Longer term: Interaction with IMEx Consortium?

- The IMEx Consortium (IntAct, DIP, MINT, BioGrid, MPact, MatrixDB and MPIDB) carry out high-quality manual annotation of protein-protein interactions (http://disber.net/imexdrupal/node/1) from peer-reviewed papers.

- The annotation format used by IMEx captures full details of participants, assay and detection methods and meets the PSI **Minimum Information about a Molecular Interaction eXperiment (MIMIx)** standard.

- IMEx groups are working to produce a complete, non-redundant annotation set, that can be downloaded from an IMEx web service.

- Many GOC groups may already work with an IMEx member, capturing interaction data that is MIMIx or IMEx compliant

Longer term: Interaction with IMEx Consortium?

- Those at the GO Consortium meeting in April agreed it would be sensible to investigate a closer interaction with IMEx curation activities.

- An IMEx central website is being developed that will incorporate an option to contact the consortium to ask for a paper to be curated, making it possible for all GO groups to have their curation requests triaged between the different IMEx databases

- Groups can decide to contribute annotations using IMEx/MIMIx standards or just integrate annotations from IMEx; and decide what types of interaction data they would prefer to display

- Curators in UniProtKB will shortly contribute all protein binding annotations directly to the IntAct group, using a dedicated editor applying MIMIx /IMEx (editor will be integrated into the protein2go tool).

- All binding annotations meeting UniProtKB quality standards will be integrated into the UniProtKB-GOA dataset from IntAct.

Annotation Survey Q1

- **27 responses, 14 skipped**

- **Part 1**
  - Protein-protein interaction
  - Column 8 or 16
  - Reciprocal IPI annotations

- **Part 2**
  - Enzyme activity
  - Column 8 or 16

Annotation Survey Q1, part 2

PubMed: 18636086 The tumour suppressor CYLD is a negative regulator of RIG-I-mediated antiviral response

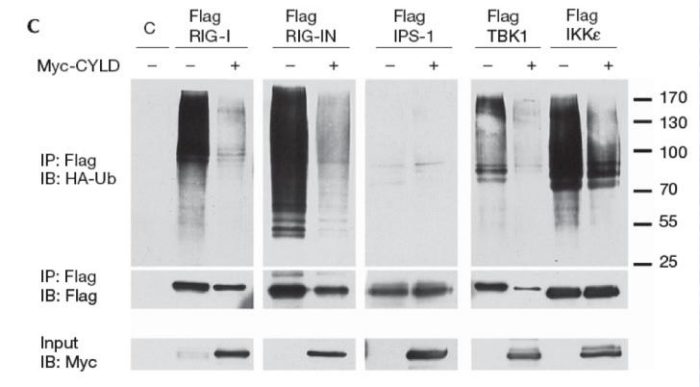

Fig 3C: EBNA cells were transfected with Flag-tagged RIG-I, RIG-IN, IPS-1, TBK1 or IKKe, together with HA-tagged K63-Ub and either empty vector or Myc-tagged CYLD. Lysates were denatured in 1% SDS and immuno-precipitated with anti-Flag. The immunoprecipitations were blotted with anti-HA to detect K63-Ub and re-probed with anti-Flag. The input lysates were blotted with anti-Myc to detect CYLD

Name	GO term	Ev.	With	C. 16	Response
CYLD	Ubiquitin specific protease activity	IPI	RIG-I		2
CYLD	Ubiquitin specific protease activity	IDA		RIG-I	14
CYLD	Protein K63-linked deubiquitination	IDA			24

Annotation Survey Q1, part 1

PubMed: 18636086 The tumour suppressor CYLD is a negative regulator of RIG-I-mediated antiviral response

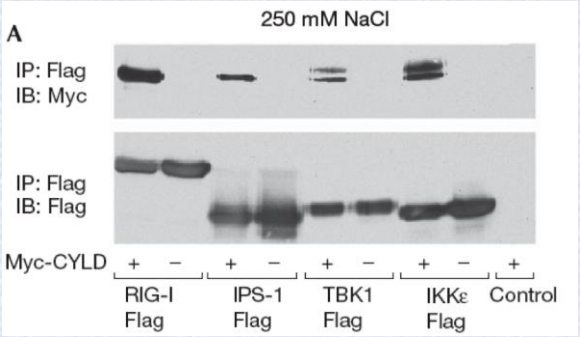

Fig.3A: Co-immunoprecipitation experiments of Myc-tagged CYLD and Flag-tagged RIG-I, IPS-1, TBK1 or IKKe in 293 EBNA cells. When the stringency of the wash was increased to 500mM NaCl, the interaction of TBK1 or IKKe with CYLD was no longer observed.

Name	GO term	Ev.	With	C. 16	Response
RIG-I	Protease binding	IPI	CYLD		21
RIG-I	Protease binding	IDA		CYLD	0
CYLD	DEAD/H-box RNA helicase binding	IPI	RIG-I		9
CYLD	DEAD/H-box RNA helicase binding	IDA		RIG-I	0
CYLD	Enzyme binding	IPI	RIG-I		6
CYLD	Enzyme binding	IDA		RIG-I	0

Annotation Survey Q1, comments

1. instead of enzyme binding why not protein binding ???

2. For the interaction of CYLD with RIG-I I would use the generic term 'protein binding'instead of 'enzyme binding' or 'DEAD..helicase' since it is not established that RIG-I has an enzymatic activity.

3. I don't think I would capture annotations to RIG-I with GO (althopugh I ticked the
most likely box because I had to tick one I would infacgt probably only use protein
binding), although I would capture the fact that RIG-I is a target of, and deubiquitinated by CYLD

4. We would not capture RIG-I as column 16

Annotation Survey Q1, comments

5. We generally try to avoid annotations that involve binding or it's children because they are difficult to interpret. What I would LIKE to say though is that CYLD has K63-linked deubiquitination activity and acts upon RIG-I. Sounds like a good use for Col. 16..but we don't have the ability to annotated into col. 16 yet...and it's gonna be a long while before we do.

6. Item 1 was chosen arbitrarily to satisfy the surveyMonkey. As suggested in the note, all of the proposed annotations take the experimental observation that two proteins stick to each other with high affinity and decorate it with hypothetical functional extrapolations - none of these data show that proteolysis, RNA unwinding, or anything else is perturbed as a result of the binding.

7. For the interaction data, I would have to read the paper to determine if the authors thought the weak interaction was significant.

Annotation Survey Q1

- **Part 1**
  - Protein-protein interaction
  - Column 8 or 16
  - Reciprocal IPI annotations

- **Part 2**
  - Enzyme activity
  - Column 8 or 16