

API

ALLEN BRAIN ATLAS API

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The **NIH Blueprint Non-Human Primate (NHP) Atlas** consists of a suite of gene expression data, neuroanatomical data and informatics tools for exploring the cellular and molecular architecture of the developing rhesus macaque brain. Data includes:

- **Microdissection Microarray:** Fine structure transcriptional profiling across prenatal and postnatal development stages for fine nuclear subdivisions of the prefrontal cortex, primary visual cortex, hippocampus, amygdala and ventral striatum
- **Macrodissection Microarray:** Gross structure transcriptional profiling across postnatal developmental stages for the same structures

From the API, you can:



Download expression values



Query the correlative and differential search services

Microdissection Microarray

Experimental Overview and Metadata

The NHP Developmental Microdissection Microarray Study is a genome-wide microarray profiling survey fine nuclear subdivisions of specific brain regions using rhesus macaque-specific DNA microarrays at four postnatal developmental stages.

Each sampling site was associated to a Structure by expert anatomists using cytoarchitectural information from multiple histological stains. Structures are organized hierarchically into a tree in which children structures are "parts of" their parent structure. Structures are assigned colors that visually emphasize the hierarchical relationships.

See the [structure ontology page](#) for more information.

Normalized microarray expression values can be downloaded in several ways:

- From the web application [Download page](#)
- From the connected data service in the API

All experimental data from this study is associated with the "Non-Human Primate LMD Microarray" Product. All probe and sampling site information can be accessed through the API using RMA queries.

Examples:

- [All donors in the Product](#)
- [All sampling sites in the Product](#)
- [All microarray probes in the Product](#)
- [All donors at age 0 months](#)

Downloading Expression Values



Normalized expression values can be obtained by specifying:

- a list of probes,
- a list of donors (optional), and
- a list of structures (optional)

See the [connected service](#) page for definitions of `service::nhp_lmd_microarray_expression` parameters.

Example:

Download expression values for all 48 mo donors in structure "V1-1" for all probes associated with gene MET.

- Find Donor ID for all 48 mo donors (id = 9878,11196,11272)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,age[name$seq'48 mo'],organism[name$seq'Macaca mulatta'],
products[name$seq'Non-Human Primate LMD Microarray'],
rma::options[only$seq'donors.id']
```

- Find Structure ID for "V1-1" (id = 10027)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Structure,
rma::criteria,[acronym$il'V1-1'],ontology[name$seq'Non-Human Primate Brain Atlas'],
rma::options[only$seq'structures.id']
```

- Find AffymetrixMacaqueProbeset IDs associated with gene MET (id = 12414,29851,29853,29854,49439)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::AffymetrixMacaqueProbeset,
rma::criteria,gene_association(gene[acronym$seq'MET']),
rma::options[only$seq'affymetrix_macaque_probesets.id'][order$seq'affymetrix_macaque_probesets.id']
```

- Use Donor, Structure and AffymetrixMacaqueProbeset IDs as parameters to the connected service

```
http://api.brain-map.org/api/v2/data/query.json?criteria=
service::nhp_lmd_microarray_expression[structures$seq10027]
[probes$seq12414,29851,29853,29854,49439][donors$seq9878,11196,11272]
```

The output of the service is two top level ordered arrays "probes" and "samples". For example:

```
"probes":[
  { "id":12414,
    "name": "MmugDNA.19034.1.S1_at",
    "gene-id":183127,
    "gene-symbol": "MET",
    "gene-name": "met proto-oncogene (hepatocyte growth factor receptor)",
    "entrez-id":704562, "chromosome": "3", "start-position": "n/a", "end-position": "n/a",
    "expression_level": [ "4.3598", "4.4762", "4.4883" ],
    "z-score": [ "-0.3668", "0.2633", "0.3287" ] },
  { "id":29851,
    "name": "MmugDNA.34584.1.S1_at",
    "gene-id":183127,
    "gene-symbol": "MET",
    "gene-name": "met proto-oncogene (hepatocyte growth factor receptor)",
    "entrez-id":704562, "chromosome": "3", "start-position": "n/a", "end-position": "n/a",
    "expression_level": [ "4.2801", "4.1808", "4.0958" ],
    "z-score": [ "0.0110", "-0.2272", "-0.4310" ] },
  ...
],
"samples": [
  { "donor": { "id":11272, "name": "MMU36322", "age": "48 mo", "color": "333333" },
    "structure": { "id":10027, "name": "layer I of V1", "abbreviation": "V1-1", "color": "EDC9C0" },
    "top_level_structure": { "id":4004, "name": "occipital cortex", "abbreviation": "Ocx", "color": "E7ACA1" } },
  { "donor": { "id":11196, "name": "MMU36358", "age": "48 mo", "color": "333333" },
    "structure": { "id":10027, "name": "layer I of V1", "abbreviation": "V1-1", "color": "EDC9C0" },
    "top_level_structure": { "id":4004, "name": "occipital cortex", "abbreviation": "Ocx", "color": "E7ACA1" } },
  { "donor": { "id":9878, "name": "MMU36468", "age": "48 mo", "color": "333333" },
    "structure": { "id":10027, "name": "layer I of V1", "abbreviation": "V1-1", "color": "EDC9C0" },
    "top_level_structure": { "id":4004, "name": "occipital cortex", "abbreviation": "Ocx", "color": "E7ACA1" } }
]
```

Each **probe** contains information about:

- the AffymetrixMacaqueProbeset (id, name), and
- the Gene (id, acronym, name, entrez-id), along with
- a vector of normalized expression values in the same order as the "samples" array.

- a vector of z-score values in the same order as the "samples" array. Note: z-score is computed independently for each probe over all donors and samples.

Each **sample** contains information about:

- the Donor (id, name, age),
- the Sample (well id and (x,y,z) coordinate in the MR volume in millimeters),
- the associated Structure (id, name, acronym and color), and
- the associated top (coarse) level Structure (id, name, acronym and color).

Differential Search

The differential search function finds probes that show the greatest difference between two sets (target and contrast) of user-defined structures and donors. For each probe, a 2-sample t-test is performed followed by Benjamini and Hochberg false discovery rate correction. The null hypothesis is that the average expression level of samples in the contrast set of structures is greater than or equal to the average expression level of samples in the target set of structures. A statistically significant result (p-value less than user-defined threshold) allows us to reject the null hypothesis and conclude that the average expression level of samples in the target set of structures is greater than the average expression level of samples in the contrast set of structures. Resulting p-values are sorted in ascending order. Search results can also be sorted by fold-change (log ratio of expression) in descending order.



The differential search function can be accessed through the [Web application](#) or using the API.

See the [connected service](#) page for definitions of `service::nhp_lmd_microarray_differential` parameters.

Example:

Differential search for genes with higher expression in "basal ganglia" than in the "neocortex"

- Find Structure ID for "basal ganglia" (id = 4001)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Structure,
rma::criteria,[name$il'*basal ganglia*'],ontology[name$eq'Non-Human Primate Brain Atlas'],
rma::options[only$eq'structures.id']
```

- Find Structure ID for "neocortex" (id = 294021746)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Structure,
rma::criteria,[name$il'neocortex'],ontology[name$eq'Non-Human Primate Brain Atlas'],
rma::options[only$eq'structures.id']
```

- Use Structure IDs as parameters to the connected service

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=service::nhp_lmd_microarray_differential
[structures1$eq294021746][structures2$eq4001][sort_by$eq'fold-change']
```

- [Visualize the same search result in the Web application](#)



Figure: Screenshot of top returns of a differential search for genes with higher expression in the basal ganglia than in the neocortex represented as a z-score heatmap ranging from green (below mean) to red (above mean).

Example:

Differential search for genes with higher expression at 0 months than at 3 months

- Find Donor ID for all 0 mo donors (id = 12149,3786,9321,12143)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,age[name$eq'0 mo'],organism[name$eq'Macaca mulatta'],
products[name$eq'Non-Human Primate LMD Microarray'],
rma::options[only$eq'donors.id']
```

- Find Donor ID for all 3 mo donors (id = 9479,2554,11197,12185)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,age[name$eq'3 mo'],organism[name$eq'Macaca mulatta'],
products[name$eq'Non-Human Primate LMD Microarray'],
rma::options[only$eq'donors.id']
```

- Use Donor IDs as parameters to the connected service

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=service::nhp_lmd_microarray_differential
[donors1$eq9479,2554,11197,12185][donors2$eq12149,3786,9321,12143][sort_by$eq'fold-change']
```

- Visualize the same search result in the Web application

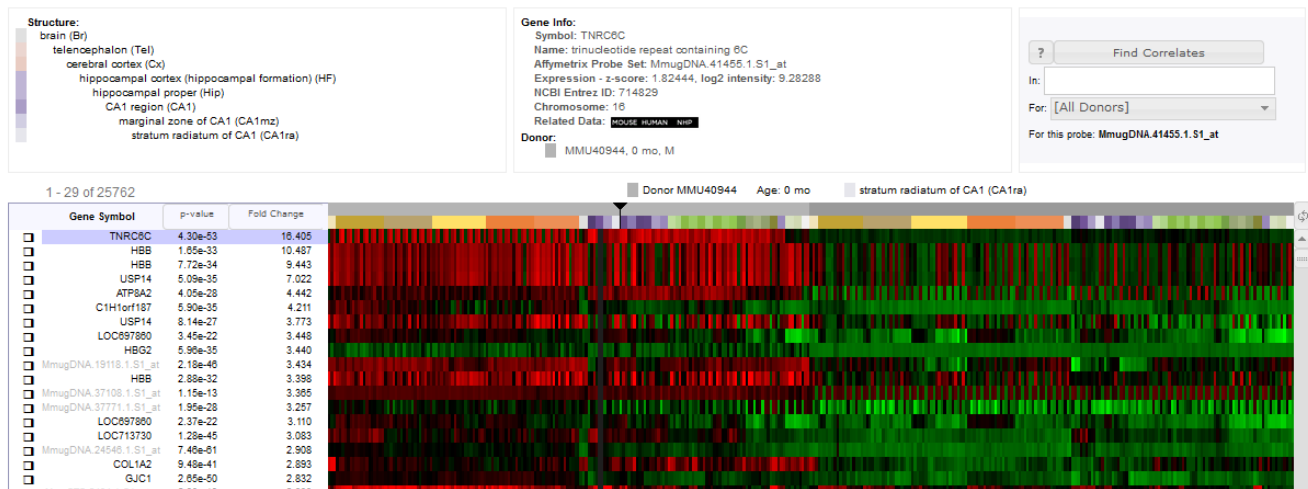


Figure: Screenshot of top returns of a differential search for genes with higher expression at 0 months than 3 months represented as a z-score heatmap ranging from green (below mean) to red (above mean).

Correlative Search

The correlative search function finds probes with expression profile similar to that of a selected seed probe over all samples within a user-specified structure and for user-specified donors. Pearson's correlation coefficient is computed for all probes and the results ranked in descending order.



The correlative search function can be accessed through the [Web application](#) or using the API.

See the [connected service](#) page for definitions of `service::nhp_lmd_microarray_correlation` parameters.

Example:

Correlative search for probes with similar expression to NTNG1 probe MmuSTS.4647.1.S1_at over the cerebral cortex

- Find AffymetrixMacaqueProbeset ID for probe "MmuSTS.4647.1.S1_at" (id = 51317)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::AffymetrixMacaqueProbeset,
rma::criteria,[displayable_id_from_affymetrix$eq'MmuSTS.4647.1.S1_at'],
rma::options[only$eq'affymetrix_macaque_probesets.id']
```

- Find Structure ID for "cerebral cortex" (id = 128011354)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Structure,
rma::criteria,[name$il'cerebral cortex'],ontology[name$eq'Non-Human Primate Brain Atlas'],
rma::options[only$eq'structures.id']
```

- Use Probe and Structure IDs as parameters to the connected service

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=service::nhp_lmd_microarray_correlation
[probes$eq51317][structures$eq128011354]
```

Macrodissection Microarray

Experimental Overview and Metadata

The NHP Developmental Macrodissection Microarray Study is a genome-wide microarray profiling survey of 5 gross brain regions using rhesus macaque-specific DNA microarrays at four postnatal developmental stages.

Normalized microarray expression values can be downloaded in several ways:

- From the web application [Download page](#)
- From the connected data service in the API

All experimental data from this study is associated with the "Non-Human Primate Macro Microarray" Product. All probe and sampling site information can be accessed through the API using RMA queries.

Examples:

- [All donors in the Product](#)
- [All sampling sites in the Product](#)
- [All microarray probes in the Product](#)
- [All donors at age 0 months](#)

Downloading Expression Values



Normalized expression values can be obtained by specifying:

- a list of probes,
- a list of donors (optional), and
- a list of structures (optional)

See the [connected service](#) page for definitions of **service::nhp_macro_microarray_expression** parameters.

Example:

Download expression values for all 48 months donors in structure "neocortex" for all probes associated with gene MET.

- Find Donor ID for all 48 mo donors (id = 9353,9481,9480)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,age[name$eq'48 mo'],organism[name$eq'Macaca mulatta'],
products[name$eq'Non-Human Primate Macro Microarray'],
rma::options[only$eq'donors.id']
```

- Find Structure ID for "neocortex" (id = 294021746)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Structure,
rma::criteria,[name$il'neocortex'],ontology[name$eq'Non-Human Primate Brain Atlas'],
rma::options[only$eq'structures.id']
```

- Find AffymetrixMacaqueProbeset IDs associated with gene MET (id = 12414,29851,29853,29854,49439)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::AffymetrixMacaqueProbeset,
rma::criteria,gene_association(gene[acronym$eq'MET']),
rma::options[only$eq'affymetrix_macaque_probesets.id'][order$eq'affymetrix_macaque_probesets.id']
```

- Use Donor, Structure and AffymetrixMacaqueProbeset IDs as parameters to the connected service

```
http://api.brain-map.org/api/v2/data/query.json?criteria=
service::nhp_macro_microarray_expression[structures$eq294021746]
[probes$eq12414,29851,29853,29854,49439][donors$eq9353,9481,9480]
```

The output of the service is two top level ordered arrays "probes" and "samples".

Each **probe** contains information about:

- the AffymetrixMacaqueProbeset (id, name), and
- the Gene (id, acronym, name, entrez-id), along with
- a vector of normalized expression values in the same order as the "samples" array.
- a vector of z-score values in the same order as the "samples" array. Note: z-score is computed independently for each probe over all donors and samples.

Each **sample** contains information about:

- the Donor (id, name, age),
- the Sample (well id and (x,y,z) coordinate in the MR volume in millimeters),
- the associated Structure (id, name, acronym and color), and
- the associated top (coarse) level Structure (id, name, acronym and color).

Differential Search

The differential search function finds probes that show the greatest difference between two sets (target and contrast) of user-defined structures and donors. For each probe, a 2-sample t-test is performed followed by Benjamini and Hochberg false discovery rate correction. The null hypothesis is that the average expression level of samples in the contrast set of structures is less than the average expression level of samples in the target set of structures. Resulting p-values are sorted in ascending order. Search results can also be sorted by fold-change (log ratio of expression) in descending order.



The differential search function can be accessed through the [Web application](#) or using the API.

See the [connected service](#) page for definitions of `service::nhp_macro_microarray_differential` parameters.

Example:

Differential search for genes with higher expression in "basal ganglia" than the "neocortex"

- Find Structure ID for "basal ganglia" (id = 4001)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Structure,
rma::criteria,[name$il'*basal ganglia*'],ontology[name$eq'Non-Human Primate Brain Atlas'],
rma::options[only$eq'structures.id']
```

- Find Structure ID for "neocortex" (id = 294021746)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Structure,
rma::criteria,[name$il'neocortex'],ontology[name$eq'Non-Human Primate Brain Atlas'],
rma::options[only$eq'structures.id']
```

- Use Structure IDs as parameters to the connected service

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=service::nhp_macro_microarray_differential
[structures1$eq294021746][structures2$eq4001][sort_by$eq'fold-change']
```

Example:

Differential search for genes with higher expression at 0 mo than 3 mo

- Find Donor ID for all 0 mo donors (id = 148141688,9590,9425)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,age[name$eq'0 mo'],organism[name$eq'Macaca mulatta'],
products[name$eq'Non-Human Primate Macro Microarray'],
rma::options[only$eq'donors.id']
```

- Find Donor ID for all 3 mo donors (id = 148141705,9639,9630)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,age[name$eq'3 mo'],organism[name$eq'Macaca mulatta'],
products[name$eq'Non-Human Primate Macro Microarray'],
rma::options[only$eq'donors.id']
```

- Use Donor IDs as parameters to the connected service

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=service::nhp_macro_microarray_differential
[donors1$eq148141705,9639,9630][donors2$eq148141688,9590,9425][sort_by$eq'fold-change']
```

Correlative Search

The correlative search function finds probes with expression profile similar to that of a selected seed probe over all samples within a user-specified structure and for user-specified donors. Pearson's correlation coefficient is computed for all probes and results ranked in descending order.



The correlative search function can be accessed through the [Web application](#) or using the API.

See the [connected service](#) page for definitions of `service::nhp_macro_microarray_correlation` parameters.

Example:

Correlative search for probes with similar expression to NTNG1 probe MmuSTS.4647.1.S1_at over the cerebral cortex

- Find AffymetrixMacaqueProbeset ID for probe "MmuSTS.4647.1.S1_at" (id = 51317)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::AffymetrixMacaqueProbeset,
rma::criteria,[displayable_id_from_affymetrix$eq'MmuSTS.4647.1.S1_at'],
rma::options[only$eq'affymetrix_macaque_probesets.id']
```

- Find Structure ID for "cerebral cortex" (id = 128011354)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Structure,
rma::criteria,[name$il'cerebral cortex'],ontology[name$eq'Non-Human Primate Brain Atlas'],
rma::options[only$eq'structures.id']
```

- Use Probe and Structure IDs as parameters to the connected service

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=service::nhp_macro_microarray_correlation
[probes$eq51317][structures$eq128011354]
```