

ASTROBIO
USER STORIES



iGEM CONCORDIA

ID	Card	Sprint	Status	Conversation	Confirmation	Points	Priority	Type	Dependency
1	As a user, I need to look up gene expressions in microgravity conditions, so that I can better select target genes for my experiments	8	Complete	MVP of AstroBio	1- Users can now freely search and cross compare results of different genes from different organisms, species and microgravity conditions	55	1	EPIC	US: 2,3 PP: 1
2	As a user, I need to be able to make a search with sufficient options, so that I can find what I am looking for	6	Complete	8 options can be used for search Testing all options	1- Users have 255 different possible queries that can be generated from this search options 2- Unit testing manually by help of all team members	44	1	EPIC	US: 4,5,6,7,12,13
3	As a user, I need to look up for genes expressed in different microgravity conditions for different species and organisms, so that I can cross compare between studies	4	Complete	Having sufficient amount of data	1- HARV/RPM/SPACEFLOWN	11	2	EPIC	8,9,10,11
4	As a user, I need to be able to search for a spicific gene symbol, so that I can view all results associated with that gene	2	Complete	Input format? Case sensitivity? What happens when no results found? What happens when input is empty? Focus of this search option	1- All capitals 2- No results found message 3- Nothing will occur 4- Looks for all genes that has the same name as the gene symbol given by the user "exact match"	2	4	Feature	
5	As a user, I need to be able to search for a specific open reading frame, so that I can view all results associated with that gene	1	Complete	Input format? Case sensitivity? What happens when no results found? What happens when input is empty? Focus of this search option	1- All capitals 2- No results found message 3- Nothing will occur 4- Looks for all genes that has the same platform open reading frame given by the user "exact match"	2	4	Feature	
6	As a user, I need to be able to search for maximum adjusted P value accepted in results, so that I can view all relevant results from the analysis	2	Complete	Input format? Case sensitivity? What happens when no results found? What happens when input is empty? Focus of this search option	1- Floating format (decimals) 2- No results found message 3- Nothing will occur 4- Looks for all gene results with equal or less adjusted value number given by the user	2	4	Feature	

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7	As a user, I need to be able to search for a gene name , platform open reading frame, and/or adjusted P value in any combination, so that I can filter accepted genes in results	2	Complete	Input format? Case sensitivity? What happens when no results found? What happens when input is empty? Focus of this search option	1- Differs from each input as specified by Cards IDS 45&6 2- No results found message will be displayed 3- Nothing will occur 4- The ability to use the three inputs, Adjusted P Value, Gene symbol and/or Platform Open Reading Frame at any combination, to filter results	4	4	Feature	
8	As a user, I need to be able to view search results and obtain more information about that gene and study overview, so that I can decide which result is more suitable for me	2	Complete	What is crucial to display initially? How can it be interpreted?	1- Display of gene name, study number, microgravity condition, expression change, assay type, generations, adjusted P Value and species 2- Users can view expression change (up or down), and associated adjusted P Value can give good info regarding DE Analysis. Also, shows microgravity condition, assay and species which give more info about the biological and experimental aspects which could be of great importance to researchers	2	3	Feature	
9	As a user, I need to be able to view search results and obtain more information about that gene, so that I can get a full information about the experiment, design, author and link to the study	2	Complete	How is it displayed? What content is provided?	1- More information are stored in Modals that can be viewed when clicked. 2-The modal page shows DE Analysis such as log2FC, t,B adj value, adj p value, Gene info, GO info and chromosome info, and study info in such as author info, study info, and link to study	4	7	Feature	
10	As a user, I need to be able to view gene ontology, gene location, assay type, microgravity conditions, NCBI GEO Accession number, organism, species and strain, so that I can get more information about the study and make sense of the results	3	Complete	What type of information can be provided?	1- All data fetched by the bioinformatics along with extra additions are now displayable in modal format according to new DB schema	3	5	Feature	
11	As a user, I need differentiate different results obtained, so that I can find which genes fits my criteria	3	Complete	How can users differentiate different results?	1- Display for genes in list provide authors and study number, which differentiate studies. Also, species, generations of study, expression change, adjusted p value and microgravity conditions are also provided	2	4	Feature	

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12	As a user, I need to search up a gene by its expression change, so that I can find genes expression changes (up or down, and by how much) in microgravity conditions	3	Complete	How can users choose this? what options?	1- Users can choose UP (means positively expression change only) or DOWN (mean negatively expression change only) that is used as a criteria by itself. Best used as filter	6	5	Feature	
13	As a user, I need to be able to search for a gene by its name, platform ORF, GEO accession number, organism, species, expression change (up or down), assay type, and microgravity type, so that I have the freedom to make my search query based on my needs and requirements	5	Complete	Users can freely use any of the search options and make search	1- Users can freely select any combination to their needs, to filter down results based on species, microgravity type, organism, expression change, assay type and more	28	3	EPIC	US: 14,15,16,17,18,19 PP: 3,13,17
14	As a user, I need to be able to search for a gene by its name, so that I can find all genes associated to that name from across all studies in DB	4	Complete	What to do about data with delimiters? Input format, what changed?	1- Split and apply map reduce operation and store results in a sperate collection in DB 2- Input now is not case sensitive	8	8	Feature	
15	As a user, I need to be able to search for a gene by its GEO Accession number, so that I can find all genes associated to that study in DB	4	Complete	Input format? Case sensitivity? What happens when no results found? What happens when input is empty? Focus of this search option	1- Input is not case sensitive, format is GSE followed by numbers found in NCBI GEO database 2- No found message is displayed 3- No input selected 4- Search by studies	4	8	Feature	
16	As a user, I need to be able to search for a gene by its organism, so that I can find all genes associated to that organism across all species found in DB	4	Complete	Input format? Case sensitivity? What happens when no results found? What happens when input is empty? Focus of this search option	1- Input is select with options yeast, plant and bacteria 2- No found message is displayed 3- No input selected 4- Search for specific organism related genes	4	8	Feature	

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17	As a user, I need to be able to search for a gene by its species, so that I can find all genes associated to that specie from across all strains found in DB	4	Complete	Input format? Case sensitivity? What happens when no results found? What happens when input is empty? Focus of this search option	1- Input is not case sensitive 2- No found message is displayed 3- No input selected 4- Search for specific a species related genes	4	8	Feature	
18	As a user, I need to be able to search for a gene by its microgravity conditions, so that I can find all genes associated to that microgravity related studies	4	Complete	Input format? Case sensitivity? What happens when no results found? What happens when input is empty? Focus of this search option	1- Input is select with options HARV, RPM, SPACEFLOWN, and HYPERBOLIC 2- No found message is displayed 3- No input selected 4- Search for genes undergone specific microgravity conditions	4	8	Feature	
19	As a user, I need to be able to search for a gene by its assay type, so that I can find all genes associated to that assay from across all studies	4	Complete	Input format? Case sensitivity? What happens when no results found? What happens when input is empty? Focus of this search option	1- Input is select with options microarray and RNAseq 2- No found message is displayed 3- No input selected 4- Search for genes studied by a specific assay type	4	8	Feature	
20	As a user, I need a user friendly gene and study information view, so that it is much clearer and easier to read	5	Complete	How will this be accomplished? View structure	1- Have dedicated page to display gene and study information. This will be accomplished by passing parameter containing unique Objected of the gene, which can display the rest of the information. 2- jQuery is used to hide and show focused field. Separated into overview, gene ontology, gene location, study overview and study information	6	15	Feature	

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21	As a user, I need to be able to view all potential results as pages, so that I can find all potential candidate genes found	6	Complete	How will the pagination be structured? What happens when no more pages? or at first page?	1- Pagination is created with the help of AJAX and API, parameters for the initial search will be passed as API GET requests, that has the format, /get-gene/:start/:limit/:query/:sort 2- Next button will be hidden when no more results can be fetched. Also, when user is in fist page, previous button will be hidden	15	7	EPIC	PP: 14,15,16,17
22	As a user, I need to be able to set the limit to results found per page, so that I can adjust results displayed per page up to my own convenience	6	Complete	How is it intended to be used? What are the options?	1- Users can make a search, then, sort and limit fields will be displayed. Using AJAX, users can directly submit addition limit and sorting criteria and the query will fetch desired results with sort and limit and previously set search conditions. Previous data will be hidden, and newly fetched results will be displayed 2- Limit number of results per page is set to 10 by default. User can choose between (10,50,100 and 500), while sorting options are based on adjusted p value by default, and user can choose between (adjusted p value, ascending expression change, and descending expression change)	6	7	Feature	PP:13
23	As a user, I need to be able to export/print results, so that I can have a soft copy of my findings	6	Complete	How will it be displayed, and print format?	1- EXPORT/PRINT can be done, as it takes all information present in screen and saved in PDFs. The extra info cannot be added given the enourmous amount of data, users can still access more info via the printed PDF as long as there is internet connection	3	12	Feature	
24	As a user, I need the interface to be attractive and user friendly. so that I am motivated to explore the site	8	In-Progress	Clear and self-explanatory Links and guide to help users find their needs to use for search	- How to section created to explain how to use the search engine - Links will be available to explore more genes, P_ORF, GSEs and so on		20	Feature	
25	As a user, I need to be notified that results query succeeded, so that I know that search has occurred	7	Complete	Notification method?	1- Change view for search results. Shrink container and show results number found for the search	4	16	Feature	

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26	As a user, I need to be able to insert FASTA file as input, so that I can get expression change values for all genes in the file for all available microgravity conditions available in the DB	-	To do	-	-	-	15	Feature	
27	As a user, I need to be guided, so that I can fully utilize the application capabilities	8	Complete	How to successfully guide users to their needs?	1- Search results now can inform users search has been done 2- Going for the simple designs, to ease use of the software	5	9	Feature	
28	As a user, I need to be able to view heatmaps and interact with metadata for yeast studies, so that I can distinguish and understand gene regulations of pathways	8	Complete	Shiny App hosted in AWS	1- User can now access the shiny app via astrobio	18	8	Feature	
29	As a user, I need to be able to print essential genes for flights, so that I do not need to get back to that section of the page	-	To do	-	-	-	20	Feature	