553	ribonucleotide binding	X	X	X	X	X	X	X	X	X	X	X	X	IDA
Molecular Function	GO:0043531	ADP binding	X	X	X	X	X	X	X	X	X	X	X	X	IDA
Cellular Component	GO:0005945	6-phosphofructokinase complex	IDA	X	X	X	X	IC	X	IDA	X	X	IMP	X	IDA
Cellular Component	GO:0005829	cytosol	IDA	IDA	X	X	X	X	X	IDA	X	IDA	X	X	X
Cellular Component	GO:0005737	cytoplasm	X	X	X	X	X	X	X	X	X	X	X	X	IDA
Cellular Component	GO:0005886	plasma membrane	X	X	X	X	X	X	X	X	X	IDA	X	X	X
Cellular Component	GO:0009507	chloroplast	X	X	X	X	X	X	X	X	X	IDA	X	X	X

summary tables

Category	ID	Term	Human	Mouse	Rat	Chicken	Zfish	Fly	Worm	Dicty	Dicot	Dicot	Yeast	Pombe	Ecoli
Biological Process	GO:0040018	positive regulation of multicellular organism growth	X	X	X	X	X	X	IMP	X	X	X	X	X	X
Biological Process	GO:0006096	glycolysis	IDA	IDA	X	X	X	IC	X	X	X	IDA ISS	IMP IDA	X	IDA
Biological Process	GO:0006002	fructose 6-phosphate metabolic process	IDA IMP	X	X	X	X	IMP	X	IDA	X	X	X	X	X
Biological Process	GO:0031115	negative regulation of microtubule polymerization	X	X	X	X	X	X	X	IDA	X	X	X	X	X
Biological Process	GO:0006007	glucose catabolic process	X	X	X	X	X	X	X	IGI	X	X	X	X	IMP
Biological Process	GO:0009792	embryonic development ending in birth or egg hatching	X	X	X	X	X	X	IMP	X	X	X	X	X	X
Biological Process	GO:0000003	reproduction	X	X	X	X	X	X	IMP	X	X	X	X	X	X
Biological Process	GO:0044275	cellular carbohydrate catabolic process	X	X	X	X	X	X	X	X	X	X	X	X	IMP
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Biological Process	GO:0046676	negative regulation of insulin secretion	X	IDA	X	X	X	X	X	X	X	X	X	X	X
Biological Process	GO:0009749	response to glucose stimulus	X	IDA	X	X	X	X	X	X	X	X	X	X	X
Molecular Function	GO:0003872	6-phosphofructokinase activity	IDA IMP	IDA	X	X	X	X	X	X	X	X	X	X	X
Molecular Function	GO:0015631	tubulin binding	X	X	X	X	X	X	X	X	X	X	X	X	X
Molecular Function	GO:0005524	ATP binding	IDA	X	X	X	X	X	X	X	X	X	X	X	X
Molecular Function	GO:0042802	identical protein binding	IPI	X	X	X	X	X	X	X	X	X	X	X	X
Molecular Function	GO:0005515	protein binding	IPI	X	X	X	X	X	X	X	X	X	X	X	X
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Molecular Function	GO:0032553	ribonucleotide binding	X	X	X	X	X	X	X	X	X	X	X	X	X
Molecular Function	GO:0043531	ADP binding	X	X	X	X	X	X	X	X	X	X	X	X	X
Cellular Component	GO:0005945	6-phosphofructokinase complex	IDA	X	X	X	X	X	X	X	X	X	X	X	X
Cellular Component	GO:0005829	cytosol	IDA	IDA	X	X	X	X	X	X	X	X	X	X	X
Cellular Component	GO:0005737	cytoplasm	X	X	X	X	X	X	X	X	X	X	X	X	IDA
Cellular Component	GO:0005886	plasma membrane	X	X	X	X	X	X	X	X	X	IDA	X	X	X
Cellular Component	GO:0009507	chloroplast	X	X	X	X	X	X	X	X	X	IDA	X	X	X



driving images



thanks to Mary Dolan @ MGI

conflict detector

Table Edit

lacZ Gene (Product(s))

See Key/Class, clicking the two arrows or clicking GO terms and GO annotations in Details

A conflict has been detected (between the version of this table in the wiki and the copy you are editing)

Rows in conflict with the working copy:

Qualifier (E)	GO ID (E)	GO term name (E)	Reference(s) (E)	Evidence Code (E)	withFrom (E)	Aspect (E)	Notes (E)	Status (E)
protein-binding	GO:0005116	protein-binding	PMID:18838888	EIA: Inferred from Sequence or Structural Similarity	UniProt			
protein-catabolism	GO:0007137	protein-catabolism	PMID:14821768	EIA: Inferred from Sequence or Structural Similarity		C	Deleted from TracCap 11.1 - required field missing	
protein-lysine kinase activity	GO:0004110	protein-lysine kinase activity	PMID:16791034	EIA: Inferred by Curator		F	This is a sample annotation - complete	

The rows shown above are different from the working copy. This includes rows that have been edited and rows that are missing in the copy you are editing. Copy desired rows to the editing session and you have what you need, then continue editing.

Working copy:

The highlighted rows are different from the copy of the table from the wiki. This includes rows that have been edited and rows that you added. You can delete rows from the working copy in this view before continuing.

Qualifier (E)	GO ID (E)	GO term name (E)	Reference(s) (E)	Evidence Code (E)	withFrom (E)	Aspect (E)	Notes (E)	Status (E)
protein-binding	GO:0005116	protein-binding	PMID:18838888	EIA: Inferred from Physical Interaction	UniProt/P30203	F	Deleted from TracCap 12.0 - complete	
protein-binding	GO:0005116	protein-binding	PMID:18838888	EIA: Inferred from Physical Interaction	UniProt/P30203	F	Deleted from TracCap 12.0 - complete	
enzymatic activity	GO:0003674	enzymatic activity	GO:REF:0000000	EIA: Inferred from Electronic Annotation	UniProt/P10102	F	Deleted from TracCap 12.0 - complete	
helicase activity, acting on G-proteins	GO:0004480	helicase activity, acting on G-proteins	GO:REF:0000000	EIA: Inferred from Electronic Annotation	UniProt/P10102	F	Deleted from TracCap 12.0 - complete	
beta-galactosidase activity	GO:0004480	beta-galactosidase activity	GO:REF:0000000	EIA: Inferred from Electronic Annotation	UniProt/P10102	F	Deleted from TracCap 12.0 - complete	
carbohydrate metabolic process	GO:0003071	carbohydrate metabolic process	GO:REF:0000000	EIA: Inferred from Electronic Annotation	UniProt/P10102	F	Deleted from TracCap 12.0 - complete	
metabolic process	GO:0003071	metabolic process	GO:REF:0000000	EIA: Inferred from Electronic Annotation	UniProt/P10102	F	Deleted from TracCap 12.0 - complete	
beta-galactosidase complex	GO:0005047	beta-galactosidase complex	GO:REF:0000000	EIA: Inferred from Electronic Annotation	UniProt/P10102	F	Deleted from TracCap 12.0 - complete	
helicase activity	GO:0114787	helicase activity	GO:REF:0000000	EIA: Inferred from Electronic Annotation	UniProt/P10102	F	Deleted from TracCap 12.0 - complete	
helicase activity, acting on glycosyl bonds	GO:0114798	helicase activity, acting on glycosyl bonds	GO:REF:0000000	EIA: Inferred from Electronic Annotation	UniProt/P10102	F	Deleted from TracCap 12.0 - complete	
carbohydrate binding	GO:0022046	carbohydrate binding	GO:REF:0000000	EIA: Inferred from Electronic Annotation	UniProt/P10102	F	Deleted from TracCap 12.0 - complete	
cell-cell signaling	GO:0043109	cell-cell signaling	GO:REF:0000000	EIA: Inferred from Electronic Annotation	UniProt/P10102	F	Deleted from TracCap 12.0 - complete	
protein-catabolism	GO:0007137	protein-catabolism				C	Deleted from TracCap 11.1 - required field missing	
carbohydrate catabolic process	GO:0114830	carbohydrate catabolic process				F	Deleted from TracCap 11.1 - required field missing	
protein-lysine kinase activity	GO:0004110	protein-lysine kinase activity	PMID:16791034	EIA: Inferred by Curator		F	This is a sample annotation - complete	

edit working copy

Cancel

Back to address

View table metadata

Show row data

ISS: Inferred from Sequence or Structural Similarity

IPI: Inferred from Physical Interaction



help links

pcnB:Gene Product(s)

[TableEdit Help](#)

Standard name	PcnB
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EC number (for enzymes)	■ 2.7.7.19 ↗ ^[1]
	<input type="button" value="Edit"/> <input type="button" value="Copy"/> <input type="button" value="Delete"/> public

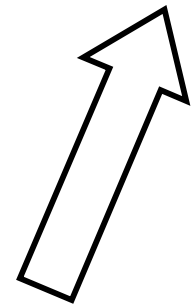


Table style

(e.g. align='right')

Heading style

(e.g. 'bgcolor = #ccccff' to make the heading background light blue)

[Cancel](#)

Extra for admins:

the loader

// Instantiate the object

```
$loader = new TableEdit_Loader;
```

// set some options

```
$loader->setVerbose(true);
```

```
$loader->setUser("WikiBot");
```

```
$loader->blah("foo");
```

*// load pretty much anything into tables from either an *.ifalt file.*

```
$loader->loadFromFile( $your_data );
```

ifalt

1. page title
2. page template
3. table template
4. row data
5. metadata
6. update type
7. misc

lacZ:Gene

Gene

Gene_nomenclature

field1 || field2 || field3

metadata-for-the-row

append

key=value&arr[]=foo+bar

...as related to GMOD

- Gbrowse roundtrip
 - requires SeqFeature::Store
 - requires valid GFF3
 - requires 'prokaryotic' genbank2gff3
 - User defined gene-models
- CHADO frontend
 - User defined everything
 - Bio::Chado::Schema / DBIx::Class

thanks

- Jim Hu, the rest of the Hu Lab
- EcoliHub(.org) & NIH
- GMOD
- Mediawiki Developers Mailing List

Daniel Renfro bluecurio@gmail.com

<http://gmod.org/TableEdit>