

MSSNG Research Portal Features

Prepared by DNASTack
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This presentation showcases the features of the MSSNG Research Portal, a project by Autism Speaks.

The MSSNG Research Portal is open source under the terms of the Apache License, version 2.0. The [source code is available on GitHub](#).

We hope that this project will be useful beyond the MSSNG dataset, and that this presentation will help you to decide if it could be useful to your project.

This presentation may be shared freely in its unaltered form.

Variant Queries

“One Box” Variant Search

The screenshot shows the MSSNG website interface for variant searching. The browser address bar shows `research.mss.ng/variant_searches/search`. The page has a dark header with the MSSNG logo and navigation links: **Variant Queries**, Sample Queries, Phenotypes, Gene Info, More, and Sign Out.

Variant Query

One Box Query

All coordinates are 0-based and use the GRCh38/hg38 reference.

[Query History](#)
[Saved Queries](#)
[Advanced Query](#)

What Can You Do?

With the one box query, you can quickly make certain queries as shown in the table below.

Query for a specific variant in all subjects
<code>2-58497678-58497679-G-A</code>
Query for all variants within a specific genomic interval (or position), in all subjects
<code>2-58724816-58724817</code>
Query for all rare high-impact variants within a specific gene, in all subjects
<code>NRXN1</code>
Query for all rare high-impact variants within a specific gene, in a specific subject
<code>NRXN1:2-1116-803</code>
Query for all rare high-impact variants within two genes, in all subjects
<code>NRXN1,NRXN3</code>
Query for a specific cDNA change within a gene, in all subjects
<code>NRXN1:c.C2653T</code>
Query for any variant modifying a specific cDNA position within a gene, in all subjects
<code>NRXN1:c..2653</code>
Query for a specific amino acid change within a gene, in all subjects
<code>NRXN1:p.H885Y</code>
Query for Query for any variant modifying a specific amino acid position within a gene, in all subjects
<code>NRXN1:p..885</code>
Query for a specific dbSNP ID in all subjects
<code>r199784139</code>

The Default Criteria

When you use the One Box Query, here is the default criteria.

Variant quality	Passing
-----------------	---------

MSS.NG `ldyllic-analyst-574.db6_release` A project by AUTISM SPEAKS

Variant Search Results

The screenshot shows the MSSNG Variant Search Results page for the gene NRXN1. The page includes a header with the MSSNG logo and navigation links. A variant query summary table is displayed, followed by a table of search results. The results table has columns for Sample, Chr, Start, End, Reference allele, Alternate allele, Genotype, Zygosity, Read depth, Allelic depth, Genotype quality, Inheritance, De Novo, RefSeq ID, and Gene Symbol. Three sample rows are visible, each with a genomic track visualization. The footer contains the MSSNG logo, a project identifier, and the Autism Speaks logo.

MSSNG [Variant Queries](#) [Sample Queries](#) [Phenotypes](#) [Gene Info](#) [More](#) [Sign Out](#)

VARIANT QUERY:
NRXN1

Symbol	NRXN1
Variant quality	Passing
Affection	affected
Control Database Frequency	<= 0.01
Damage Potential	High
BigQuery SQL	Show

73 results 119,948 GB processed

[Export as TSV](#) [Save this query](#) [Edit this query](#) [Show/hide columns](#)

Sample	Chr	Start	End	Reference allele	Alternate allele	Genotype	Zygosity	Read depth	Allelic depth	Genotype quality	Inheritance	De Novo	RefSeq ID	Gene Symbol
1-0201-004	chr2													
1-0201-005	chr2													
1-0225-003	chr2													

MSSNG [Kyllic-analyst-574.db6_release](#) [A project by AUTISM SPEAKS](#)

Advanced Variant Query Builder & Editor (1/2)

The screenshot shows a web browser window with the URL `research.mss.ng/variant_searches/150502/edit`. The page features a dark header with the MSSNG logo and navigation links: **Variant Queries**, Sample Queries, Phenotypes, Gene Info, More, and Sign Out. The main content area is a form for editing a variant query. The **Query Name** field contains "NRXN1". The **Search Scope** section has a checked option for "Only passing variants". The **Select Genomic Interval** section offers five methods:
1. **by Genomic Coordinate**: Includes fields for Chromosome (a dropdown menu), Start Position, End Position, Reference Allele, and Alternate Allele.
2. **by 0-based UCSC-like formatted string**: Includes a Variant field with the example "chr-start-end-ref-alt" and a note "Example: 2-50497878-50497879-G-A".
3. **by File**: Includes a BED File field with a "Choose File" button and the text "No file chosen".
4. **by Gene**: Includes a Symbol(s) field with the example "NRXN1" and an Upload Gene Symbol File section with a "Choose File" button and the text "No file chosen".
5. **by dbSNP ID**: Includes a dbSNP ID field with the example "rs199784139".
At the bottom of the browser window, a status bar shows "MSS.NG" on the left, "Idyllic-analyst-574.db6_release" in the center, and "A project by AUTISM SPEAKS" on the right.

Query Name *

NRXN1

Search Scope

☒ Only passing variants

Select Genomic Interval

by Genomic Coordinate

Chromosome Start Position End Position Reference Allele Alternate Allele

Chromosome Start Position End Position Reference Allele Alternate Allele

by 0-based UCSC-like formatted string

Variant

chr-start-end-ref-alt

Example: 2-50497878-50497879-G-A

by File

BED File

Choose File No file chosen

by Gene

Symbol(s)

NRXN1

Upload Gene Symbol File

Choose File No file chosen

by dbSNP ID

dbSNP ID

rs199784139

MSS.NG Idyllic-analyst-574.db6_release A project by AUTISM SPEAKS

Advanced Variant Query Builder & Editor (2/2)

The screenshot displays the MSSNG Advanced Variant Query Builder & Editor interface within a web browser. The browser's address bar shows the URL `research.mss.ng/variant_searches/150502/edit`. The MSSNG logo is in the top left, and a navigation menu in the top right includes **Variant Queries**, Sample Queries, Phenotypes, Gene Info, More, and Sign Out.

The main content area is titled "Optional Filters" and is organized into three sections:

- by Sample(s)**: Includes a text input for "Sample(s)" with the placeholder "e.g. 1-0022-001" and an "Upload Sample File" button with a "Choose File" option.
- by Subject(s)**: Includes a text input for "Subject(s)" with the placeholder "e.g. 1-0022-001" and an "Upload Subject File" button with a "Choose File" option. Below this are four dropdown menus: "DNA Source" (set to "All Sources"), "Platform" (set to "All Platforms"), "Gender" (set to "Both Genders"), and "Affection" (set to "affected").
- by Variant Annotation**: Includes a "De Novo" checkbox, a "Frequency Operator" dropdown (set to "<="), a "Control Database Frequency" input (set to "0.01"), a "Zygosity" dropdown (set to "Any Zygosity"), an "Effect On Gene Product" dropdown (set to "Click to select Effects"), a "Damage Potential" dropdown (set to "High"), and a "Pathogenicity" dropdown (set to "Click to select Pathogenicity").

The footer of the interface shows the MSSNG logo, a project identifier "ldyllic-analyst-574.db6_release", and the text "A project by AUTISM SPEAKS".

Sample Queries

“One Box” Sample Query

The screenshot shows a web browser window with the URL `research.mss.ng/trios/search`. The page features a dark header with the MSSNG logo and navigation links: Variant Queries, Sample Queries (highlighted), Phenotypes, Gene Info, More, and Sign Out. The main content area is titled "Sample Query" and includes a search box labeled "One Box Query" with a blue submit button. Below the search box is a placeholder text: "Please enter one subject ID, e.g., 1-0027-004". To the left of the search box are links for "Query History", "Saved Queries", and "Advanced Query". To the right, under the heading "What Can You Do?", a paragraph explains that the one box query is used for Family (Trio) with subject ID, e.g., 1-0027-004. Below this, "The Default Criteria" section states that when using the One Box Query, the default criteria are as follows:

Variant quality	Passing
Control Database Frequency	<= 0.05
Damage Potential	High or Medium

Below the table, it says: "Use the Advanced Query for alternative query parameters."

The footer of the page includes the MSSNG logo, a project ID `idyllic-analyst-574.db6_release`, and a statement "A project by AUTISM SPEAKS" with the Autism Speaks logo.

Sample Query Results

The screenshot displays the MSSNG web interface for a sample query. The browser address bar shows `research.mss.ng/trios/150503`. The page header includes the MSSNG logo and navigation links: Variant Queries, Sample Queries (highlighted), Phenotypes, Gene Info, More, and Sign Out.

SAMPLE QUERY:
1-0627-004

Variant quality	Passing
Subject ID	1-0627-004
Control Database Frequency	≤ 0.05
Damage Potential	High, Medium
BigQuery SQL	Show

This query has exceeded the maximum of 500 variants; the first 500 are being returned. To obtain all search results, please export the data as TSV.

Showing 500 of 923 results 119.948 GB processed

[Export as TSV](#) [Save this query](#) [Edit this query](#) [Show/hide columns](#)

	Sample	Chr	Start	End	Reference allele	Alternate allele	Genotype	Zygosity	Read depth	Allelic depth	Genotype quality	Inheritance	De Novo	RefSeq ID
☰	1-0627-004	chr1												
■	1-0627-004	chr1												
■	1-0627-004	chr1												
■	1-0627-004	chr1												

MSSNG Idyllic-analyst-574.db6_release A project by AUTISM SPEAKS

Advanced Sample Query Builder & Editor

The screenshot shows a web browser window with the URL `research.mss.ng/trios/150503/edit`. The page features a dark header with the MSSNG logo and navigation links: Variant Queries, Sample Queries (highlighted), Phenotypes, Gene Info, More, and Sign Out.

The main form is titled "Query Name" and contains a text input field with the value "1-0627-004". Below this is a "Select Subject" section with a "Subject ID" dropdown menu also set to "1-0627-004".

The "Select Risk Gene(s)" section has two options: "by File" and "by Gene Symbol(s)". The "by File" option includes a "Risk Genes File" section with a "Choose File" button and a note: "Text file of gene symbols (one gene symbol per line)". The "by Gene Symbol(s)" option includes a "Symbol(s)" text input field with the example text "e.g. SHANK1".

The "Optional Filters" section is divided into three columns:

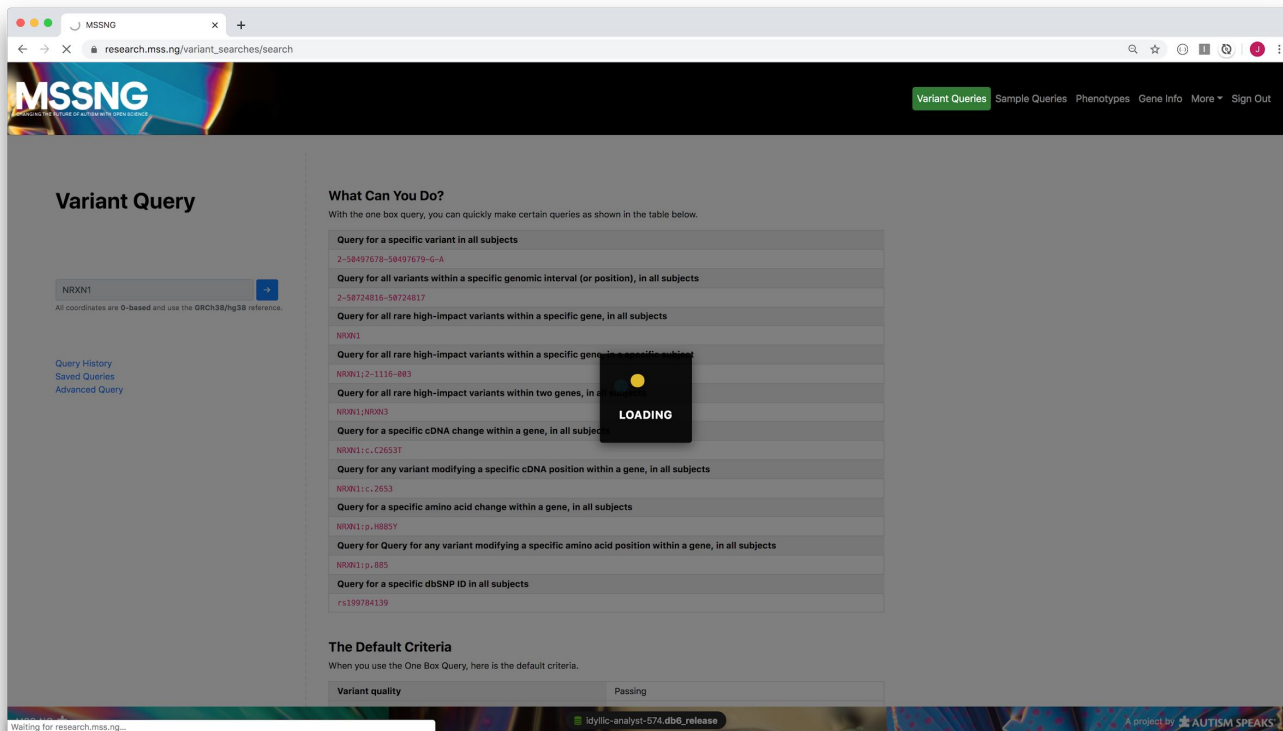
- by Variant Annotation:** Includes a "Frequency Operator" dropdown set to "<=", a "Control Database Frequency" input field set to "0.05", and a "Zygosity" dropdown set to "Zygosity".
- Effect On Gene Product:** Includes a button labeled "Click to select Effects".
- Damage Potential:** Includes a dropdown menu set to "High | Medium".
- Pathogenicity:** Includes a button labeled "Click to select Pathogenicity".

At the bottom of the form, there are two buttons: "Update this query" and "Cancel".

The footer of the page includes the MSSNG logo, a project identifier "ldyllic-analyst-574.db6_release", and a statement "A project by AUTISM SPEAKS".

Common to
Variant Queries
and Sample Queries

Animated Indicator While Query is Running



Choose Which Columns to Include in the Query

The screenshot displays the MSSNG research platform interface. At the top, the browser address bar shows the URL `research.mss.ng/variant_searches/150502`. The main header features the MSSNG logo and navigation links: **Variant Queries**, Sample Queries, Phenotypes, Gene Info, More, and Sign Out.

The central section is titled "VARIANT QUERY: NRXN1". It contains a table of query parameters:

Symbol	NRXN1
Variant quality	Passing
Affection	affected
Control Database Frequency	<= 0.01
Damage Potential	High
BigQuery SQL	Show

Below the parameters, it indicates "73 results" and provides an "Export as TSV" button. A table of results is shown with columns: Sample, Chr, Start, End, Reference allele, Alternate allele, and Genotype. The first three rows are visible:

Sample	Chr	Start	End	Reference allele	Alternate allele	Genotype
1-0201-004	chr2					
1-0201-005	chr2					
1-0225-003	chr2					

A "Column Visibility" dialog box is open in the center, listing various columns with checkboxes. The "Defaults" button is highlighted in blue. The columns listed are:

- ☒ Sample
- ☒ Chr
- ☒ Start
- ☒ End
- ☒ Reference allele
- ☒ Alternate allele
- ☒ Genotype
- ☒ Zygosity
- ☒ Read depth
- ☒ Allelic depth
- ☒ Genotype quality
- ☒ Inheritance
- ☒ De Novo
- ☒ RefSeq ID
- ☒ Gene Symbol
- ☒ Effect - Impact
- ☒ Max frequency (1000 Genomes)
- ☒ Max frequency GnomAD genome
- ☒ Max frequency (MSSNG)
- ☒ Sex
- ☒ Sequencing platform
- ☐ Clinvar Significance Simple
- ☐ Clinvar significance
- ☐ Max frequency GnomAD exome
- ☐ Max frequency EXAC
- ☐ Filter
- ☐ Entrez Id
- ☐ dbSNP ID

On the right side of the interface, a "Show/hide columns" button is visible. The bottom of the page features the MSSNG logo and the text "A project by AUTISM SPEAKS".

View/Copy Underlying BigQuery SQL Statement

The screenshot displays the MSSNG research portal interface. On the left, a sidebar shows the variant query 'NRXN1' and a table of variant details. The main panel shows a table of variant results. A modal window titled 'BigQuery SQL' is open, displaying the underlying SQL query. The query is a complex SELECT statement with multiple joins and filters. A 'Copy to Clipboard' button is visible at the top of the modal. The background interface includes a search bar, navigation links, and a footer with the MSSNG logo and 'A project by AUTISM SPEAKS'.

Variant Query: NRXN1

Symbol	NRXN1
Variant quality	Passing
Affection	affected
Control Database Frequency	<= 0.01
Damage Potential	High
BigQuery SQL	Show

73 results

Export as TSV

Sample	Chr	Start	End	Reference allele	Alternate allele
1-0201-004	chr2				
1-0201-005	chr2				
1-0225-003	chr2				

BigQuery SQL

Copy to Clipboard

```
WITH
  annotations AS (
    SELECT
      "idyllic-analyst-574.db6_release.annotations_ilen" AS source,
      "base" AS select_scope,
      id AS annotation_id, reference_name, start, "end", reference_bases, al
    FROM "idyllic-analyst-574.db6_release.annotations_ilen"
    WHERE entrez_id IN (9378) AND freq_max <= 0.01 AND effect_impact > 0 AND
  ) UNION ALL (
    SELECT
      "idyllic-analyst-574.db6_release.annotations_cg" AS source,
      "cg" AS select_scope,
      id AS annotation_id, reference_name, start, "end", reference_bases, al
    FROM "idyllic-analyst-574.db6_release.annotations_cg"
    WHERE entrez_id IN (9378) AND freq_max <= 0.01 AND effect_impact > 0 AND
  )
),
annotated_variants AS (
  SELECT
    -- [From Annotation]
    a.*,
    -- [From Variant]
    v.* EXCEPT(
      annotation_id,
      alternate_bases,
      filter, # relies on call.filter instead
      call,
      no_call,
      hom_ref_call
    ),
    v.alternate_bases AS associated_alternate_bases,
    c.* EXCEPT(ad, genotype),
    -- [From Sample]
    ss.SUBMITTEDID AS sample_id,
    ss.INDEXID AS subject_id,
    ss.DNASOURCE,
    ss.PLATFORM,
    -- [From Subject]
    s.SEX AS sex,
    s.FAMILYID,
    s.FAMILYTYPE,
    ss.father.SUBMITTEDID,
    ss.mother.SUBMITTEDID,
```

119,948 GB processed

Show/Hide columns

De Novo RefSeq ID Gene Symbol

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Jump to Related Resources for a Sample Variant

The screenshot displays the MSSNG research website interface. At the top, the MSSNG logo is on the left, and navigation links for 'Variant Queries', 'Sample Queries', 'Phenotypes', 'Gene Info', 'More', and 'Sign Out' are on the right. The main content area shows a 'VARIANT QUERY: NRXN1' section with a table of variant details: Symbol (NRXN1), Variant quality (Passing), Affection (affected), Control Database Frequency (<= 0.01), Damage Potential (High), and BigQuery SQL (with a 'Show' link). Below this, it indicates '73 results' and '119.948 GB processed'. A table of variant results is shown with columns: Sample, Chr, Start, End, Reference allele, Alternate allele, Genotype, Zygosity, Read depth, Allelic depth, Genotype quality, Inheritance, De Novo, RefSeq ID, and Gene Symbol. A tooltip is visible over the first row (Sample 1-0201-004, Chr2), providing links to 'See the annotation for chr2', 'Open in the Read Viewer', and 'Search for similar variants on the Beacon Network*'. The footer includes the URL 'https://research.mss.ng/annotations/chr2...', a source link 'source=idyllic-analyst-574.db6_release', and a project logo for 'A project by AUTISM SPEAKS'.

MSSNG
Variant Queries Sample Queries Phenotypes Gene Info More Sign Out

VARIANT QUERY:
NRXN1

Symbol	NRXN1
Variant quality	Passing
Affection	affected
Control Database Frequency	<= 0.01
Damage Potential	High
BigQuery SQL	Show

73 results 119.948 GB processed

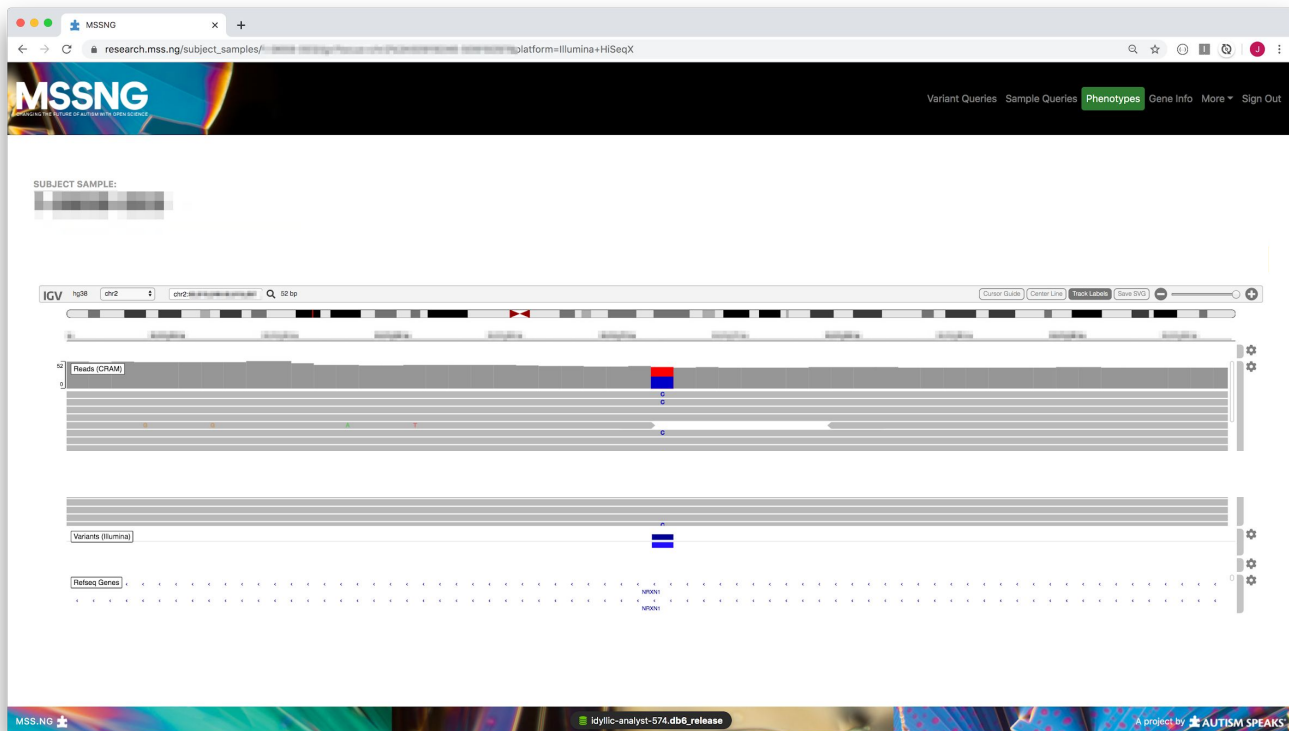
Export as TSV Save this query Edit this query Show/hide columns

Sample	Chr	Start	End	Reference allele	Alternate allele	Genotype	Zygosity	Read depth	Allelic depth	Genotype quality	Inheritance	De Novo	RefSeq ID	Gene Symbol
1-0201-004	chr2													
1-0275-003	chr2													

See the annotation for chr2
Open in the Read Viewer
Search for similar variants on the Beacon Network*
Beacon Network uses the 1-based coordinate system.

source=idyllic-analyst-574.db6_release A project by AUTISM SPEAKS

IGV Read Viewer



History of Past Queries

The screenshot shows a web browser window with the URL `research.mss.ng/variant_searches`. The page features a dark header with the MSSNG logo and navigation links: [Variant Queries](#) (highlighted in green), [Sample Queries](#), [Phenotypes](#), [Gene Info](#), [More](#), and [Sign Out](#).

Variant Queries History

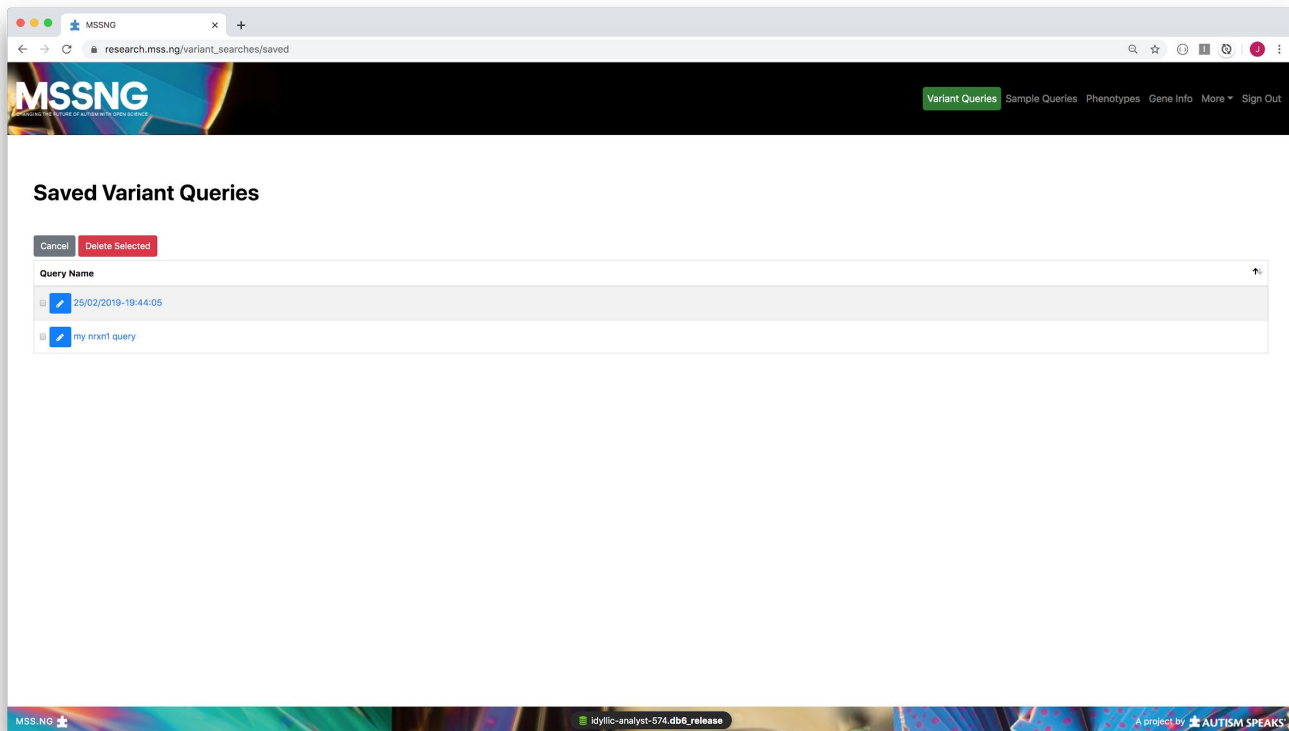
At the top of the history section are two buttons: [Cancel](#) and [Delete All](#).

The main content is a table with the following structure:

Query Name	
	03/06/2019-13:50:50
	[blurred]
	[blurred]
	[blurred]
	[blurred]
	[blurred]
	[blurred]
	[blurred]
	[blurred]
	[blurred]
	[blurred]
	[blurred]
	NRXN1
	NRXN1
	[blurred]

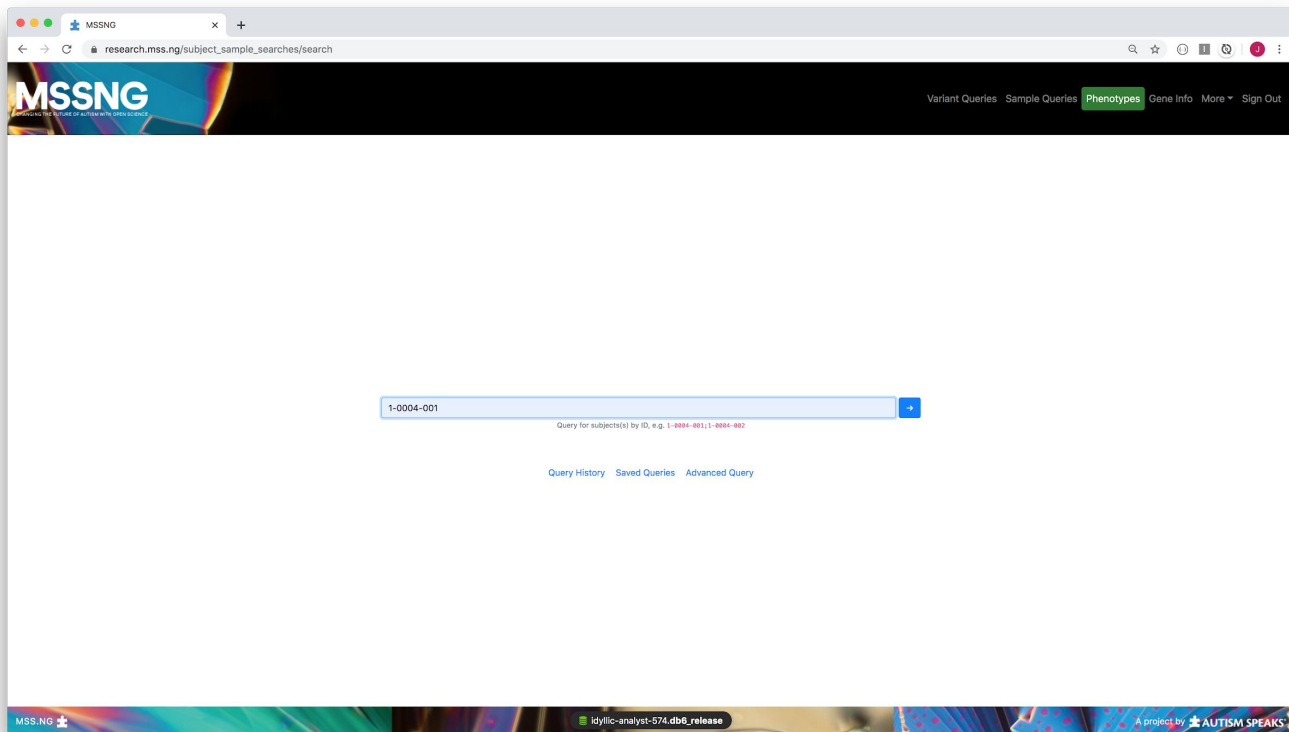
The footer of the browser window includes the MSSNG logo, a user profile icon, a text label `ldyllic-analyst-574.db6_release`, and a project credit: [A project by AUTISM SPEAKS](#).

Saved Queries (separate from history)



Subject Phenotype Query

“One Box” Subject Query



Sample Info and Subject Phenotypes

The screenshot displays the MSSNG research portal interface. At the top, the browser address bar shows the URL `research.mss.ng/subject_samples/1-0004-002?sample=1-0004-002`. The MSSNG logo is on the left, and navigation links for Variant Queries, Sample Queries, Phenotypes, Gene Info, More, and Sign Out are on the right. The main content area is titled 'SUBJECT 1-0004-002'. Below this, a section '1 Sample Found' contains a table with sample details. Further down, a 'Measures' section contains a table of various tests and their results. The bottom of the page features a footer with the MSSNG logo, a project ID 'ldyllic-analyst-574.db6_release', and the text 'A project by AUTISM SPEAKS'.

SUBJECT
1-0004-002

1 Sample Found

Sample	DNA Source	Platform
1-0004-002	White blood cell	Complete Genomics

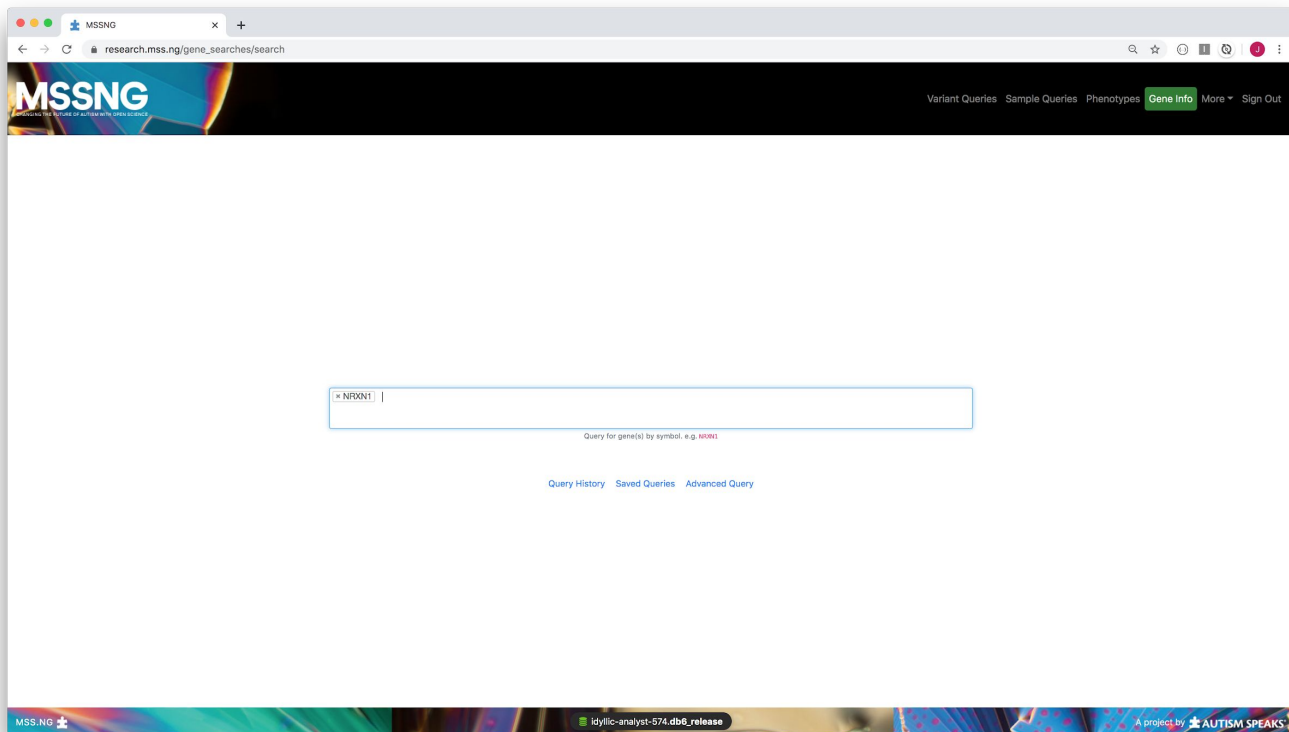
Measures

Relevance	Date	Test	Question	Value	Legend
Low		Personality Styles and Preferences Questionnaire: BAP-Q Part 1 Self Ratings	Age at time questionnaire completed (months)		(No information available)
Low		Social Responsiveness Scale - Adult Research Version: 2005	Age at testing (months)		(No information available)
Low		Personality Styles and Preferences Questionnaire: BAP-Q Part 2 Informant Ratings	Age at time questionnaire completed (months)		(No information available)
Low		Personality Styles and Preferences Questionnaire: BAP-Q Part 1 Self Ratings	Aloud: total		(No information available)
Low		Personality Styles and Preferences Questionnaire: BAP-Q Part 1 Self Ratings	Pragmatic language: total		(No information available)
Low		Personality Styles and Preferences Questionnaire: BAP-Q Part 1 Self Ratings	Rigid: total		(No information available)
Low		Social Responsiveness Scale - Adult Research	Total Raw Score		(No information available)

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Gene Info

“One Box” Gene Info Query



Gene Info (1/4)

The screenshot shows a web browser window with the URL `research.mss.ng/genes/9378`. The page header features the MSSNG logo and navigation links: Variant Queries, Sample Queries, Phenotypes, Gene Info (highlighted), More, and Sign Out. The main content area displays the gene name **NRXN1** under the heading "GENE:". Below this, the "Entrez" section contains a table with the following data:

Entrez Gene ID	9378
Gene Symbol	NRXN1
Chromosome	2
Map Location	2p16.3
Synonyms	Hs.22998, PTHSL2, SCZD17
Description	neurexin 1
Type	protein-coding
Cross References	MM-600565, HGNC:HGNC:8008, Ensembl:ENSG00000179915

Below the Entrez section is the "RefSeq Gene" section, which includes a table with the following data:

Chromosome	Start Position	End Position
2	49918504	51032536

Below this table is a section for "RNA Accession Numbers" with a list containing `NM_001330077` and `NM_001330078`. The footer of the page includes the MSSNG logo, a link to `ldyllic-analyst-574.db6_release`, and a project by AUTISM SPEAKS logo.

Gene Info (2/4)

The screenshot shows a web browser window with the URL `research.mss.ng/genes/9378`. The page features the MSSNG logo and navigation links: Variant Queries, Sample Queries, Phenotypes, Gene Info (highlighted), More, and Sign Out. The main content area is titled "RefSeq Gene" and contains a table with the following data:

Chromosome	Start Position	End Position
2	49918504	51032536

Below the table, there is a section titled "RNA Accession Numbers" listing 18 accession numbers:

- NM_001330077
- NM_001330078
- NM_001330081
- NM_001330086
- NM_001330082
- NM_001330095
- NM_001330091
- NM_001330093
- NM_001330092
- NM_004801
- NM_001330088
- NM_001320157
- NM_001320156
- NM_001330079
- NM_001330087
- NM_001330097
- NM_001330096

The footer of the page includes the MSSNG logo, a project identifier "ldyllic-analyst-574.db6_release", and the text "A project by AUTISM SPEAKS".

Gene Info (3/4)

The screenshot shows a web browser window with the URL `research.mss.ng/genes/9378`. The page header features the MSSNG logo and navigation links: Variant Queries, Sample Queries, Phenotypes, Gene Info (highlighted), More, and Sign Out.

Clinical Genomics Database

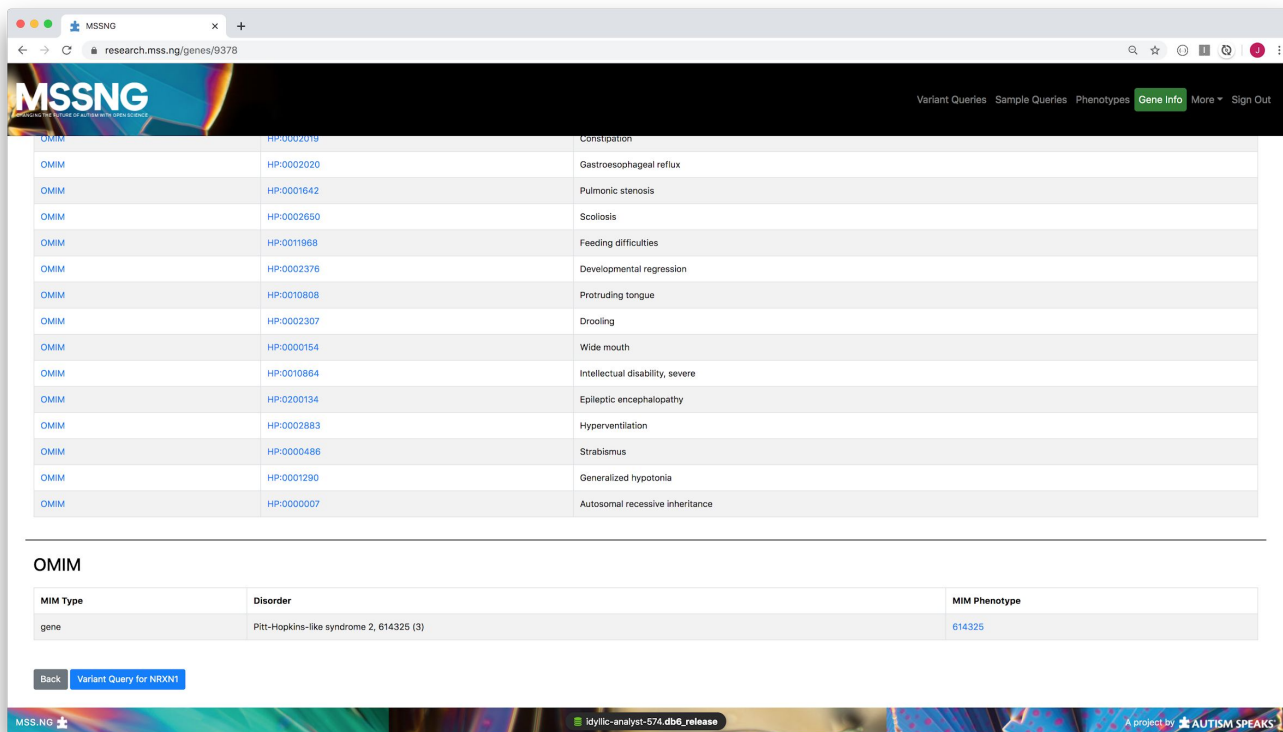
Condition	Schizophrenia 17; Pitt-Hopkins-like syndrome 2
Inheritance	AD/AR
Age Group	N/A
Allelic Conditions	N/A
Manifestation Categories	Craniofacial; Neurologic
Intervention Categories	General
Intervention Rationale	Genetic knowledge may be beneficial related to issues such as selection of optimal supportive care, informed medical decision-making, prognostic considerations, and avoidance of unnecessary testing
Comments	(No information available)
References	18369103, 17989066, 18945720, 19896112, 21424692

Human Phenotype Ontology

Disease	HPO ID	HPO Name
OMIM	HP:0002019	Constipation
OMIM	HP:0002020	Gastroesophageal reflux
OMIM	HP:0001642	Pulmonic stenosis
OMIM	HP:0002650	Scoliosis
OMIM	HP:0011968	Feeding difficulties
OMIM	HP:0002376	Developmental regression
OMIM	HP:0010808	Protruding tongue

The footer of the page includes the MSSNG logo, a release identifier `ldyllic-analyst-574.db6_release`, and a project credit: "A project by AUTISM SPEAKS".

Gene Info (4/4)



MSSNG

Variant Queries Sample Queries Phenotypes **Gene Info** More Sign Out

OMIM	HP:0002019	Constipation
OMIM	HP:0002020	Gastroesophageal reflux
OMIM	HP:0001642	Pulmonic stenosis
OMIM	HP:0002650	Scoliosis
OMIM	HP:0011968	Feeding difficulties
OMIM	HP:0002376	Developmental regression
OMIM	HP:0010808	Protruding tongue
OMIM	HP:0002307	Drooling
OMIM	HP:0000154	Wide mouth
OMIM	HP:0010864	Intellectual disability, severe
OMIM	HP:0200134	Epileptic encephalopathy
OMIM	HP:0002883	Hyperventilation
OMIM	HP:0000486	Strabismus
OMIM	HP:0001290	Generalized hypotonia
OMIM	HP:0000007	Autosomal recessive inheritance

OMIM

MIM Type	Disorder	MIM Phenotype
gene	Pitt-Hopkins-like syndrome 2, 614325 (3)	614325

[Back](#) [Variant Query for NRXN1](#)

MSSNG

Idyllic-analyst-574.db6_release

A project by AUTISM SPEAKS