

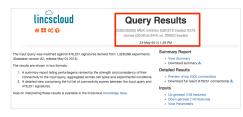
lincscloud > Tools and Apps > Interpreting Results

### Query App Results

This page is dedicated to aid in interpreting results from the LINCSCLOUD Query App. For information on how the application works and the underlying algorithms, please see our support page.

The Query App takes as input one or two gene sets and computes the connectivity between these sets with all of the gene expression signatures in the LINCS database. There are a number of different results generated by the Query App, each of which is accessible from an index page, as listed in the examples below.

#### The Query Title



The name you assigned your query and the time at which it was run are displayed at the top of the page.

Summary Report

#### RECENTLY VIEWED ARTICLES

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Signature Generation and Analysis (L1000)
sig\_introspect (examines similarities between a group of gene expression signatures)
sig\_query (interrogate with gene sets)

# RELATED ARTICLES

Query App
Perturbation Types
Query App Report
Santagata S. and Mendillo M.L. et al.
(Science 2013)
sig\_query (interrogate with gene sets)



The tool outputs a summary report like the one seen below. This report can be viewed by clicking the 'View Summary' link or by clicking the download icon to download the report as a text file.

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1	MD-CHTRNS	9-0126	99.673	99.35	97.605	- 1	
6	860-853454580	P0-0325903	99.529	99.203	98.795	-	
7	840-480614967	AS-793005	99.529	99.111	56.45		-
	860-605804844	A2-628	99.4	96.963	98.019		
9	890-412244279	MDI1-2-IMIDIN	99,346	96.80	98.172		
22	840-405204953	PD-184352	99.325	96.776	62.153		
11	BID-K14581868	BM5-138924	19.647	98.679	97.442		
12	840-400134438	PF-110	96.879	98.621	94,363		
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4	CC8061-6845	NAMP7	97.245	96.119	93.62		
5	C03061-8243	SMCLA	96.89	55.962	89.197		- 1
6	CC8061-5591	PP100	98.331	95.654	76.639	6	
2	CG50E1-3845	696	96276	55.437	86.54)	9	
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40	00000-110244	6,944	00.000	64-463	88-607		
11	CORRESPINA	ARRENZ	99.088	96.479	24.885		- 1
12	CC8061-9604	MARKE	99.819	\$4.475	88.908	9	
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This report has three main sections, as labeled in the figure above. There is one section for each major group of pertubation type in the LINCS database (chemical compounds, gene knockdowns, and gene over-expressions). In each section, perturbagens are scored as to how well they connect to the query signature. In the example above, the the pertubagens are scored as to how well they connect

to the gene expression signature derived by treating A375 cells with GSK212 at 30nM for 24 hours (relative to DMSO).

The tables list a number of metrics, each of which is described below:

Query App Results - lincscloud

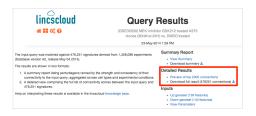
Range	Description
n/a	A unique identifier for the given pertubagen
n/a	The common name for the pertubagen
-100 to 100	The mean connectivity score across the two cell lines in which the pertubagen connected most strongly to the query
-100 to 100	The mean connectivity score across the four cell lines in which the pertubagen connected most strongly to the query
-100 to 100	The mean connectivity score across the six cell lines in which the pertubagen connected most strongly to the query
4 to 9	The number of cell lines over which the connectivity between the query and the perturbagen have been summarized
	n/a  n/a  -100 to 100  -100 to 100

The different score metrics indicate how well a particular pertubagen connected to the query in the given best number of cell lines. In practice, we have found the score\_best4 metric to be a reasonable compromise between too many and too few cell types over which to summarize, and hence the tables are sorted by this value to start. The scores in these columns range from -100 (complete anti-connection) to 100 (complete connection). Positive values indicate that the pertubation gave a similar signature to the query, and negative values indicate that the pertubation gave a signature opposite to that of the query. -666 means that no information is available. We have generally found that scores with a magnitude of greater than 90 correspond to significant connections.

The underlying space of perturbagens in the summary report corresponds to the subset of perturbagens that have been profiled systematically across multiple cell types and have given reproducible signatures.

If we continue with the MEK inhibitor example above, we see in the 'Compound Connections' section that there are a number of compounds with strong positive connectivity scores, many of which are known MEK inhibitors (selumetinib, PD-0325901, U0126, AS-703026, PD-184352, known PI3-K inhibitor AS-605240 and known RAF inhibitor AZ-628). If we look in the 'Consensus Knockdown Connections' section, we also observe that knockdowns of known MEK pathway members (KRAS, MAP2K1) connect strongly to the query MEK inhibitor signature.

#### Detailed Results

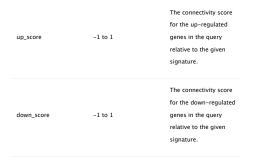


In addition to the summarized results described above, in which connections have been aggregated across cell types, it is also possible to view a detailed list of connections in which different cell types remain unaggregated. The top 2,000 connections can be previewed in the web browser by clicking the corresponding link, or a list of all connections can be downloaded as a text file by clicking the download icon.

The detailed report contains a number of fields, described in the table below:

Query App Results - lincscloud

Metric	Range	Description
rank	1 to 4,000	The rank by connectivity score of the particular signature
sig_id	n/a	A unique identifier for the signature
pert_id	n/a	A unique identifier for perturbation used to generate the signature
pert_iname	n/a	The common name for the perturbation
pert_type	n/a	A code for the type of pertubation. Please see this table for a list of all the pert_type values.
cell_id	n/a	The cell line in which the signature was generated
pert_itime	3 to 144 h	The treatment time that generated the signature
pert_idose	n/a	The treatment dose that generated the signature
connectivity_score	-1 to 1	The integrated connectivity score for the query relative to the given signature.



#### Inputs



Lastly, the index page allows you to view and download the inputs and parameters for the query by clicking the links in this section.

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query_index_title.png (90 KB)
query_index_summary.png (90 KB)
query_index_detail.png (90 KB)
query_result_table_numbered.png (200 KB)

Was this article helpful?

# 1 out of 1 found this helpful
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Have more questions? Submit a request

query\_index\_inputs.png (90 KB)

# Comments

http://support.lincscloud.org/hc/en-us/articles/202231633-Quer...



# Jeanette McClintick

January 07, 2015 16:07

The reports on this page are unreadable. The columns identified by this knowledge base article no longer match the query report output. Is "score best 2" equivalent to "mean rank2". etc? What does a value of -666 mean. Reports are meaningless if you don't have a key to interpret them.

7 of 7 12/1/15, 2:12 PM