Last Update: 2012-12-19

Editor – The IntAct Curation Interface

User Guide

Contact: intact-developers@googlegroups.com

1. Opening the IntAct Production Editor

   URL: http://www.ebi.ac.uk/intact/editor

   Log on using your given user name and password

   In the case of a local instance, you can log in the first time with the following credential: admin/admin (we recommend you immediately create your own admin user and disable the default credential)

The dashboard – currently shows a listing of all papers you have curated lately. Colour coding:

a. Light green – under curation
b. Red – has been checked, entry needs correction
c. Yellow – entry has been corrected and is in the rechecking process.
d. Dark green – Accepted and will be/has been released

You may select the following options

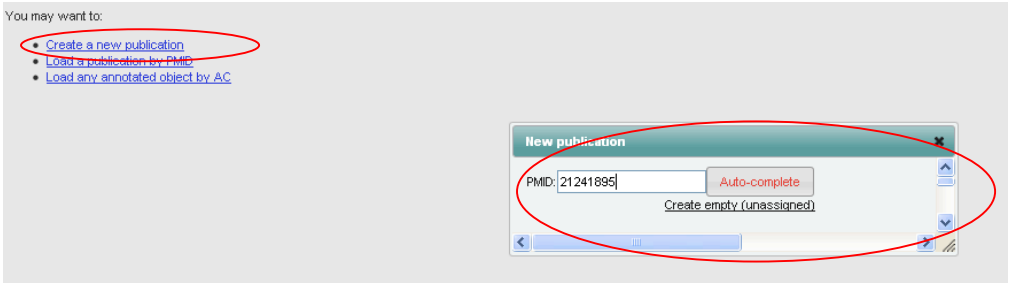
For normal working, keep the first 2 boxes checked but you may be interested in following the progress of a paper through to publication which is possible by selecting other check boxes.

You can now open an existing entry or start a new one.
To search for an existing entry

a. Find it on the dashboard.
b. Search by PMID
c. Search by first authors surname e.g.'smith' or, more specifically surname + publication year 'smith-2004'

The full curation manual can be found at
www.ebi.ac.uk/~intact/site/doc/IntActAnnotationRules.pdf

2. Creating a new entry
    a. Press button labelled ‘Curate’
    b. Select ‘Create a new publication’
    c. Enter the PMID in the box
    d. Hit Auto-complete



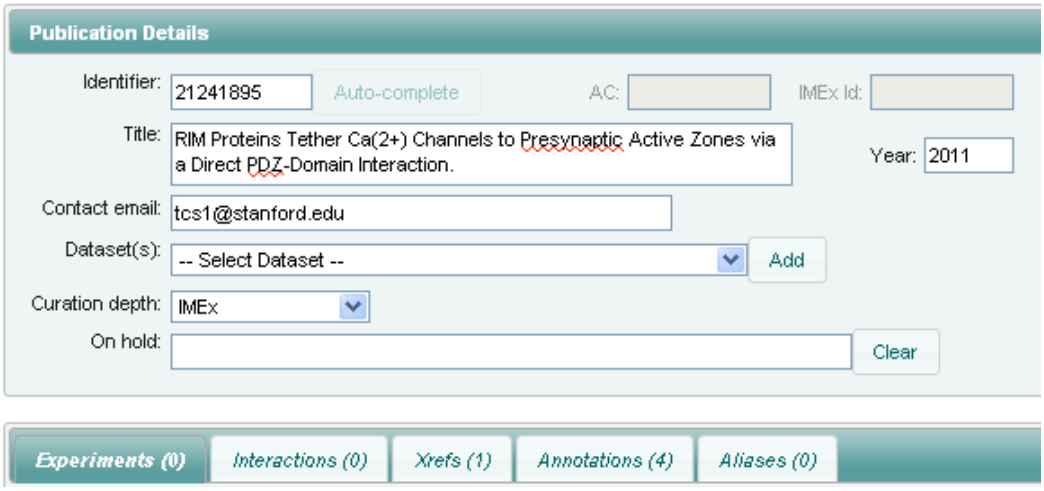
The editor will now access and complete the basic journal details. The orange Save button will now be visible, hitting this will save all existing annotation at the publication level.

Depending on the journal, this may not include the contact e-mail of the author. If this is missing, it needs to be added to the box headed ‘Contact e-mail’. Multiple author e-mails should all be added, and separated by a comma “smith@somewhere.com, jones@elsewhere.ac.uk’.

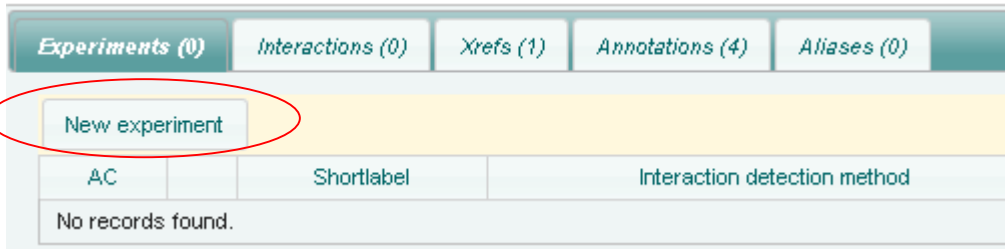
IMEx/MIMx – check your pre-set default. If you select IMEx, the entire paper must be annotated to this standard. You may change the selection at any point.

Dataset annotation should only be added to IMEx entries (see **4.8.10**). IMEx entries may be annotated to multiple datasets.

Save before moving on



3. Adding the first experiment
    a. Open the 'Experiment' tab
    b. Click on 'New experiment' – the short label will be automatically generated



    c. Select the appropriate host organism (**see 4.4**)
    d. Select the appropriate 'Interaction detection method' (see **4.5**). If you cannot find the term, use the Browse button which appears when you hover the mouse to the right of the drop down menu. Walk the hierarchy until you find the correct term and then select it. Clicking on the term will load it into the editor.
    e. Select the appropriate 'Participant detection method' (see 4.6). Again a Browse button will let you walk the hierarchy.

Depending on the entry, and your individual work style, you may choose to add annotation to the experiment at this point. This will normally only apply to IMEx entries. Annotations commonly added are:

Data-processing – to explain the processes you may have gone through to map proteins to UniProtKB accession numbers (see 4.8.9)

Exp-modification – describe a non-standard procedure which does not exactly match the interaction detection method selected (see 4,8,11)

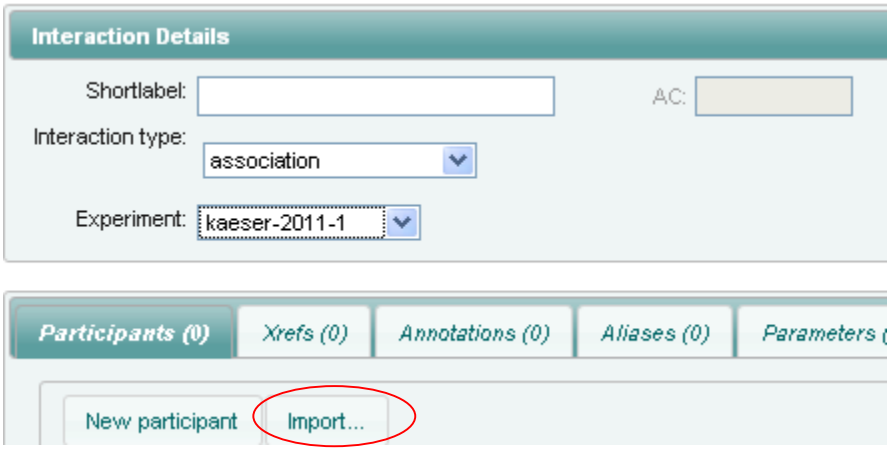
Library-used – screening assays, give some detail of the construct or phage library (see 4.8.12)

Please note, the annotation must relate to ALL the interactions you attach to the experiment. If it does not apply to one or more interactions, attach these to a separate experiment.

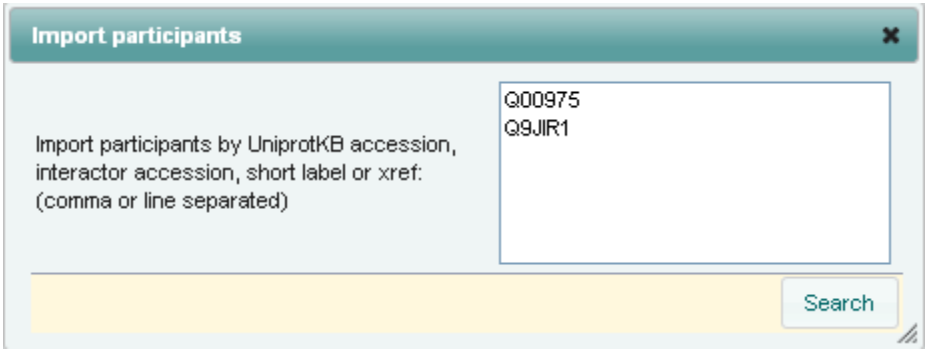
a. Open Annotation tab
b. Press 'New Annotation' button
c. Select Topic from pull-down menu
d. Add Free text annotation

Save before moving on.

4. Adding the first interaction
    a. Open the 'Interaction' tab
    b. The short label will be auto-generated for you.
    c. Select the 'Interaction type' (see 5.5). Again a Browse button will allow you to access the controlled vocabularies.
        i. 'Direct interaction' should only be used for in vitro interactions involving only two proteins
        ii. 'Physical association' should be used for 2-hybrid (and related) assays and coips or pulldowns where only a single bait has been identified
        iii. 'Association' should be used for coips and pulldowns with two baits or more.
    d. Press the 'Import' button. N.B. do not use ADD PARTICIPANT – it does not work yet.



    e. List all the interactors. The editor recognises UniProtKB accession numbers, ChEBI identifiers, internal IntAct identifiers and UniProtKB identifiers, but the last ONLY if the protein is already in IntAct. Accession numbers are your best option. Press Search



    f. Your list of interactors are displayed as a table. De-select any which are incorrect and they will not be imported. Move to the bottom on the entry and select
        i. Experimental Role (see 5.9.2)

2-hybrid – bait is the protein with the DNA binding domain tag, prey have the transcriptional activiator domain

Co-ips – the bait is the Ab used to bring down the complex, prey are the proteins subsequently identified by western blot or mass spec.

Pulldowns – the bait is the protein which binds to the column, prey are the proteins subsequently identified by western blot or mass spec.

Gel filtration, co-purifications and colocalisation – use Neutral

Once the experimental role has been selected, a sensible biological role will be set as default.

Note – you can only select one role for all the interactors in this screen. For n-ary interactions, it is least work to select 'prey', then amend the appropriate protein to 'bait' once the proteins have been imported.

ii. Biological Role (see 5.9.1)

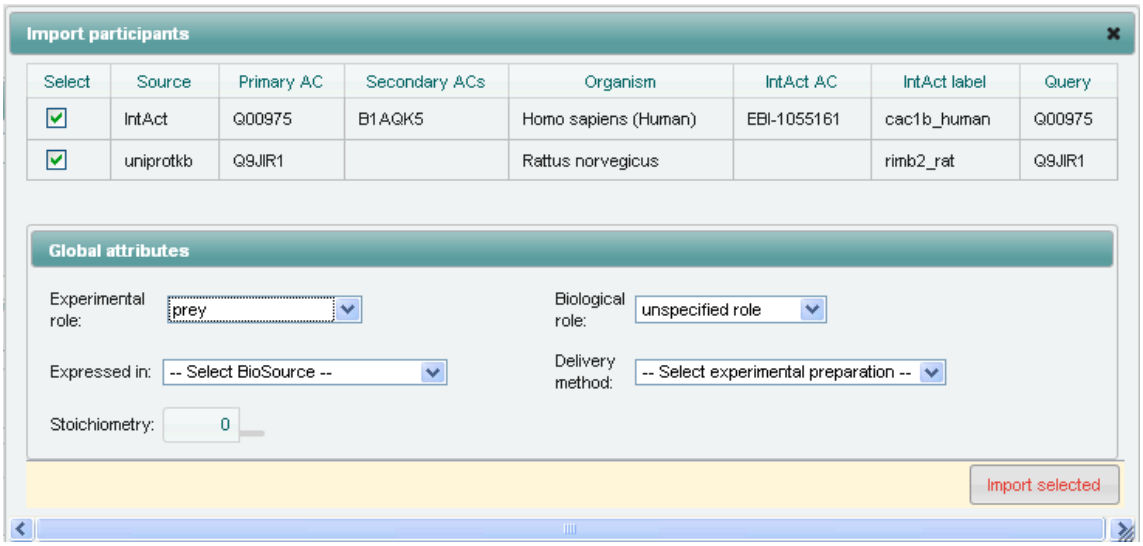
Usually enzyme/enzyme target

iii. Expressed-in (see 5.10)

This need only be done for experiments with host organism=in vitro.

Note – the prey may be from a different host organism from the bait. Again, it is least work to set for the multiple prey then amend the bait following import.

g. When all is chosen, press 'Import selected entries' – once entries have imported, amend any individual entries.



Save before moving on.

You may choose to add annotation/cross-references to the interaction at this point. This will normally only apply to IMEx entries. Annotations commonly added are:

Figure legend – indicates where the data was taken from e.g. Table 1, Fig. 2a. Data may have been summarised from multiple location e.g. Figs 1a, 2b and Supp. Table 1

Agonist/Antagonist – generally added to whole cells, and in some undefined way increase/decrease the interaction

Stimulation/inhibition – directly modulate the interaction by binding to a participant

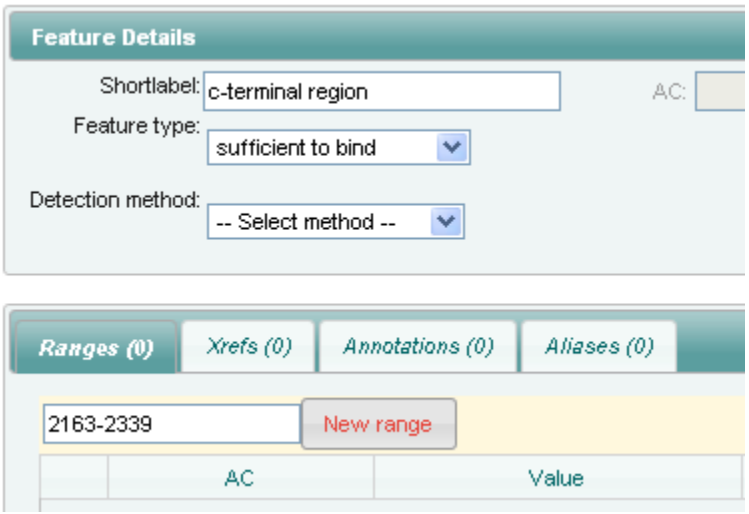
3d-resolution/3d-r-factor – for x-ray crystallography only. Copy for PDBe entry.

Cross-references (see **5.13)** – for colocalisations or interactions performed in a defined subcellular location e.g. nuclear extracts, add the appropriate GO component term (e.g. GO:0005634, nucleus – add the correct qualifier)

For enzyme assays add the appropriate GO Function and Process terms (e.g GO:0004672, protein kinase activity; GO:0006468, protein amino acid phosphorylation – add the correct qualifier)

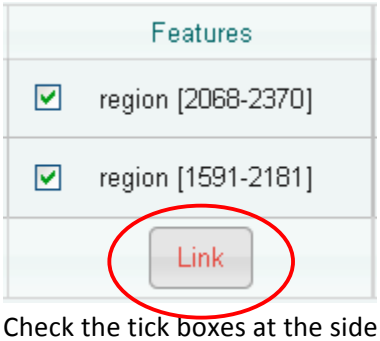
Adding a feature (normally only IMEx entries)

h. Open the appropriate participant via the hyper-link
i. Press 'New Feature'
j. Add a short name – if in doubt use 'region' but more specific terms may be used. For point mutations, use to indicate the nature of the mutations (see **6.2.5**)
k. Select the Feature Type (see **6.1.3**)
l. If appropriate, add a 'Feature detection method'. Features present on the construct at the start of the experiment e.g. tags, radio-labels do not need this added
m. Add the range in the box. This can be '?-?' if unknown, 'n-n', 'c-c' or '40-199'. If amino acids are known, please check mapping to current UniProt sequence is correct. If a cross-reference corresponds to an InterPro domain (80% overlap as a rough estimate) add the InterPro accession number as a cross-reference, qualifier='identity' (see **6.1.6**).



Common tags – pulldowns His GST, TAP, anti-tag coips Myc, Flag, HA

If you have two domains which have been shown to interact with each other in the experiment that you are annotating, please Link these domains as they will then be shown as linked in the new graphical display on the website.

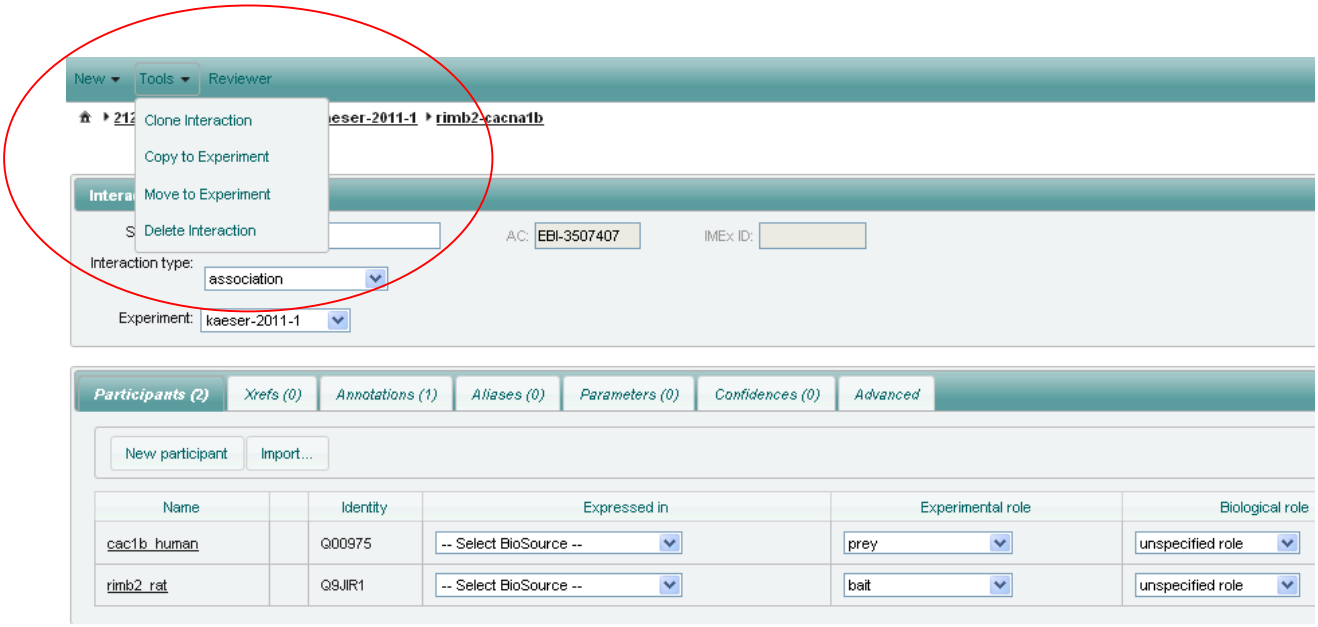


Check the tick boxes at the side of each feature and then press the button 'Link'. To unlink, press on the link symbol which subsequently appears to the side of the feature.

5. Cloning

You may clone an experiment, an interaction or an experiment plus all its interactions. This is a quick way of dealing with very repetitive data.

To clone an experiment, open the appropriate experiments then use the 'Tools' option on the menu bar. To clone an interaction, open the interaction first, then again use the 'Tools' option.



In all cases, will have to change something on the first page before he system will allow you to Save. Remember you will have cloned all the Annotations, Cross-references and Features associated with the experiment/interaction/interactors so you must make any necessary changes to ensure they are all relevant for the new experiment. Experiment short label will update incrementally, interaction short labels will change as you make any changes to the interactor set.

Once your entry is finished

when you have completed a paper and are ready for the entire entry to go forward to checking, go to the Publication level (e.g. Press on `9605687 (imex curation)' in the breadcrumb trail) and hit the button "Ready for Checking". This will immediately assign you a reviewer and the entry will appear on your reviewer's dashboard.

If your reviewer immediately Accepts your entire paper, it will disappear from the dashboard tab "Publications owned by you" but will still be accessible if you select " Ready for release".

If your reviewer rejects one or more experiments, the entry will appear red in your dashboard view, as before, with the reviewer's comments visible when you open each experiment. Correct the entry - there is a new annotation topic "correction comment" in which you can send any message to the reviewer you wish. You can access this by pressing the yellow button which is present on the experiment page. Please do not clear the 'To-be-reviewed' comment, as this will remind your checker what they asked you to correct.

Once your corrections are complete, hit the 'Ready for (re) checking' button and the entry will both turn an exciting shade of yellow, and re-appear in your reviewer's dashboard.

Hopefully, at this point it will finally be Accepted and disappear from view. Keep an eye on the Status of the entry in your dashboard - if it now changes back to 'Curation in progress', it is a signal to you that you have another round of correction to do.

Requesting new PSI-MI CV terms

https://sourceforge.net/tracker/?group_id=65472&atid=612426

IMEx	MIMIx
Capture all PPI experimental data in publication - includes colocalisations but NOT genetic interactions	
Publication	
PMID + autocomplete	PMID + autocomplete
Author contact details	Author contact details
IMEx designator	MIMIx designator
Dataset	
Experiment	
Host organism-tissue/cell	Host organism
Interaction Detection method	Interaction Detection method
Participant Detection method	Participant Detection method
Additional annotation – experimental modification, data processing	
Interaction	
Interaction Type	Interaction Type
Figure legend(s)	Figure legend(s)
Additional annotation – Comments, Caution	
Location xref (GO) – usually only colocalisations	
Participants	
Experimental/Biological role	Experimental/Biological role
Expressed in (in vitro expts only)	
Features – tags, radio/isotope labels, deletion mutants, point mutations	

Binding site xrefs (InterPro)	

Sample IMEx Entries

Y2H screen	
Directed Y2H	EBI-4406557
Anti-bait coimmunopreciptiation	
Anti-tag coimmunopreciptiation	
Pulldown	
Far Western	EBI-593412