MageComet

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1 Purpose

MageComet is a web application designed for quick annotation and manipulation of MAGE-TAB files. The webapp features tools that allow curators to easily edit MAGE-TAB documents, without spending excessive time and effort formating files to MAGE-TAB specifications. MageComet's goal is to reduce the amount of time editing MAGE-TAB documents by automating tasks commonly encountered during curation. This automation allows curators to focus more on the biological data presented instead of spending time formating the document.

2 Loading Files

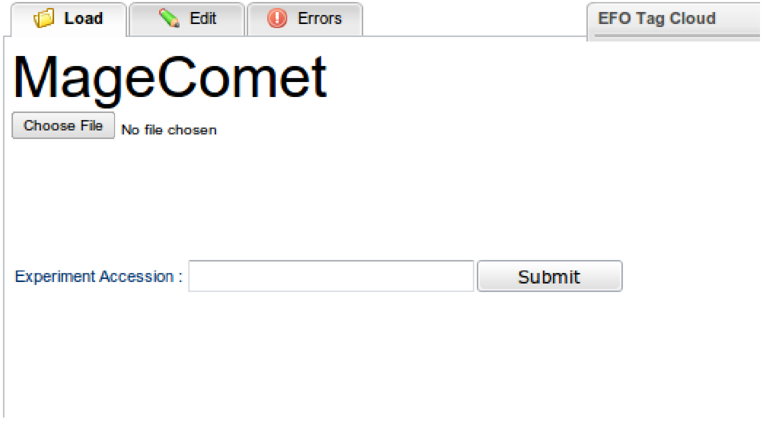
There are two ways to begin editing a set of MAGE-TAB files.

Direct Loading

Direct loading is used when MAGE-TAB documents are locally stored on the client machine. There are two files required to proceed, namely the the SDRF, and IDF files which are usually appended by ”sdrf.txt” and ”idf.txt” respectively. Though the MAGE-TAB specification does not mandate that SDRF and IDF files have these suffixes, MageComet uses these suffixes during load, and will not proceed without them.

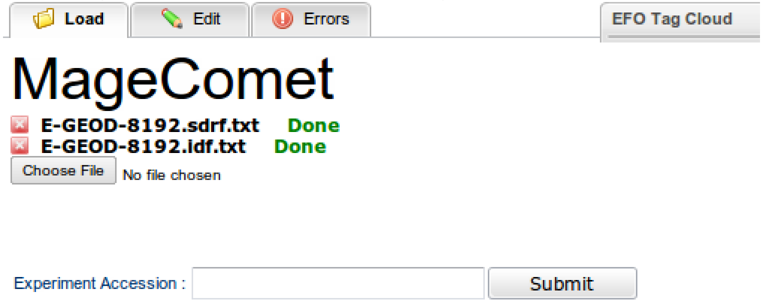
When starting the MageComet webapp, the user will be presented with the ”Load Tab”. This can be seen in Figure 1.

Figure 1: The opening load tab



To load the MAGE-TAB files to the server, the user must click the ”Choose File” button. A popup will appear and the user can select either the SDRF file or the IDF file to upload first. The same ”Choose File” button must be clicked after the first file has loaded. When both files have successfully been loaded, the screen should like like Figure 2.

Figure 2: Snapshot after loading IDF and SDRF files



E-GEOD-8192.sdrf.txt Done
E-GEOD-8192.idf.txt Done

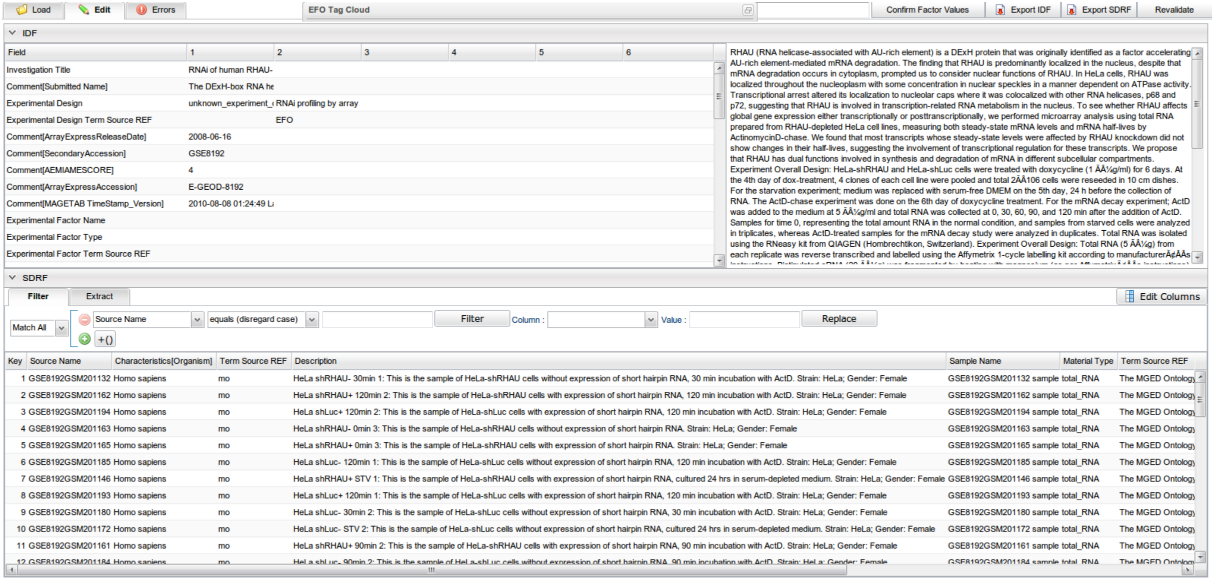
ArrayExpress FTP

To load a file via the ArrayExpress FTP service the user can use the form directly below the "Choose File" button. The user can simply type in the experiment accession and click submit, which will automatically fetch and load the IDF and SDRF files.

3 Filtering Data

Once the files have been loaded the user can proceed to the "Edit" tab. If loading has been successful, the page should resemble Figure 3.

Figure 3: Edit after successful load



Field	1	2	3	4	5	6
Investigation Title	RNAi of human RHAU-					
Comment[Submitted Name]	The DExH-box RNA he					
Experimental Design	unknown_experiment_(	RNAi profiling by array				
Experimental Design Term Source REF		EFO				
Comment[ArrayExpressReleaseDate]	2008-06-16					
Comment[SecondaryAccession]	GSE8192					
Comment[AEMIAMESCORE]	4					
Comment[ArrayExpressAccession]	E-GEOD-8192					
Comment[MAGETAB TimeStamp_Version]	2010-08-08 01:24:49 La					
Experimental Factor Name						
Experimental Factor Type						
Experimental Factor Term Source REF						

RHAU (RNA helicase-associated with AU-rich element) is a DExH protein that was originally identified as a factor accelerating AU-rich element-mediated mRNA degradation. The finding that RHAU is predominantly localized in the nucleus, despite that mRNA degradation occurs in cytoplasm, prompted us to consider nuclear functions of RHAU. In HeLa cells, RHAU was localized throughout the nucleoplasm with some concentration in nuclear speckles in a manner dependent on ATPase activity. Transcriptional arrest altered its localization to nucleolar caps where it was colocalized with other RNA helicases, p68 and p72, suggesting that RHAU is involved in transcription-related RNA metabolism in the nucleus. To see whether RHAU affects global gene expression either transcriptionally or posttranscriptionally, we performed microarray analysis using total RNA prepared from RHAU-depleted HeLa cell lines, measuring both steady-state mRNA levels and mRNA half-lives by ActinomycinD-chase. We found that most transcripts whose steady-state levels were affected by RHAU knockdown did not show changes in their half-lives, suggesting the involvement of transcriptional regulation for these transcripts. We propose that RHAU has dual functions involved in synthesis and degradation of mRNA in different subcellular compartments. Experiment Overall Design: HeLa-shRHAU and HeLa-shLuc cells were treated with doxycycline (1 ÃÂ¼g/ml) for 6 days. At the 4th day of dox-treatment, 4 clones of each cell line were pooled and total 2ÃÂ106 cells were reseeded in 10 cm dishes. For the starvation experiment; medium was replaced with serum-free DMEM on the 5th day, 24 h before the collection of RNA. The ActD-chase experiment was done on the 6th day of doxycycline treatment. For the mRNA decay experiment; ActD was added to the medium at 5 ÃÂ¼g/ml and total RNA was collected at 0, 30, 60, 90, and 120 min after the addition of ActD. Samples for time 0, representing the total amount RNA in the normal condition, and samples from starved cells were analyzed in triplicates, whereas ActD-treated samples for the mRNA decay study were analyzed in duplicates. Total RNA was isolated using the RNeasy kit from QIAGEN (Hombrechtikon, Switzerland). Experiment Overall Design: Total RNA (5 ÃÂ¼g) from each replicate was reverse transcribed and labelled using the Affymetrix 1-cycle labelling kit according to manufacturerÃ¢ÂÂs

Key	Source Name	Characteristics[Organism]	Term Source REF	Description	Sample Name	Material Type	Term Source REF
1	GSE8192GSM201132	Homo sapiens	mo	HeLa shRHAU- 30min 1: This is the sample of HeLa-shRHAU cells without expression of short hairpin RNA, 30 min incubation with ActD. Strain: HeLa; Gender: Female	GSE8192GSM201132 sample	total_RNA	The MGED Ontology
2	GSE8192GSM201162	Homo sapiens	mo	HeLa shRHAU+ 120min 2: This is the sample of HeLa-shRHAU cells with expression of short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female	GSE8192GSM201162 sample	total_RNA	The MGED Ontology
3	GSE8192GSM201194	Homo sapiens	mo	HeLa shLuc+ 120min 2: This is the sample of HeLa-shLuc cells with expression of short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female	GSE8192GSM201194 sample	total_RNA	The MGED Ontology
4	GSE8192GSM201163	Homo sapiens	mo	HeLa shRHAU- 0min 3: This is the sample of HeLa-shRHAU cells without expression of short hairpin RNA. Strain: HeLa; Gender: Female	GSE8192GSM201163 sample	total_RNA	The MGED Ontology
5	GSE8192GSM201165	Homo sapiens	mo	HeLa shRHAU+ 0min 3: This is the sample of HeLa-shRHAU cells with expression of short hairpin RNA. Strain: HeLa; Gender: Female	GSE8192GSM201165 sample	total_RNA	The MGED Ontology
6	GSE8192GSM201185	Homo sapiens	mo	HeLa shLuc- 120min 1: This is the sample of HeLa-shLuc cells without expression of short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female	GSE8192GSM201185 sample	total_RNA	The MGED Ontology
7	GSE8192GSM201146	Homo sapiens	mo	HeLa shRHAU+ STV 1: This is the sample of HeLa-shRHAU cells with expression of short hairpin RNA, cultured 24 hrs in serum-depleted medium. Strain: HeLa; Gender: Female	GSE8192GSM201146 sample	total_RNA	The MGED Ontology
8	GSE8192GSM201193	Homo sapiens	mo	HeLa shLuc+ 120min 1: This is the sample of HeLa-shLuc cells with expression of short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female	GSE8192GSM201193 sample	total_RNA	The MGED Ontology
9	GSE8192GSM201180	Homo sapiens	mo	HeLa shLuc- 30min 2: This is the sample of HeLa-shLuc cells without expression of short hairpin RNA, 30 min incubation with ActD. Strain: HeLa; Gender: Female	GSE8192GSM201180 sample	total_RNA	The MGED Ontology
10	GSE8192GSM201172	Homo sapiens	mo	HeLa shLuc- STV 2: This is the sample of HeLa-shLuc cells without expression of short hairpin RNA, cultured 24 hrs in serum-depleted medium. Strain: HeLa; Gender: Female	GSE8192GSM201172 sample	total_RNA	The MGED Ontology
11	GSE8192GSM201161	Homo sapiens	mo	HeLa shRHAU+ 90min 2: This is the sample of HeLa-shRHAU cells with expression of short hairpin RNA, 90 min incubation with ActD. Strain: HeLa; Gender: Female	GSE8192GSM201161 sample	total_RNA	The MGED Ontology
12	GSE8192GSM201184	Homo sapiens	mo	HeLa shLuc- 90min 2: This is the sample of HeLa-shLuc cells without expression of short hairpin RNA, 90 min incubation with ActD. Strain: HeLa; Gender: Female	GSE8192GSM201184 sample	total_RNA	The MGED Ontology

The first tool that is visible to the user is the filter and replace tool as shown in Figure 4. This tool is very similar to the search and replace tool in excel, but it is designed to be more specific for editing columns of data.

There are 5 components of this tool that a user can customize.

A Filter Column - This is the column that has a trait of interest. Usually this is the "Description" column.

B Logic - This dropdown box determines the logic a user wants to apply on the filter column It contains a list of items such "equals", "contains", "does not contain" and more.

C Filter Value - This is the value the user will filter on.

Parts A, B, and C contain the logic for filtering.

Example: A user wants to filter for all the rows that contain female in the description column. The values for the A, B, and C would be A:Description, B:Contains, C:Female

D Target Column - The column whose value will be set

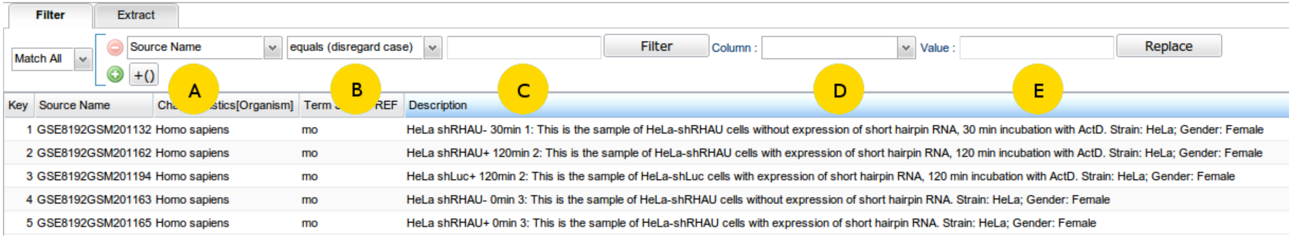
E New Value - The value that the target column will be set to.

Parts D and E contain the logic for replacing.

Example: A user wants to replace all the values in the column Characteristics[sex] with female. The values for D and E would be D:Characteristic[sex], E:female.

Note: The value for D must be a column that already exists

Figure 4: Filter and Replace



Key	Source Name	Ch stics[Organism]	Term REF	Description
1	GSE8192GSM201132	Homo sapiens	mo	HeLa shRHAU- 30min 1: This is the sample of HeLa-shRHAU cells without expression of short hairpin RNA, 30 min incubation with ActD. Strain: HeLa; Gender: Female
2	GSE8192GSM201162	Homo sapiens	mo	HeLa shRHAU+ 120min 2: This is the sample of HeLa-shRHAU cells with expression of short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female
3	GSE8192GSM201194	Homo sapiens	mo	HeLa shLuc+ 120min 2: This is the sample of HeLa-shLuc cells with expression of short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female
4	GSE8192GSM201163	Homo sapiens	mo	HeLa shRHAU- 0min 3: This is the sample of HeLa-shRHAU cells without expression of short hairpin RNA. Strain: HeLa; Gender: Female
5	GSE8192GSM201165	Homo sapiens	mo	HeLa shRHAU+ 0min 3: This is the sample of HeLa-shRHAU cells with expression of short hairpin RNA. Strain: HeLa; Gender: Female

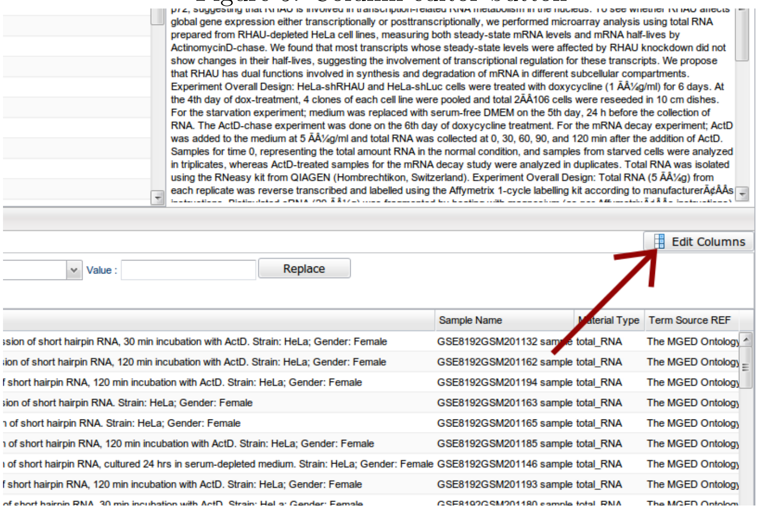
4 Column Manipulation

All column manipulation must be performed from the "Column Editor". The button to activate this editor is shown in Figure 5 and the popup editor is shown in Figure 6.

In this column editor, all of the rows are represented as rows. The left side of the editor designated by **A** is the clipboard. This section of the popup acts as a scratch buffer where columns are discarded to. In addition, new columns also appear in this clipboard before they are placed.

The right side of the editor designated by **C** is the representation of the SDRF columns. This section shows what columns are in the SDRF and in what order it appears.

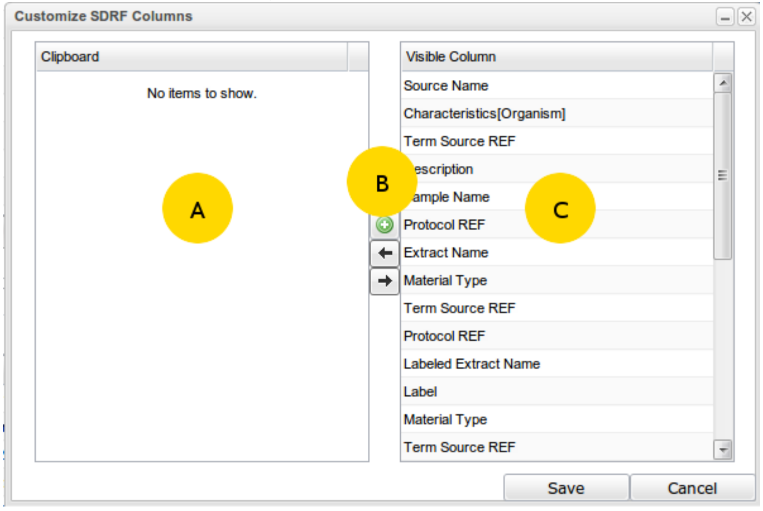
Figure 5: Column editor button



p72, suggesting that RHAU is involved in transcription-related RNA metabolism in the nucleus. To see whether RHAU affects global gene expression either transcriptionally or posttranscriptionally, we performed microarray analysis using total RNA prepared from RHAU-depleted HeLa cell lines, measuring both steady-state mRNA levels and mRNA half-lives by ActinomycinD-chase. We found that most transcripts whose steady-state levels were affected by RHAU knockdown did not show changes in their half-lives, suggesting the involvement of transcriptional regulation for these transcripts. We propose that RHAU has dual functions involved in synthesis and degradation of mRNA in different subcellular compartments. Experiment Overall Design: HeLa-shRHAU and HeLa-shLuc cells were treated with doxycycline (1 ÃÂ¼g/ml) for 6 days. At the 4th day of dox-treatment, 4 clones of each cell line were pooled and total 2ÃÂ106 cells were reseeded in 10 cm dishes. For the starvation experiment; medium was replaced with serum-free DMEM on the 5th day, 24 h before the collection of RNA. The ActD-chase experiment was done on the 6th day of doxycycline treatment. For the mRNA decay experiment; ActD was added to the medium at 5 ÃÂ¼g/ml and total RNA was collected at 0, 30, 60, 90, and 120 min after the addition of ActD. Samples for time 0, representing the total amount RNA in the normal condition, and samples from starved cells were analyzed in triplicates, whereas ActD-treated samples for the mRNA decay study were analyzed in duplicates. Total RNA was isolated using the RNeasy kit from QIAGEN (Hombrechtikon, Switzerland). Experiment Overall Design: Total RNA (5 ÃÂ¼g) from each replicate was reverse transcribed and labelled using the Affymetrix 1-cycle labelling kit according to manufacturerÃ¢ÂÂs instructions. Biotinylated cRNA (20 ÃÂ¼g) was fragmented by heating with magnesium (as per AffymetrixÃ¢ÂÂs instructions).

	Sample Name	Material Type	Term Source REF
ssion of short hairpin RNA, 30 min incubation with ActD. Strain: HeLa; Gender: Female	GSE8192GSM201132 sample	total_RNA	The MGED Ontology
sion of short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female	GSE8192GSM201162 sample	total_RNA	The MGED Ontology
f short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female	GSE8192GSM201194 sample	total_RNA	The MGED Ontology
sion of short hairpin RNA. Strain: HeLa; Gender: Female	GSE8192GSM201163 sample	total_RNA	The MGED Ontology
n of short hairpin RNA. Strain: HeLa; Gender: Female	GSE8192GSM201165 sample	total_RNA	The MGED Ontology
n of short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female	GSE8192GSM201185 sample	total_RNA	The MGED Ontology
n of short hairpin RNA, cultured 24 hrs in serum-depleted medium. Strain: HeLa; Gender: Female	GSE8192GSM201146 sample	total_RNA	The MGED Ontology
f short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female	GSE8192GSM201193 sample	total_RNA	The MGED Ontology
of short hairpin RNA, 30 min incubation with ActD. Strain: HeLa; Gender: Female	GSE8192GSM201180 sample	total_RNA	The MGED Ontology

Figure 6: Column editor



Adding Columns

To add a column, click the green plus sign below **B**. This will add a row to the clipboard **A**.

Removing Columns

To remove a column, drag the desired column from section **C** to section **A**. In addition, a user can also select the column from section **C** and click the ← button.

Reordering Columns

To reorder column orders, drag and drop the row to the desired position.

Renaming Columns

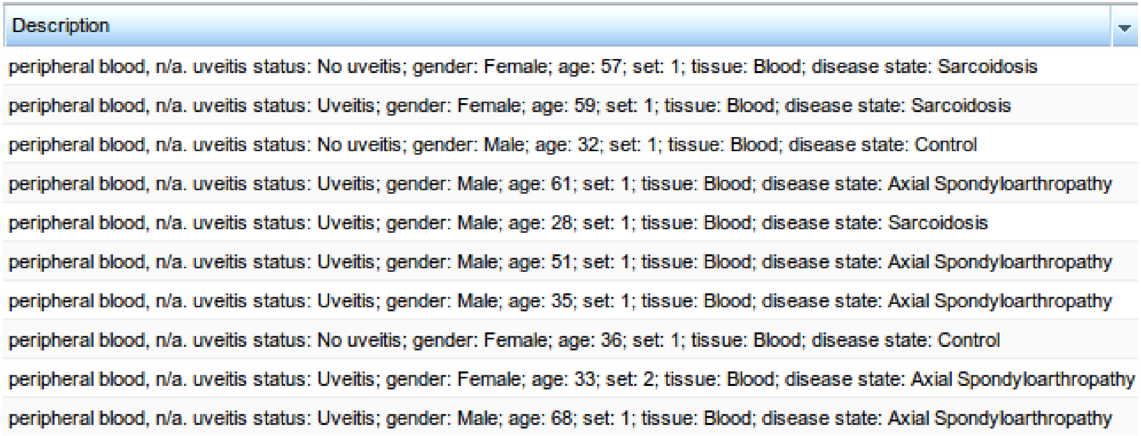
To rename a column, double click the row.

5 Extracting Data

The extract tool is a feature that splits row values formated with delimiters. If all of the rows in a column are formated similarly, this tool allows the user to separate a single column into many. An example of splittable column is seen in Figure 7.

In this example the ”Description” column should be separated into new columns for organism part, disease stage, sex, age, set, and disease state. Automatic splitting is difficult and avoided because a single column could have many different combinations of delimiters. In this example alone, there are commas, semicolons, colons, and text delimiters in a single row. However, because this format is consistent throughout the column, the extract feature implemented in MageComet works well in these situations.

Figure 7: Example of a splittable column



Description
peripheral blood, n/a. uveitis status: No uveitis; gender: Female; age: 57; set: 1; tissue: Blood; disease state: Sarcoidosis
peripheral blood, n/a. uveitis status: Uveitis; gender: Female; age: 59; set: 1; tissue: Blood; disease state: Sarcoidosis
peripheral blood, n/a. uveitis status: No uveitis; gender: Male; age: 32; set: 1; tissue: Blood; disease state: Control
peripheral blood, n/a. uveitis status: Uveitis; gender: Male; age: 61; set: 1; tissue: Blood; disease state: Axial Spondyloarthropathy
peripheral blood, n/a. uveitis status: Uveitis; gender: Male; age: 28; set: 1; tissue: Blood; disease state: Sarcoidosis
peripheral blood, n/a. uveitis status: Uveitis; gender: Male; age: 51; set: 1; tissue: Blood; disease state: Axial Spondyloarthropathy
peripheral blood, n/a. uveitis status: Uveitis; gender: Male; age: 35; set: 1; tissue: Blood; disease state: Axial Spondyloarthropathy
peripheral blood, n/a. uveitis status: No uveitis; gender: Female; age: 36; set: 1; tissue: Blood; disease state: Control
peripheral blood, n/a. uveitis status: Uveitis; gender: Female; age: 33; set: 2; tissue: Blood; disease state: Axial Spondyloarthropathy
peripheral blood, n/a. uveitis status: Uveitis; gender: Male; age: 68; set: 1; tissue: Blood; disease state: Axial Spondyloarthropathy

The extract tool is located in the same panel as the filter tool. By clicking on the "Extract" tab, the user can activate the panel that should resemble Figure 8. Like the filter tool, the extract tool has 5 components which the user must fill in.

A From Column - This is the column that is splittable. Usually this is the "Description" column.

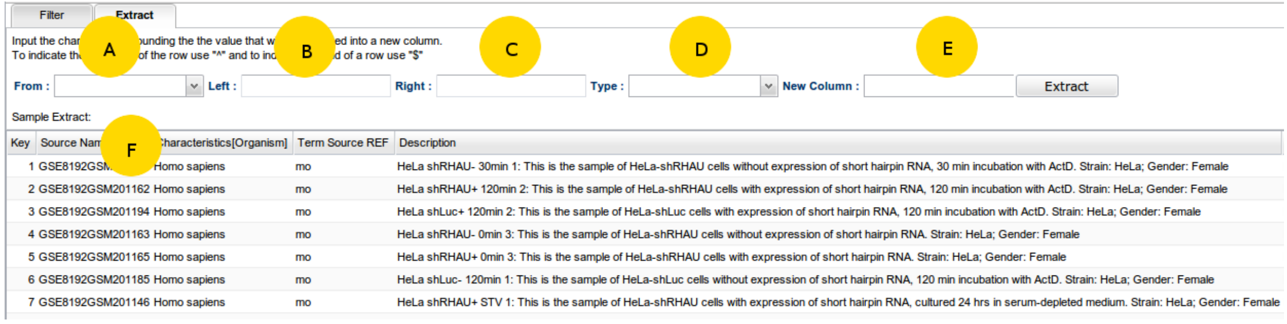
B Left Input - This field should be filled in with the text that is left of the value that should be extracted. The input however should be **unique** as it will only match the first input found.

C Right Input - This field should be filled in with the text that is right of the value that should be extracted.

D Type Column - This field is the target column type. The possible choices are "Clipboard", "Characteristic", Factor Value", or "Both".

E Column Name- This field is the target column name. This is the value that will fit in between the brackets [ ].

Figure 8: Extract



Input the char unding the the value that w ed into a new column.
To indicate th of the row use "^" and to ind d of a row use "$"

Sample Extract:

Key	Source Nam	haracteristics[Organism]	Term Source REF	Description
1	GSE8192GSM	Homo sapiens	mo	HeLa shRHAU- 30min 1: This is the sample of HeLa-shRHAU cells without expression of short hairpin RNA, 30 min incubation with ActD. Strain: HeLa; Gender: Female
2	GSE8192GSM201162	Homo sapiens	mo	HeLa shRHAU+ 120min 2: This is the sample of HeLa-shRHAU cells with expression of short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female
3	GSE8192GSM201194	Homo sapiens	mo	HeLa shLuc+ 120min 2: This is the sample of HeLa-shLuc cells with expression of short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female
4	GSE8192GSM201163	Homo sapiens	mo	HeLa shRHAU- 0min 3: This is the sample of HeLa-shRHAU cells without expression of short hairpin RNA. Strain: HeLa; Gender: Female
5	GSE8192GSM201165	Homo sapiens	mo	HeLa shRHAU+ 0min 3: This is the sample of HeLa-shRHAU cells with expression of short hairpin RNA. Strain: HeLa; Gender: Female
6	GSE8192GSM201185	Homo sapiens	mo	HeLa shLuc- 120min 1: This is the sample of HeLa-shLuc cells without expression of short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female
7	GSE8192GSM201146	Homo sapiens	mo	HeLa shRHAU+ STV 1: This is the sample of HeLa-shRHAU cells with expression of short hairpin RNA, cultured 24 hrs in serum-depleted medium. Strain: HeLa; Gender: Female

When the user completes values for **B** and **C**, the section designated by **F** will show the sample values that will be extracted.

More Examples

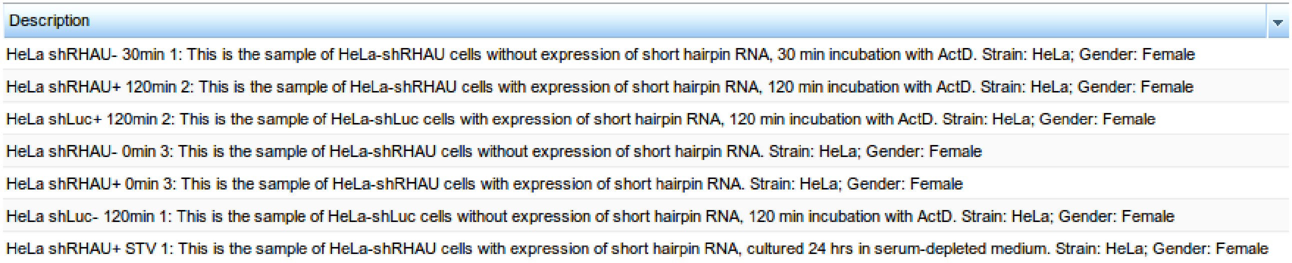
The following lists the input values for **B** and **C** that will extract the targeted value successfully for Figure 7.

Left	Right	Sample Extract Row 1
ˆ	,	peripheral blood
status:	;	No uveitis
gender:	;	Female
set:	;	1
tissue:	;	Blood
state:	$	Sarcoidosis

Table 1: Sample inputs and outputs for Figure 7

The following lists the input values for **B** and **C** that will extract the targeted value successfully for Figure 9.

Figure 9: Another example of a splittable column (intermediate difficulty)



Description

HeLa shRHAU- 30min 1: This is the sample of HeLa-shRHAU cells without expression of short hairpin RNA, 30 min incubation with ActD. Strain: HeLa; Gender: Female

HeLa shRHAU+ 120min 2: This is the sample of HeLa-shRHAU cells with expression of short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female

HeLa shLuc+ 120min 2: This is the sample of HeLa-shLuc cells with expression of short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female

HeLa shRHAU- 0min 3: This is the sample of HeLa-shRHAU cells without expression of short hairpin RNA. Strain: HeLa; Gender: Female

HeLa shRHAU+ 0min 3: This is the sample of HeLa-shRHAU cells with expression of short hairpin RNA. Strain: HeLa; Gender: Female

HeLa shLuc- 120min 1: This is the sample of HeLa-shLuc cells without expression of short hairpin RNA, 120 min incubation with ActD. Strain: HeLa; Gender: Female

HeLa shRHAU+ STV 1: This is the sample of HeLa-shRHAU cells with expression of short hairpin RNA, cultured 24 hrs in serum-depleted medium. Strain: HeLa; Gender: Female

Left	Right	Sample Extract Row 1
ˆ	[0-9]	HeLa shRHAU-
[+-]	min	30
gender:	;	Female
RNA,	min	30
Strain:	;	HeLa
Gender:	$	Female

Table 2: Sample inputs and outputs for Figure 9

6 Tag Cloud

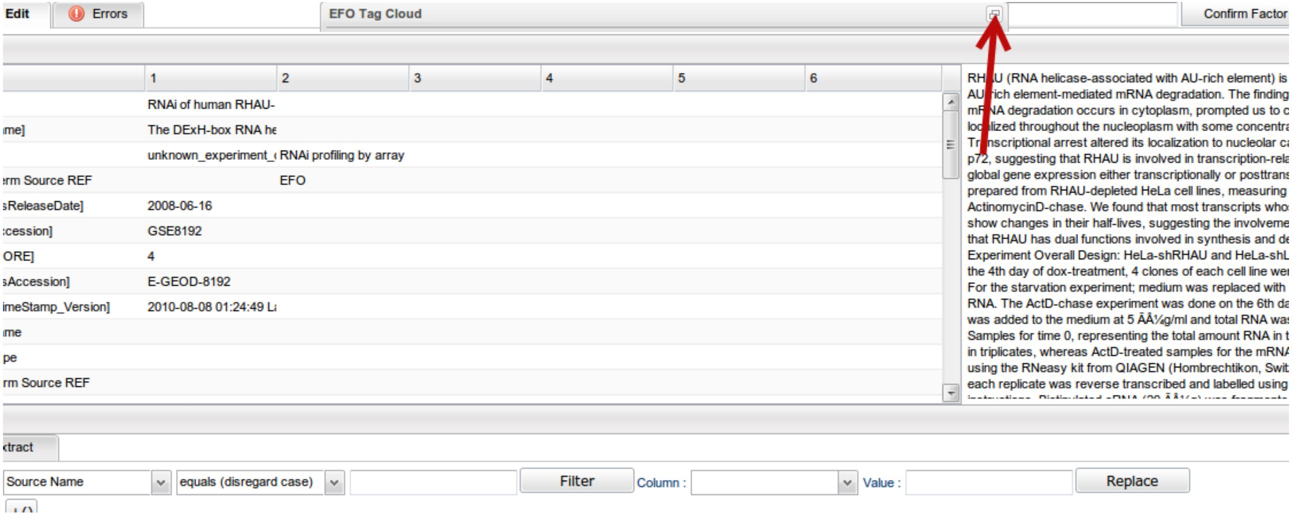
The tag cloud is a feature that helps curators identify important biological information text-mined from the IDF and SDRF text. To open the window, click on the button designated by Figure 10. A window should pop up that resembles Figure 11.

In the tagcloud representation of the text, each item represents an EFO ontology term that has been mined from 2 documents. The size of an item corresponds to where the term came from. The smallest size, indicates that only the IDF mentions the word. The medium sized text indicates that the text was mined from the SDRF, and the largest sized text indicates that both the IDF and SDRF mention the ontology term.

Adding characteristics via tagcloud

A sub feature of the tag cloud is the ability to add a characteristic term to all rows in a document. This feature is useful when some vital information is mentioned in the experiment description but is not mentioned in the SDRF document. By clicking on the term in the tag cloud, a new popup will show up, giving the user the option of adding the selected term to the SDRF. Figure 12.

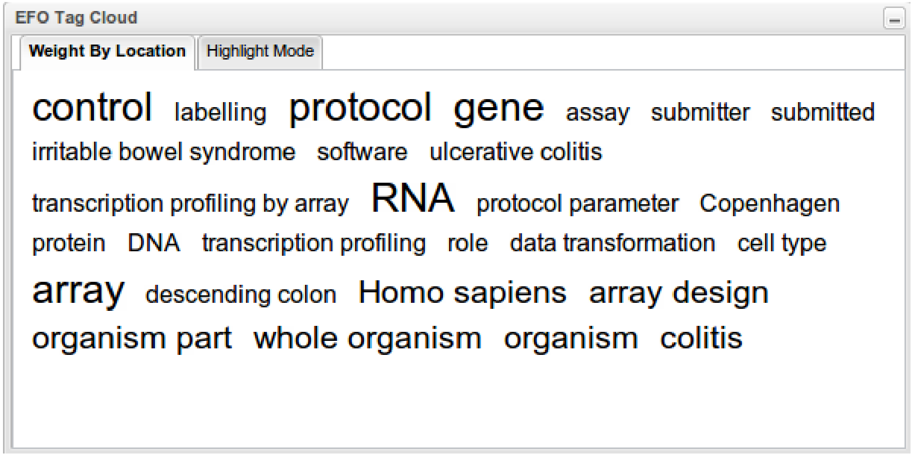
Figure 10: Default tagcloud position



	1	2	3	4	5	6
	RNAi of human RHAU-					
ime]	The DExH-box RNA he					
	unknown_experiment_(	RNAi profiling by array				
erm Source REF		EFO				
sReleaseDate]	2008-06-16					
ccession]	GSE8192					
ORE]	4					
sAccession]	E-GEOD-8192					
imeStamp_Version]	2010-08-08 01:24:49 La					
ime						
pe						
rm Source REF						

RHAU (RNA helicase-associated with AU-rich element) is
AU-rich element-mediated mRNA degradation. The finding
mRNA degradation occurs in cytoplasm, prompted us to c
localized throughout the nucleoplasm with some concentra
Transcriptional arrest altered its localization to nucleolar ca
p72, suggesting that RHAU is involved in transcription-rela
global gene expression either transcriptionally or posttrans
prepared from RHAU-depleted HeLa cell lines, measuring
ActinomycinD-chase. We found that most transcripts who
show changes in their half-lives, suggesting the involveme
that RHAU has dual functions involved in synthesis and de
Experiment Overall Design: HeLa-shRHAU and HeLa-shL
the 4th day of dox-treatment, 4 clones of each cell line wer
For the starvation experiment; medium was replaced with
RNA. The ActD-chase experiment was done on the 6th da
was added to the medium at 5 ÃÂ¼g/ml and total RNA was
Samples for time 0, representing the total amount RNA in t
in triplicates, whereas ActD-treated samples for the mRNA
using the RNeasy kit from QIAGEN (Hombrechtikon, Swit
each replicate was reverse transcribed and labelled using

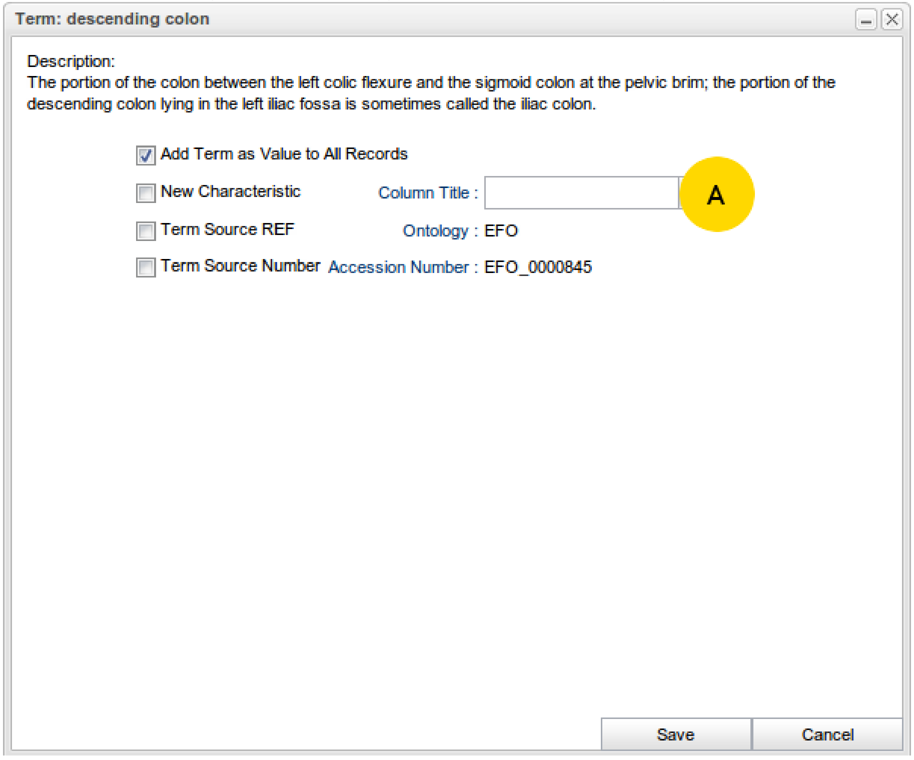
Figure 11: The TagCloud Window



When a tag cloud item is clicked, a popup will appear, providing some useful information about the term. It usually provides a description near the top, which is pulled from the EFO ontology and the term source number.

The user can choose to add a characteristic column, term source ref column, or a term source number column to the SDRF, depending on how granular the curation is. The input field designated by **A** in Figure 12 is the value that will be placed in the brackets [ ].

Figure 12: Adding a characteristic via tagcloud



Term: descending colon

Description:
The portion of the colon between the left colic flexure and the sigmoid colon at the pelvic brim; the portion of the descending colon lying in the left iliac fossa is sometimes called the iliac colon.

☑ Add Term as Value to All Records

☐ New Characteristic Column Title :

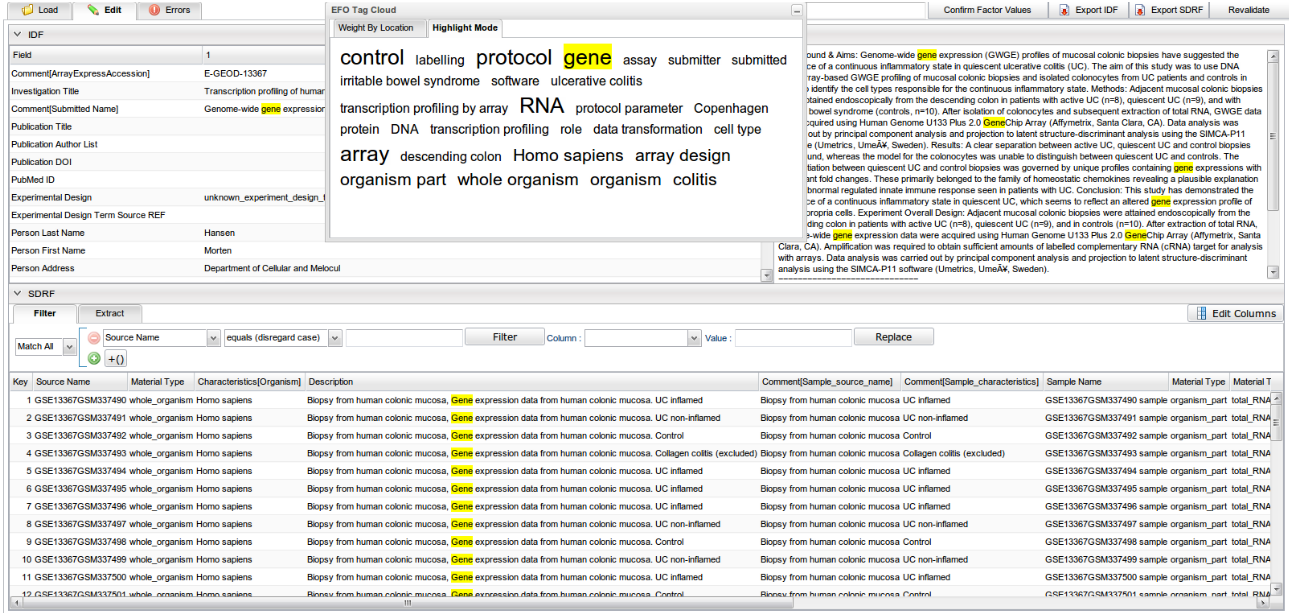
☐ Term Source REF Ontology : EFO

☐ Term Source Number Accession Number : EFO_0000845

Highlighting text via tagcloud

Another sub feature of the tag cloud is to highlight text. This feature can be accessed by clicking the ”Highlight Mode” tab in Figure 11. The same cloud will appear, but clicking on a term will cause it to highlight on the page. This is demonstrated by Figure 13.

Figure 13: Tagcloud highlight feature



Field	1
Comment[ArrayExpressAccession]	E-GEOD-13367
Investigation Title	Transcription profiling of human
Comment[Submitted Name]	Genome-wide gene expression
Publication Title	
Publication Author List	
Publication DOI	
PubMed ID	
Experimental Design	unknown_experiment_design_t
Experimental Design Term Source REF	
Person Last Name	Hansen
Person First Name	Morten
Person Address	Department of Cellular and Melocul

control labelling protocol gene assay submitter submitted irritable bowel syndrome software ulcerative colitis transcription profiling by array RNA protocol parameter Copenhagen protein DNA transcription profiling role data transformation cell type array descending colon Homo sapiens array design organism part whole organism organism colitis

ound & Aims: Genome-wide gene expression (GWGE) profiles of mucosal colonic biopsies have suggested the
ce of a continuous inflammatory state in quiescent ulcerative colitis (UC). The aim of this study was to use DNA
ray-based GWGE profiling of mucosal colonic biopsies and isolated colonocytes from UC patients and controls in
identify the cell types responsible for the continuous inflammatory state. Methods: Adjacent mucosal colonic biopsies
btained endoscopically from the descending colon in patients with active UC (n=8), quiescent UC (n=9), and with
bowel syndrome (controls, n=10). After isolation of colonocytes and subsequent extraction of total RNA, GWGE data
cquired using Human Genome U133 Plus 2.0 GeneChip Array (Affymetrix, Santa Clara, CA). Data analysis was
out by principal component analysis and projection to latent structure-discriminant analysis using the SIMCA-P11
e (Umetrics, UmeÃ¥, Sweden). Results: A clear separation between active UC, quiescent UC and control biopsies
und, whereas the model for the colonocytes was unable to distinguish between quiescent UC and controls. The
tiation between quiescent UC and control biopsies was governed by unique profiles containing gene expressions with
ant fold changes. These primarily belonged to the family of homeostatic chemokines revealing a plausible explanation
bnormal regulated innate immune response seen in patients with UC. Conclusion: This study has demonstrated the
ce of a continuous inflammatory state in quiescent UC, which seems to reflect an altered gene expression profile of
propria cells. Experiment Overall Design: Adjacent mucosal colonic biopsies were attained endoscopically from the
ding colon in patients with active UC (n=8), quiescent UC (n=9), and in controls (n=10). After extraction of total RNA,
e-wide gene expression data were acquired using Human Genome U133 Plus 2.0 GeneChip Array (Affymetrix, Santa
Clara, CA). Amplification was required to obtain sufficient amounts of labelled complementary RNA (cRNA) target for analysis
with arrays. Data analysis was carried out by principal component analysis and projection to latent structure-discriminant
analysis using the SIMCA-P11 software (Umetrics, UmeÃ¥, Sweden).

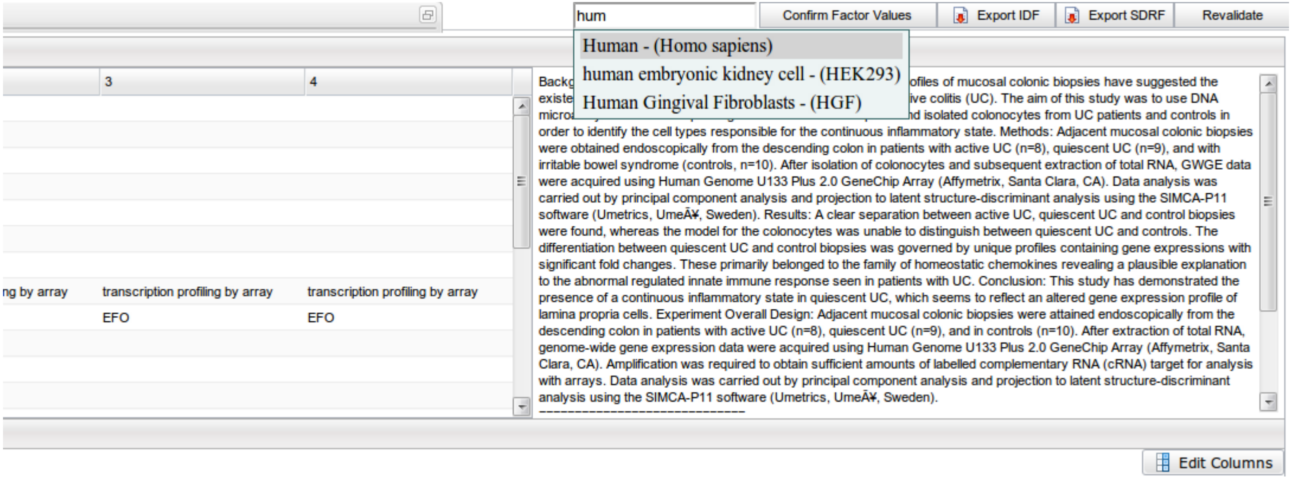
Key	Source Name	Material Type	Characteristics[Organism]	Description	Comment[Sample_source_name]	Comment[Sample_characteristics]	Sample Name	Material Type	Material T
1	GSE13367GSM337490	whole_organism	Homo sapiens	Biopsy from human colonic mucosa, Gene expression data from human colonic mucosa. UC inflamed	Biopsy from human colonic mucosa	UC inflamed	GSE13367GSM337490 sample	organism_part	total_RNA
2	GSE13367GSM337491	whole_organism	Homo sapiens	Biopsy from human colonic mucosa, Gene expression data from human colonic mucosa. UC non-inflamed	Biopsy from human colonic mucosa	UC non-inflamed	GSE13367GSM337491 sample	organism_part	total_RNA
3	GSE13367GSM337492	whole_organism	Homo sapiens	Biopsy from human colonic mucosa, Gene expression data from human colonic mucosa. Control	Biopsy from human colonic mucosa	Control	GSE13367GSM337492 sample	organism_part	total_RNA
4	GSE13367GSM337493	whole_organism	Homo sapiens	Biopsy from human colonic mucosa, Gene expression data from human colonic mucosa. Collagen colitis (excluded)	Biopsy from human colonic mucosa	Collagen colitis (excluded)	GSE13367GSM337493 sample	organism_part	total_RNA
5	GSE13367GSM337494	whole_organism	Homo sapiens	Biopsy from human colonic mucosa, Gene expression data from human colonic mucosa. UC inflamed	Biopsy from human colonic mucosa	UC inflamed	GSE13367GSM337494 sample	organism_part	total_RNA
6	GSE13367GSM337495	whole_organism	Homo sapiens	Biopsy from human colonic mucosa, Gene expression data from human colonic mucosa. UC inflamed	Biopsy from human colonic mucosa	UC inflamed	GSE13367GSM337495 sample	organism_part	total_RNA
7	GSE13367GSM337496	whole_organism	Homo sapiens	Biopsy from human colonic mucosa, Gene expression data from human colonic mucosa. UC inflamed	Biopsy from human colonic mucosa	UC inflamed	GSE13367GSM337496 sample	organism_part	total_RNA
8	GSE13367GSM337497	whole_organism	Homo sapiens	Biopsy from human colonic mucosa, Gene expression data from human colonic mucosa. UC non-inflamed	Biopsy from human colonic mucosa	UC non-inflamed	GSE13367GSM337497 sample	organism_part	total_RNA
9	GSE13367GSM337498	whole_organism	Homo sapiens	Biopsy from human colonic mucosa, Gene expression data from human colonic mucosa. Control	Biopsy from human colonic mucosa	Control	GSE13367GSM337498 sample	organism_part	total_RNA
10	GSE13367GSM337499	whole_organism	Homo sapiens	Biopsy from human colonic mucosa, Gene expression data from human colonic mucosa. UC non-inflamed	Biopsy from human colonic mucosa	UC non-inflamed	GSE13367GSM337499 sample	organism_part	total_RNA
11	GSE13367GSM337500	whole_organism	Homo sapiens	Biopsy from human colonic mucosa, Gene expression data from human colonic mucosa. UC inflamed	Biopsy from human colonic mucosa	UC inflamed	GSE13367GSM337500 sample	organism_part	total_RNA
12	GSE13367GSM337501	whole_organism	Homo sapiens	Biopsy from human colonic mucosa, Gene expression data from human colonic mucosa. Control	Biopsy from human colonic mucosa	Control	GSE13367GSM337501 sample	organism_part	total_RNA

7 EFO Search Box

The EFO search box is a convenience feature implemented into MageComet. If the user wants to confirm that an EFO term exists in the EFO ontology, the EFO search box can be used as shown in Figure 14.

The search field autocompletes based on the query text and displays 3 terms that match the query. If an item is in parentheses as shown with human, the value in parentheses is the standard name for the synonym found. If the user wants to copy the standard ontology name, pressing enter while over the term will fill in the field, making it copyable.

Figure 14: EFO searchbox



hum

Human - (Homo sapiens)
human embryonic kidney cell - (HEK293)
Human Gingival Fibroblasts - (HGF)

	3	4
ng by array	transcription profiling by array	transcription profiling by array
	EFO	EFO

Backg ofiles of mucosal colonic biopsies have suggested the
existe ive colitis (UC). The aim of this study was to use DNA
micro nd isolated colonocytes from UC patients and controls in
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analysis using the SIMCA-P11 software (Umetrics, UmeÃ¥, Sweden).
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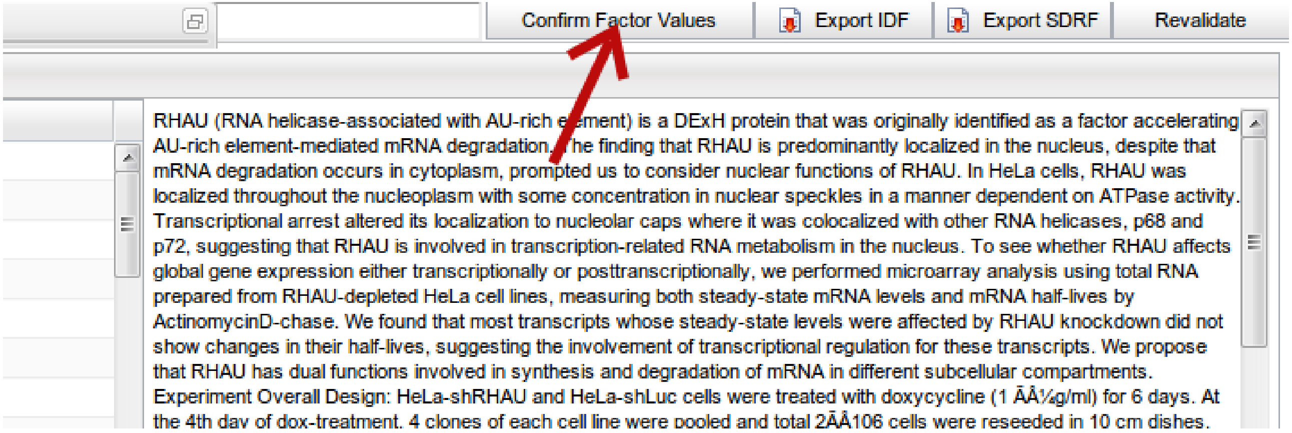
8 Adding Factor Values

When the user has finished extracting the factor values in the SDRF document, the IDF document must be updated to reflect the changes. The IDF document can be updated via the ”Confirm Factor Value” button as shown in Figure 15.

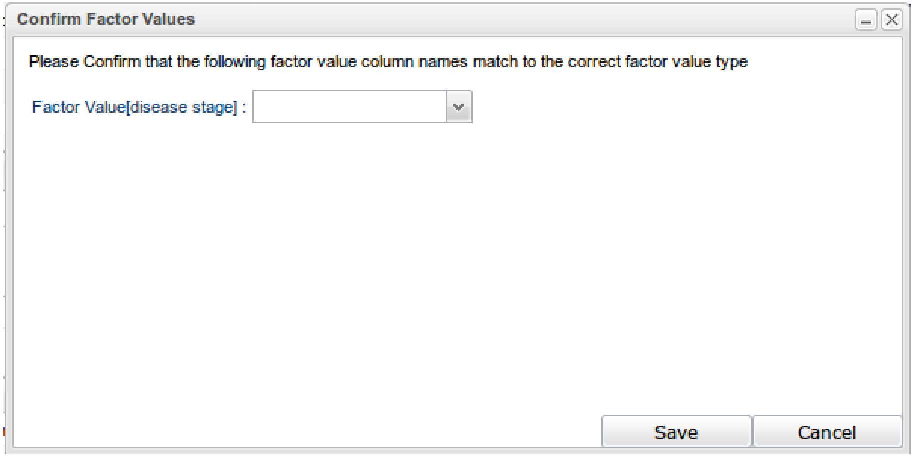
Once clicked a window will appear that shows all of the Factor Values in the SDRF. Figure 16. After filling in the corresponding Factor Value Types and clicking save, the IDF document will have the correct values automatically inserted.

Figure 15: Confirm factor value button



RHAU (RNA helicase-associated with AU-rich element) is a DExH protein that was originally identified as a factor accelerating AU-rich element-mediated mRNA degradation. The finding that RHAU is predominantly localized in the nucleus, despite that mRNA degradation occurs in cytoplasm, prompted us to consider nuclear functions of RHAU. In HeLa cells, RHAU was localized throughout the nucleoplasm with some concentration in nuclear speckles in a manner dependent on ATPase activity. Transcriptional arrest altered its localization to nucleolar caps where it was colocalized with other RNA helicases, p68 and p72, suggesting that RHAU is involved in transcription-related RNA metabolism in the nucleus. To see whether RHAU affects global gene expression either transcriptionally or posttranscriptionally, we performed microarray analysis using total RNA prepared from RHAU-depleted HeLa cell lines, measuring both steady-state mRNA levels and mRNA half-lives by ActinomycinD-chase. We found that most transcripts whose steady-state levels were affected by RHAU knockdown did not show changes in their half-lives, suggesting the involvement of transcriptional regulation for these transcripts. We propose that RHAU has dual functions involved in synthesis and degradation of mRNA in different subcellular compartments. Experiment Overall Design: HeLa-shRHAU and HeLa-shLuc cells were treated with doxycycline (1 ÃÂ¼g/ml) for 6 days. At the 4th day of dox-treatment. 4 clones of each cell line were pooled and total 2ÃÂ106 cells were reseeded in 10 cm dishes.

Figure 16: Confirm factor value window



Please Confirm that the following factor value column names match to the correct factor value type

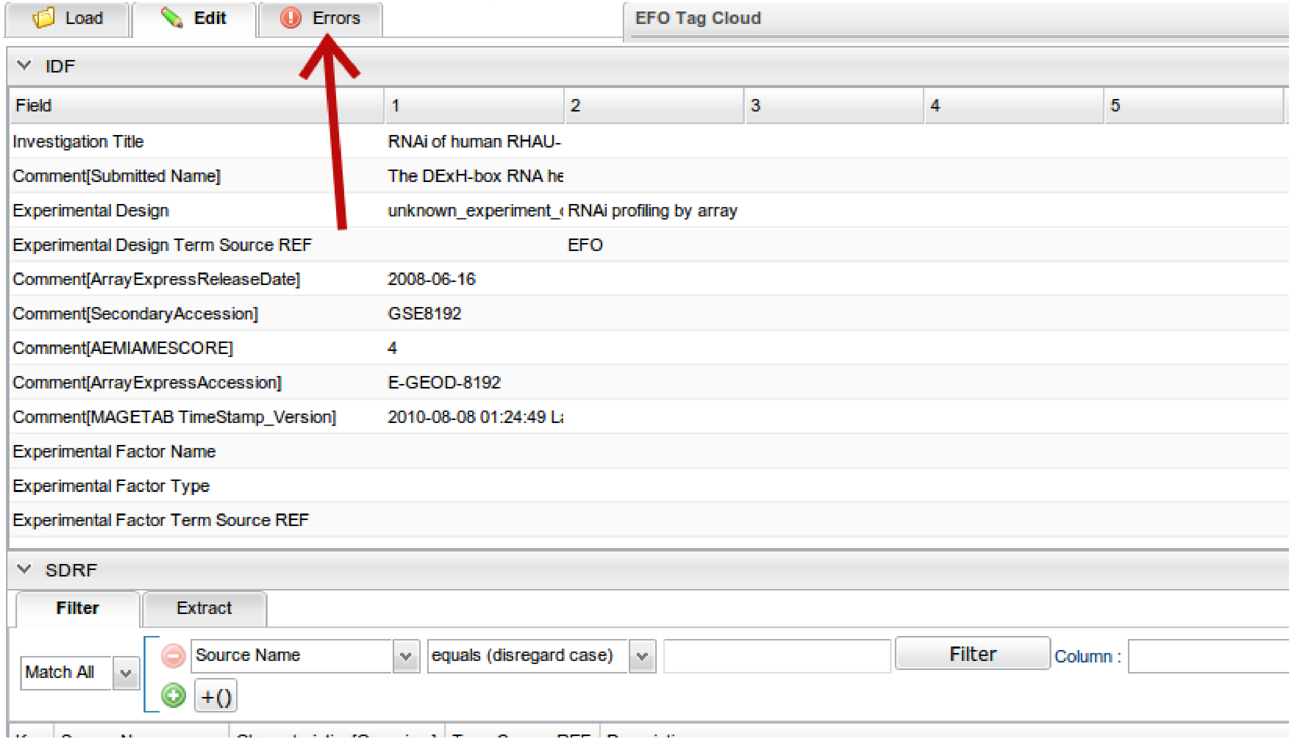
Factor Value[disease stage] :

9 Revalidation/Validation

MageComet also has implementation of the Limpopo validators. A user can see all the of the errors by clicking on the Errors tab as shown in Figure 17.

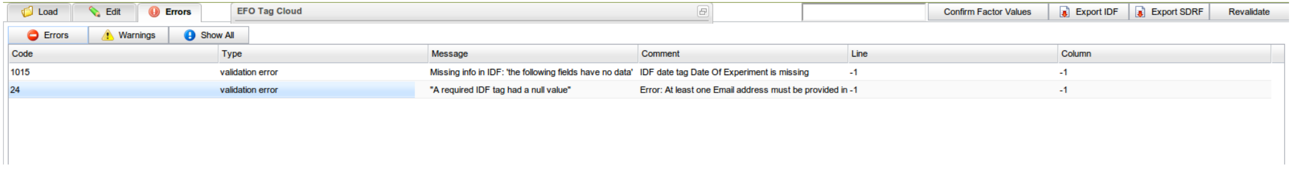
In the errors tab, the user can selectively view errors, warnings, missing information, and revalidate the current MAGE-TAB documents after changes have been made.

Figure 17: Errors button



Field	1	2	3	4	5
Investigation Title	RNAi of human RHAU-				
Comment[Submitted Name]	The DExH-box RNA he				
Experimental Design	unknown_experiment_(	RNAi profiling by array			
Experimental Design Term Source REF		EFO			
Comment[ArrayExpressReleaseDate]	2008-06-16				
Comment[SecondaryAccession]	GSE8192				
Comment[AEMIAMESCORE]	4				
Comment[ArrayExpressAccession]	E-GEOD-8192				
Comment[MAGETAB TimeStamp_Version]	2010-08-08 01:24:49 L:				
Experimental Factor Name					
Experimental Factor Type					
Experimental Factor Term Source REF					

Figure 18: Errors tab

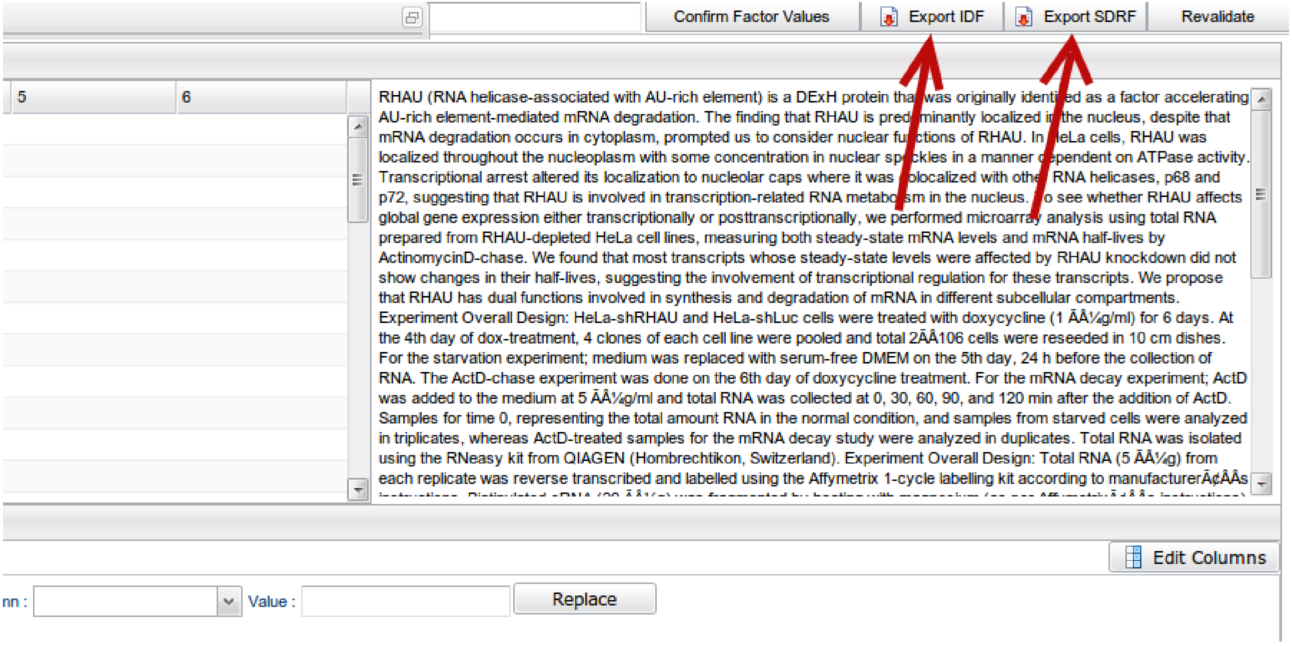


Code	Type	Message	Comment	Line	Column
1015	validation error	Missing info in IDF: 'the following fields have no data'	IDF date tag Date Of Experiment is missing	-1	-1
24	validation error	"A required IDF tag had a null value"	Error: At least one Email address must be provided in	-1	-1

10 Exporting

The final stage in editing is exporting the changes. To save a file locally, the user can click either ”Export” button as designated by Figure 19.

Figure 19: Export buttons



RHAU (RNA helicase-associated with AU-rich element) is a DExH protein that was originally identified as a factor accelerating AU-rich element-mediated mRNA degradation. The finding that RHAU is predominantly localized in the nucleus, despite that mRNA degradation occurs in cytoplasm, prompted us to consider nuclear functions of RHAU. In HeLa cells, RHAU was localized throughout the nucleoplasm with some concentration in nuclear speckles in a manner dependent on ATPase activity. Transcriptional arrest altered its localization to nucleolar caps where it was colocalized with other RNA helicases, p68 and p72, suggesting that RHAU is involved in transcription-related RNA metabolism in the nucleus. To see whether RHAU affects global gene expression either transcriptionally or posttranscriptionally, we performed microarray analysis using total RNA prepared from RHAU-depleted HeLa cell lines, measuring both steady-state mRNA levels and mRNA half-lives by ActinomycinD-chase. We found that most transcripts whose steady-state levels were affected by RHAU knockdown did not show changes in their half-lives, suggesting the involvement of transcriptional regulation for these transcripts. We propose that RHAU has dual functions involved in synthesis and degradation of mRNA in different subcellular compartments. Experiment Overall Design: HeLa-shRHAU and HeLa-shLuc cells were treated with doxycycline (1 ÃÂ¼g/ml) for 6 days. At the 4th day of dox-treatment, 4 clones of each cell line were pooled and total 2ÃÂ106 cells were reseeded in 10 cm dishes. For the starvation experiment; medium was replaced with serum-free DMEM on the 5th day, 24 h before the collection of RNA. The ActD-chase experiment was done on the 6th day of doxycycline treatment. For the mRNA decay experiment; ActD was added to the medium at 5 ÃÂ¼g/ml and total RNA was collected at 0, 30, 60, 90, and 120 min after the addition of ActD. Samples for time 0, representing the total amount RNA in the normal condition, and samples from starved cells were analyzed in triplicates, whereas ActD-treated samples for the mRNA decay study were analyzed in duplicates. Total RNA was isolated using the RNeasy kit from QIAGEN (Hombrechtikon, Switzerland). Experiment Overall Design: Total RNA (5 ÃÂ¼g) from each replicate was reverse transcribed and labelled using the Affymetrix 1-cycle labelling kit according to manufacturerÃ¢ÂÂs