Supplementary File S2: Extraction of gene-disease associations from literature using MeSH descriptors

Note: The users can click the "+" symbol to expand the class/node of interest and view the available nodes/classes within.

Step 1: Click the "QueryBuilder" tab in the tab panel

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Home	Templates	Lists	QueryBuilder	Data Sources	ΑΡΙ

Step 2: Select "Gene" from the drop-down menu of data types and click the "Select" button.

	Search: e.g. STAT1, TP53
QueryBuilder Advanced users can use a flexible query interface to construct their own data mining queries. The QueryBuilder lets you view the data model, apply constraints and select output. You can also export queries to share them with others. Browse data model O Import query from XML O View saved queries O	Select a Data Type to Begin a Query Click on a class name for a description or double click on a class name to create a new query starting at that class Gene Protein Activity Aleie Alloing Site BioAssay Interaction Bio-Entity CATH Classification Select

Step 3-A: In model browser, select "Publication>MeSH Terms" and click the "SUMMARY" label to display the default MeSH term attributes.

	Search: e.g. STAT1, TP53 GO
	Show results
Model browser	Query Overview
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Step 3-B: To restrict the search to a specific gene (e.g. PPARG; Organism- H. sapiens), click the "CONSTRAIN" label next to "Symbol" tab and enter the gene symbol and click "Add to query".

	Search: e.g. STAT1, TP53 GO
	Show results
Model browser	Query Overview
Browse through the classes and attributes. Click on [UNITARY] links to add summary of fields to the results table or on [NUNA] links to add individual fields to the results. Use [CONSTRAINS] links to constrain a value in the query. Cene ⁰ [UNITARY = [CONSTRAINS] Browse [CONSTRAINS] Browse [CONSTRAINS] NCBI Gene ID ⁰ [ROWS [CONSTRAINS] Symbol [SOWS [CONSTRAINS] Symbol [SOWS [CONSTRAINS] Condary Identifier ⁰ [SOWS [CONSTRAINS] Symbol [SOWS [CONSTRAINS] Chromosome Chromosome ⁰ [UNITARY = [CONSTRAINS] E Cross References Cross Reference ⁰ [CONSTRAINS] E Gene Disease Plairs Gene Disease Plair [Constrains] E Gene Disease Plairs Gene Disease Plair [Constrains] E Integrated Pathway Clusters Integrated Pathway Cluster [Constrains] E Integrated Pathway Cl	Cene Symbol PPARC PARC Conscription Constraint logie: Some constraint

Constrain for gene (Gene Symbol; PPARG):

Model browser	Constraint for Gene > Symbol x	
Browse through the classes and a links to add summary of fields to links to add individual fields to th to constrain a value in the query.	Constrain Choose a filter	fields constrained
Gene Summary + CONSTRAIN+ - Brief Description (SHOWE) CONSTRAIN+ - Description (SHOWE) CONSTRAIN+ - Name (SHOWE) CONSTRAIN+ - NCBI Gene ID - DB identifier - DB identifier - Secondary Identifier - Symbol (SHOWE) CONSTRAIN+ - Type (SHOWE) CONSTRAIN+ - Type (SHOWE) CONSTRAIN+ - H Alleles Allele - Extended Constrain+ - H Alleles Allele - H Allele -	Filter query results on this field having a specific value Gene > Symbol = O PPARG Add to query Filter query results on this field having any value or not • Has no value Has a value Add to query	
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Search: e.g. STAT1, TP53 GO

Constrain for organism (by Short Name- H. sapiens)

		Search: e.g. STAT1, TP53 GO
		Show results
Model browser	Query Overview	
Symbol SHOW# CONSTRAINT# Type SHOW# CONSTRAINT# Type SHOW# CONSTRAINT# Alleles Allele " CONSTRAINT# Constraint for Gene > Organi Constraint Constraint Constraint Constrain	sm > Short Name >	
	nis field having a specific value ort Name ens 😧 Add to query	(B) Ilection Co m collection Co
- H Locations Locations miRNA Interactions - MiRNA Interactions miRNA Interactions - MiRNA Interactions - Mirna Mir	his field having any value or not- a value Add to query	SH Tree collection 😂 h Category ତ
- Name SHOUND CONSTRAINT - Short Name SHOUND CONSTRAINT - Species [SHOUND [CONSTRAINT] - Taxon Id Integer [SHOUND [CONSTRAINT] - H Taxonomy Taxonomy @ SAMMARY & CONSTRAINT] - H Pathways Pathway " [SUMMARY & CONSTRAINT] - H Probe Sets Probe Set " [SUMMARY & CONSTRAINT] - H Probe Sets Pr	Constraint logic: A and B and A and B and C and C and C	Diseases 🛛 🖉 (C) I C and C and C and C and C and C and C and C?

Step 4: To restrict the output to gene-disease associations, select "Publication->MeSH Terms->Tree Numbers->Category" and click the "CONSTRAIN" label next to "Name". Select "Diseases" from the list of items in the drop-down menu and click "Add to query".

	Search: e.g. STAT1, TP53 GO
	Show results
Model browser	Query Overview
 PubMed ID records and the second seco	Tree Numbers > Category > Name x c value c value bers > Category > Name bers > Category > Name c or not
Holdring(Inters)(CONSTRAINS) Parents McSH Tree SUMMARY *)(CONSTRAINS) Publication Types McSH Term SUMMARY *)(CONSTRAINS) Pelations Relation * (SUMMARY *)(CONSTRAINS) Sequence Ontology Term SO Term * Summary *)(CONSTRAINS) SNPs Variation Annotation (SUMMARY *)(CONSTRAINS)	= Diseases 😵 🖉 (C) Constraint logic: A and B and C and C and C and C and C and C A and B and C and C and C and C and C and C

Step 5: Click the "Show results" button on upper right of the panel to view the output.



Step 6: The users can export the results by "Export" button on the top-right.