

Outreach: Users' requests

Target release	Not applicable (to be released when/if it fits)
Document status	Ongoing
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Goal

- This document is to keep track of wishes and requests from users via **support email** and **from the feedback survey completed at the end Open Targets hands-on workshops**
- This document is **NOT** an inventory of feedback gathered through usability testings of new or current aspects of the Platform. This is available elsewhere in [Google Docs](#).

Background and strategic fit

- Collate into one place users' requests from support and hands-on workshops
- Check how frequent the request is made by independent users
- See **IF/WHEN** we can implement the changes (to be discussed in internal meetings)
- If the changes get implemented, usability testing will be carried out and the feedback of those will be available in [Google Docs](#).

Assumptions

- *Users of the Open Targets Platform may explore other sites/resources and suggest ways to **replicate** some of their data (e.g. LD from Ensembl), widgets (graphs from GTEx) or tables (gene centric GWAS catalog association table)*
- *Users of the Open Targets Platform will explore other sites/resources and ask us to **link out** to the external sources*

Requests suggested by users:

#	Title	User Story	Source of the request	GitHub feature (if applicable)	Notes
1	LD	I'd like to have the LD tables from Ensembl in Open Targets (Paola Bronson - Biogen).	support email		We already link out to the Variant tab in Ensembl which has among other things link to LD.
2	All associations	I'd like to be able to view in a table (and download) the associations for a gene (or SNP) all in one place (Paola Bronson - Biogen).	support email		We display the genomic context of a gene and its SNPs with associations upon clicking the lollipops. Could a table be provided? GWAS catalog provides this. Shall we replicate it? Shall we link out to them (https://www.ebi.ac.uk/gwas/search?query=clec16a). Need to be careful: we may want to change the focus of people: instead of looking at every single SNP to taking the whole genomic region at once.
3	odds ratio	I'd like to be get other stats from GWAS data e.g. odds ratio, 95% CI, B coefficient (Paola Bronson - Biogen).	support email		This information is already somewhere else e.g. Ensembl who we link out to.
4	GTEx	It'd be helpful to show the gene expression and exon expression plots from GTEx (images below) on the open targets target profile page. I also like how the default GTEx grouping is by body region (e.g. brain) (Paola Bronson - Biogen).	support email		GTEx preferred widget is http://www.gtexportal.org/home/gene/LIX1

5	BioGPS	It'd be helpful to provide a link to biogps static images for human expression data of the gene of interest (Paola Bronson - Biogen).	support email		overall biogps website: http://biogps.org/#goto=genereport&id=4261 specific link that has images to download: http://ds.biogps.org/?data set=BDS_00001&gene=4261
6	Quantitative expression data	I'd like to see quantitative data for genes on which cell types they are expressed in. For example, "Gene A" is expressed highly in "Cell type B" but not at all in "Cell type C".	workshop 17/10/16		Quantitative expression data could be extracted from http://www.immgen.org/databrowser/index.html for lymphocytes and http://servers.binf.ku.dk/bloodspot/ for other blood cells
7	mouse strains SNPs and the data for the Sanger Knockout project	I'd like to see the Sanger database on polymorphisms in different inbred mouse strains. It might be good when looking for tools to investigate a certain gene. The Sanger Mouse Genome Project also has a data base with all the data from their various knock out mice with information about all aspects of physiology (neurology tests, blood cell count, infection resistance) that might be useful if incorporated.	workshop 17/10/16		
8	ENSG IDs downloaded from the web interface	Previously when downloading the genes associations, the Ensembl gene ID was included. Now it seems not to be available. It would make downstream use easier if the Ensembl ID were included in the download from the web interface.	support email		e.g. https://www.targetvalidation.org/disease/EFO_0003843/associations . User has been informed there is an API for getting more detail, but claims is not quite as easy as clicking a download link.
9	zebrafish models	here are zebrafish mutants openly available in US and EU for the vast majority of genes, so I think it is important to include them as open models for target valid.	support email		Damian Smedley's told this user that "For up to date disease mappings to all species it is now better to use the Monarch Initiative website http://monarchinitiative.org which I am part of. They regularly update from ZFIN which takes data imports from ZMP.

Next steps:

- If the team agrees in implementing these requests, mock ups will be created and usability testing will be carried out for these new features (or data).
- Feedback on the new rounds of usability testing will be collated and available at a later stage. When this happens, we can get back to the user and say we have implemented their request.

Questions

Below is a list of questions that could be addressed as we gather more users' requests:

Question	Rationale
How many users would like the features above?	The more people request one feature, the stronger the argument to implement it
How can we prioritise the new features to be implemented?	Be wary of the cockroach effect, hence check Kano Model for prioritisation

We will not be doing

- To be announced