

# API

## ALLEN BRAIN ATLAS API

- [Developmental Transcriptome](#)
  - [Experimental Overview and Metadata](#)
  - [Downloading Expression Values](#)
  - [Differential Search](#)
  - [Correlative Search](#)
- [Prenatal LMD Microarray](#)
  - [Experimental Overview and Metadata](#)
  - [Downloading Expression Values](#)
  - [Differential Search](#)
  - [Correlative Search](#)



The **BrainSpan Atlas of the Developing Human Brain** is a foundational resource for studying transcriptional mechanisms involved in human brain development. The data includes:

- **Developmental Transcriptome:** RNA sequencing and exon microarray data profiling up to sixteen cortical and subcortical structures across the full course of human brain development
- **Prenatal LMD Microarray:** High-resolution neuroanatomical transcriptional profiles of ~300 distinct structures spanning the entire brain for four midgestational prenatal specimens

From the API, you can:



**Download expression values**



**Query the correlative and differential search services**

## Developmental Transcriptome

### Experimental Overview and Metadata

The Developmental Transcriptome Study is a broad developmental survey of gene expression in specific brain regions using RNA sequencing and exon microarray techniques. The survey profiles up to sixteen targeted cortical and subcortical structures across the full course of human brain development, spanning pre- and postnatal-development in both males and females.

Each sampling site is associated with a Structure. For convenience, surveyed structures are grouped together in the "Developing Human - Transcriptome" StructureSet.

Typically, for each sample four types of expression values are available:

- RNA-Seq RPKM values summarized to the gene level
- RNA-Seq RPKM values summarized to the exon level
- Normalized exon microarray expression values summarized to the gene level
- Normalized exon microarray expression values summarized to the probeset level

Normalized expression values can be downloaded in several ways:

- From the web application [Download page](#).
- From the "Download this data" link below the heatmap in the web application.
- From the connected data service in the API

All experimental data from this study is associated with the "Developing Human Transcriptome" Product. All gene, exon, probeset, donor and sampling site information can be accessed through the API using RMA queries.

#### Examples:

- All donors in the Product

```
http://api.brain-map.org/api/v2/data/Donor/query.xml?include=age&criteria=products[id$eq24]
```

- All samples in the Product

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Specimen,
rma::criteria,donor(products[id$eq24]),
well_known_files(well_known_file_type[name$eqRNASeqSummarizedToGenes]),
rma::include,donor(age)
```

- All prenatal donors in the Product

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,products[id$eq24],rma::include,age[embryonic$eqtrue]
```

- All postnatal donors in the Product

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,products[id$eq24],rma::include,age[embryonic$eqfalse]
```

- All surveyed structures

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Structure,
rma::criteria,structure_sets[name$eq'Developing Human - Transcriptome'],
rma::options[only$eq'structures.id,structures.acronym,structures.name,structures.color_hex_triplet']
```

## Downloading Expression Values



Normalized expression values can be obtained by specifying:

- the required expression type ("set"),
- a list of "probes",
- a list of donors (optional), and
- a list of structures (optional)

See the [connected service](#) page for definitions of **service::dev\_human\_expression** parameters.

Expression Type	"set" parameter	"probe" object
RNA-Seq RPKM values summarized to the gene level	rna_seq_genes	Gene (ensembl_id not null)
RNA-Seq RPKM values summarized to the exon level	rna_seq_exons	GoExons
Exon microarray expression values summarized to the gene level	exon_microarray_genes	Gene (entrez_id not null)
Exon microarray expression values summarized to the probeset level	exon_microarray_exons	AffymetriProbesets

### RNA-Seq RPKM values summarized to the gene level

#### Example:

Download RNA-Seq expression values for samples from donor "H376.VI.52" associated with gene CARTPT

- Find Donor ID for "H376.VI.52" (id = 12890)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,[name$eq'H376.VI.52'],
rma::options[only$eq'donors.id']
```

- Find Gene ID associated with gene CARTPT (id = 1098278)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Gene,
rma::criteria,[acronym$eq'CARTPT'] [type$eq'EnsemblGene'],organism[name$eq'Homo Sapiens'],
rma::options[only$eq'genes.id']
```

- Use **set = rna\_seq\_genes**, Gene ("probe") and Donor IDs as parameter to the **service::dev\_human\_expression**

```
http://api.brain-map.org/api/v2/data/query.json?criteria=service::dev_human_expression
[set$seq'rna_seq_genes'][probes$seq1098278][donors$seq12890]
```

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

```
"probes":[
  {
    "id":1098278,
    "name":"ENSG00000164326",
    "gene-id":9463,
    "gene-symbol":"CARTPT","gene-name":"CART prepropeptide",
    "entrez-id":9607,"chromosome":"5","start-position":"n/a","end-position":"n/a",
    "expression_level":["5.5566","4.9466","5.6331",...]
  },
  ...
]
"samples":[
  {
    "donor":{"id":12890,"name":"H376.VI.52","age":"4 mos","color":"76EB76"},
    "structure":{"id":10173,"name":"dorsolateral prefrontal cortex","abbreviation":"DFC","color":"D4B235"},
    "top_level_structure":{"id":10153,"name":"neural plate","abbreviation":"NP","color":"D7D8D8"}},
  {
    "donor":{"id":12890,"name":"H376.VI.52","age":"4 mos","color":"76EB76"},
    "structure":{"id":10185,"name":"ventrolateral prefrontal cortex","abbreviation":"VFC","color":"C2A335"},
    "top_level_structure":{"id":10153,"name":"neural plate","abbreviation":"NP","color":"D7D8D8"}},
  {
    "donor":{"id":12890,"name":"H376.VI.52","age":"4 mos","color":"76EB76"},
    "structure":{"id":10278,"name":"anterior (rostral) cingulate (medial prefrontal) cortex","abbreviation":"MFC","color":"E26880"},
    "top_level_structure":{"id":10153,"name":"neural plate","abbreviation":"NP","color":"D7D8D8"}}, ...
  ],
  ...
]
```

Each **probe** (Gene) contains information about:

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

Each **sample** contains information about:

- the Donor (id, name, age),
- the associated Structure (id, name, acronym and color), and
- the associated top (coarse) level Structure (id, name, acronym and color).

## RNA-Seq RPKM values summarized to the exon level

**Example:**

Download RNA-Seq expression values for samples from donor "H376.VI.52" and all exons associated with gene CARTPT

- Find Donor ID for "H376.VI.52" (id = 12890)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,[name$seq'H376.VI.52'],
rma::options[only$seq'donors.id']
```

- Find GoExons ID associated with gene CARTPT (id = 279330730,279330740,279330735)

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

- Use **set = rna\_seq\_exons**, GoExon ("probe") and Donor IDs as parameter to the **service::dev\_human\_expression**

```
http://api.brain-map.org/api/v2/data/query.json?criteria=service::dev_human_expression
[set$seq'rna_seq_exons'][probes$seq279330730,279330740,2793307356][donors$seq12890]
```

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

```

"probes": [
  { "id": 279330730,
    "name": "ENSG00000164326",
    "gene-id": 1098278,
    "gene-symbol": "CARTPT",
    "gene-name": "CART prepropeptide",
    "entrez-id": 9607, "chromosome": "5", "start-position": 71014989, "end-position": 71015279,
    "expression_level": [ "5.7282", "4.8102", "5.7152", ... ] },
  { "id": 279330735,
    "name": "ENSG00000164326",
    "gene-id": 1098278, "gene-symbol": "CARTPT",
    "gene-name": "CART prepropeptide",
    "entrez-id": 9607, "chromosome": "5", "start-position": 71015405, "end-position": 71015790,
    "expression_level": [ "4.4128", "3.8230", "4.3135", ... ] },
  { "id": 279330740,
    "name": "ENSG00000164326",
    "gene-id": 1098278, "gene-symbol": "CARTPT",
    "gene-name": "CART prepropeptide",
    "entrez-id": 9607, "chromosome": "5", "start-position": 71016334, "end-position": 71016875,
    "expression_level": [ "5.9593", "5.4664", "6.1137", ... ] }
],
"samples": [
  { "donor": { "id": 12890, "name": "H376.VI.52", "age": "4 mos", "color": "76EB76" },
    "structure": { "id": 10173, "name": "dorsolateral prefrontal cortex", "abbreviation": "DFC", "color": "D4B235" },
    "top_level_structure": { "id": 10153, "name": "neural plate", "abbreviation": "NP", "color": "D7D8D8" } },
  { "donor": { "id": 12890, "name": "H376.VI.52", "age": "4 mos", "color": "76EB76" },
    "structure": { "id": 10185, "name": "ventrolateral prefrontal cortex", "abbreviation": "VFC", "color": "C2A335" },
    "top_level_structure": { "id": 10153, "name": "neural plate", "abbreviation": "NP", "color": "D7D8D8" } },
  { "donor": { "id": 12890, "name": "H376.VI.52", "age": "4 mos", "color": "76EB76" },
    "structure": { "id": 10278, "name": "anterior (rostral) cingulate (medial prefrontal) cortex", "abbreviation": "MFC", "color": "E26880" },
    "top_level_structure": { "id": 10153, "name": "neural plate", "abbreviation": "NP", "color": "D7D8D8" } }, ...
],

```

Each **probe** (GoExon) contains information about:

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

Each **sample** contains information about:

- the Donor (id, name, age),
- the associated Structure (id, name, acronym and color), and
- the associated top (coarse) level Structure (id, name, acronym and color).

## Normalized exon microarray expression values summarized to the gene level

### Example:

Download exon microarray expression values for samples from donor "H376.VI.50" associated with gene CARTPT

- Find Donor ID for "H376.VI.50" (id = 12296)

```

http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,[name$eq'H376.VI.50'],
rma::options[only$eq'donors.id']

```

- Find Gene ID associated with gene CARTPT (id = 9463)

```

http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Gene,
rma::criteria,[acronym$eq'CARTPT'] [type$eq'NcbiGene'],organism[name$eq'Homo Sapiens'],
rma::options[only$eq'genes.id']

```

- Use **set = exon\_microarray\_genes**, Gene ("probe") and Donor IDs as parameter to the **service::dev\_human\_expression**

```
http://api.brain-map.org/api/v2/data/query.json?criteria=service::dev_human_expression
[set$eq'exon_microarray_genes'] [probes$eq9463] [donors$eq12296]
```

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

```
"probes": [
  { "id": 9463,
    "name": "ENSG00000164326",
    "gene-id": 9463,
    "gene-symbol": "CARTPT",
    "gene-name": "CART prepropeptide",
    "entrez-id": 9607, "chromosome": "5", "start-position": "n/a", "end-position": "n/a",
    "expression_level": [ "8.1073", "5.9564", "6.3102", "7.0532", "9.6157", "7.1290", "5.1168", "4.4212", "4.2779" ],
    "z-score": [ "1.3547", "0.0538", "0.2678", "0.7172", "2.2670", "0.7630", "-0.4541", "-0.8748", "-0.9615" ]
  },
  ...
]
"samples": [
  { "donor": { "id": 12296, "name": "H376.VI.50", "age": "4 mos", "color": "80FF80" },
    "structure": { "id": 10278, "name": "anterior (rostral) cingulate (medial prefrontal) cortex", "abbreviation": "MFC", "color": "E26880" },
    "top_level_structure": { "id": 10153, "name": "neural plate", "abbreviation": "NP", "color": "D7D8D8" },
    { "donor": { "id": 12296, "name": "H376.VI.50", "age": "4 mos", "color": "80FF80" },
    "structure": { "id": 10243, "name": "posterior (caudal) superior temporal cortex (area 22c)", "abbreviation": "STC", "color": "D670A0" },
    "top_level_structure": { "id": 10153, "name": "neural plate", "abbreviation": "NP", "color": "D7D8D8" }, ...
  },
  ...
]
```

Each **probe** (Gene) contains information about:

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

Each **sample** contains information about:

- the Donor (id, name, age),
- the associated Structure (id, name, acronym and color), and
- the associated top (coarse) level Structure (id, name, acronym and color).

## Normalized exon microarray expression values summarized to a probeset level

Download exon microarray expression values for samples from donor "H376.VI.50" for all probesets associated with gene CARTPT

- Find Donor ID for "H376.VI.50" (id = 12296)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,[name$eq'H376.VI.50'],
rma::options[only$eq'donors.id']
```

- Find AffymetrixProbeset ID associated with gene CARTPT (id = 280550735,280550750,280550740,280550730,280550745)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::AffymetrixProbeset,
rma::criteria,gene_association(gene[acronym$eq'CARTPT'](organism[name$eq'Homo Sapiens'])),
rma::options[only$eq'affymetrix_probesets.id']
```

- Use **set = exon\_microarray\_exons**, AffymetrixProbeset ("probe") and Donor IDs as parameter to the **service::dev\_human\_expression**

```
http://api.brain-map.org/api/v2/data/query.json?criteria=service::dev_human_expression
[set$eq'exon_microarray_exons'] [probes$eq280550735,280550750,280550740,280550730,280550745]
[donors$eq12296]
```

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

```

"probes": [
  { "id": 280550735,
    "name": "ENSG00000164326",
    "gene-id": 9463,
    "gene-symbol": "CARTPT",
    "gene-name": "CART prepropeptide",
    "entrez-id": 9607, "chromosome": "5", "start-position": 71015125, "end-position": 71015265,
    "expression_level": [ "8.1073", "6.4681", "6.3102", "7.0532", "9.4350", "7.1290", "5.1560", "5.0550", "4.9879" ],
    "z-score": [ "1.4783", "0.0367", "-0.1021", "0.5513", "2.6458", "0.6179", "-1.1171", "-1.2059", "-1.2649" ] },
  { "id": 280550750,
    "name": "ENSG00000164326",
    "gene-id": 9463,
    "gene-symbol": "CARTPT",
    "gene-name": "CART prepropeptide",
    "entrez-id": 9607, "chromosome": "5", "start-position": 71016613, "end-position": 71016799,
    "expression_level": [ "10.1951", "8.8021", "7.7846", "9.4317", "11.8110", "10.0210", "6.1850", "5.6075", "4.5526" ],
    "z-score": [ "1.2342", "0.6566", "0.2348", "0.9177", "1.9041", "1.1620", "-0.4284", "-0.6678", "-1.1052" ] },
  ],
"samples": [
  { "donor": { "id": 12296, "name": "H376.VI.50", "age": "4 mos", "color": "80FF80" },
    "structure": { "id": 10278, "name": "anterior (rostral) cingulate (medial prefrontal) cortex", "abbreviation": "MFC", "color": "E26880" },
    "top_level_structure": { "id": 10153, "name": "neural plate", "abbreviation": "NP", "color": "D7D8D8" } },
  { "donor": { "id": 12296, "name": "H376.VI.50", "age": "4 mos", "color": "80FF80" },
    "structure": { "id": 10243, "name": "posterior (caudal) superior temporal cortex (area 22c)", "abbreviation": "STC", "color": "D670A0" },
    "top_level_structure": { "id": 10153, "name": "neural plate", "abbreviation": "NP", "color": "D7D8D8" } }, ...
  ]

```

Each **probe** (Gene) contains information about:

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

Each **sample** contains information about:

- the Donor (id, name, age),
- the associated Structure (id, name, acronym and color), and
- the associated top (coarse) level Structure (id, name, acronym and color).

## Differential Search

Differential search find "probes" that show the greatest difference in expression values between two sets (target and contrast) of user-defined structures. 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::dev_human_differential` parameters.

### Example:

Differential search for genes with higher expression in "striatum" than in the whole "neural plate" over all donors for each of the four types of expression data.

- Find Structure ID for "striatum" (id = 10333)

```

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

```

- Find Structure ID for "neural plate" (id = 10153)

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

- Differential search for gene-level RNA-Seq data (set = rna\_seq\_genes)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=service::dev_human_differential
[set$eq'rna_seq_genes'][structures1$eq10153][structures2$eq10333][sort_by$eq'fold-change']
```

- Differential search for exon-level RNA-Seq data (set = rna\_seq\_exons)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=service::dev_human_differential
[set$eq'rna_seq_exons'][structures1$eq10153][structures2$eq10333][sort_by$eq'fold-change']
```

- Differential search for gene-level exon microarray data (set = exon\_microarray\_genes)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=service::dev_human_differential
[set$eq'exon_microarray_genes'][structures1$eq10153][structures2$eq10333][sort_by$eq'fold-change']
```

- Differential search for probeset-level exon microarray data (set = exon\_microarray\_exons)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=service::dev_human_differential
[set$eq'exon_microarray_exons'][structures1$eq10153][structures2$eq10333][sort_by$eq'fold-change']
```

- Visualize the gene-level RNA-Seq differential search result in the Web application



Figure: Screenshot of top returns of a differential search for genes with higher expression in the striatum than in the whole neural plate.

#### Example:

Differential search for genes with higher expression at 8-9 pcw than at 10-12 pcw over the whole "neural plate" for each of the four types of expression data.

- Find Structure ID for "neural plate" (id = 10153)

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

- Find Donor IDs for donors within age 8-9 pcw (id = 12833,13058)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,products[name$eq'Developing Human Transcriptome'],age[embryonic$eqtrue][days$ge56]
[days$le63],
rma::options[only$eq'donors.id']
```

- Find Donor IDs for donors within age 10-12 pcw (id = 12835,12960,13060)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,products[name$eq'Developing Human Transcriptome'],age[embryonic$eqtrue][days$ge70]
[days$le84],
rma::options[only$eq'donors.id']
```

- Differential search for gene-level RNA-Seq data (set = rna\_seq\_genes)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=service::dev_human_differential
[set$eq'rna_seq_genes'] [donors1$eq12835,12960,13060][donors2$eq12833,13058]
[structures1$eq10153][structures2$eq10153][sort_by$eq'fold-change']
```

- Differential search for exon-level RNA-Seq data (set = rna\_seq\_exons)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=service::dev_human_differential
[set$eq'rna_seq_exons'] [donors1$eq12835,12960,13060][donors2$eq12833,13058]
[structures1$eq10153][structures2$eq10153][sort_by$eq'fold-change']
```

- Differential search for gene-level exon microarray data (set = exon\_microarray\_genes)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=service::dev_human_differential
[set$eq'exon_microarray_genes'] [donors1$eq12835,12960,13060][donors2$eq12833,13058]
[structures1$eq10153][structures2$eq10153][sort_by$eq'fold-change']
```

- Differential search for probeset-level exon microarray data (set = exon\_microarray\_exons)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=service::dev_human_differential
[set$eq'exon_microarray_exons'] [donors1$eq12835,12960,13060][donors2$eq12833,13058]
[structures1$eq10153][structures2$eq10153][sort_by$eq'fold-change']
```

## Correlative Search

Correlative search finds "probes" with expression profile similar that of a to 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::dev_human_correlation` parameters.

### Example:

Correlative search for "probes" with similar expression to PVALB over the whole brain

- Correlative search for gene-level RNA-Seq data ( seed ?Ensembl Gene id = 1089164, set = rna\_seq\_genes )

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_correlation[set$eq'rna_seq_genes][probes$eq1089164][structures$eq10153]
```

- Correlative search for exon-level RNA-Seq data ( seed GoExon id = 278724739, set = rna\_seq\_exons )



```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_correlation[set$eqrna_seq_exons][probes$eq278724739][structures$eq10153]
```

- Correlative search for gene-level exon microarray data (seed NCBI Gene id = 5784, set = exon\_microarray\_genes )

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_correlation[set$eqexon_microarray_genes][probes$eq5784][structures$eq10153]
```

- Correlative search for probeset-level exon microarray data ( seed AffymetrixProbeset id = 281337753, set = exon\_microarray\_exons )

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_correlation[set$eqexon_microarray_exons][probes$eq281337753][structures$eq10153]
```

## Prenatal LMD Microarray

### Experimental Overview and Metadata

The Prenatal LMD Microarray Study is a genome-wide microarray data profiling of gene expression in finely dissected regions spanning the entire prenatal human brain and isolated using laser microdissection (LMD).

RNA isolated from each sample area was hybridized to a custom Agilent 8x60k microarray chip to measure gene expression over the transcriptome. All least two different probes were available for 93% of genes. Probes were located on different exons as much as possible when multiple probes were available for a gene. For 60 genes, sets of tiling probes were designed. This study uses the same chip design as the [Human Brain Microarray Survey](#).

Each sampling site was associated with 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](#). Each zip file contains the normalized values for all probes and all samples for one donor )
- From the "Download this data" link below the heatmap in the web application.
- From the connected data service in the API

All experimental data from this study is associated with the "Developing Human Prenatal 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](#)

### 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::dev_human_microarray_expression` parameters.

#### Example:

Download expression values for donor "H376.IIIA.02" in structure "cerebellar cortex" for all probes associated with gene SLC6A.

- Find Donor ID for "H376.IIIA.02" (id = 12840)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Donor,
rma::criteria,[name$eq'H376.IIIA.02'],
rma::options[only$eq'donors.id']
```

- Find Structure ID for "cerebellar cortex" (id = 10657)

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

- Find Probes associated with gene SLC6A2(id = 1023146,1023147 )

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Probe,
rma::criteria,[probe_type$eq'DNA'],products[abbreviation$eq'HumanMA'],gene[acronym$eq'SLC6A2'],
rma::options[only$eq'probes.id']
```

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

```
http://api.brain-map.org/api/v2/data/query.json?criteria=
service::dev_human_microarray_expression[probes$eq1023146,1023147][donors$eq12840][structures$eq10657]
```

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

```
"probes": [
  { "id": 1023146,
    "name": "A_23_P358345",
    "gene-id": 6494,
    "gene-symbol": "SLC6A2",
    "gene-name": "solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2",
    "entrez-id": 6530, "chromosome": "16", "start-position": "n/a", "end-position": "n/a",
    "expression_level": [ "5.6462", "5.9486", "3.1022" ],
    "z-score": [ "2.4164", "2.6249", "0.6624" ] },
  { "id": 1023147,
    "name": "CUST_16472_PI416261804",
    "gene-id": 6494, "gene-symbol": "SLC6A2",
    "gene-name": "solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2",
    "entrez-id": 6530, "chromosome": "16", "start-position": "n/a", "end-position": "n/a",
    "expression_level": [ "2.8149", "1.2956", "1.7658" ],
    "z-score": [ "0.8169", "-0.9788", "-0.4231" ] }
],
"samples": [
  { "donor": { "id": 12840, "name": "H376.IIIA.02", "age": "15 pcw", "color": "0080FF" },
    "structure": { "id": 10658, "name": "cerebellar vermis", "abbreviation": "CBV", "color": "76A2D5" },
    "top_level_structure": { "id": 10657, "name": "cerebellar cortex", "abbreviation": "CBC", "color": "89ADDB" } },
  { "donor": { "id": 12840, "name": "H376.IIIA.02", "age": "15 pcw", "color": "0080FF" },
    "structure": { "id": 12384, "name": "paravermis of cerebellum", "abbreviation": "CBPV", "color": "4A8ECC" },
    "top_level_structure": { "id": 10657, "name": "cerebellar cortex", "abbreviation": "CBC", "color": "89ADDB" } },
  { "donor": { "id": 12840, "name": "H376.IIIA.02", "age": "15 pcw", "color": "0080FF" },
    "structure": { "id": 12390, "name": "lateral hemisphere of cerebellum", "abbreviation": "CBL", "color": "4A8ECC" },
    "top_level_structure": { "id": 10657, "name": "cerebellar cortex", "abbreviation": "CBC", "color": "89ADDB" } }
]
```

Each **probe** contains information about:

- the Probe(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 associated Structure (id, name, acronym and color), and
- the associated top (coarse) level Structure (id, name, acronym and color).

## Differential Search

Differential search finds probes that show the greatest difference between two sets (target and contrast) of user-defined structures. 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::dev_human_microarray_differential` parameters.

**Example:**

Differential search for genes with higher expression in "thalamus" than the "transient structures of forebrain"

- Find Structure ID for "thalamus" (id = 10390)

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

- Find Structure ID for "transient structures of forebrain" (id = 10506)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Structure,
rma::criteria,[name$il'transient structures of forebrain'],ontology[name$eq'Developing Human 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::dev_human_microarray_differential
[structures1$eq10506][structures2$eq10390][sort_by$eq'fold-change']
```

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

Gene Search  
 Differential Search  
 Gene Classification

Target Structure(s)     
 Contrast Structure(s)    
 Selected Donor(s)

- Structure:
- forebrain (prosencephalon) (F)
  - gray matter of forebrain (FGM)
  - diencephalon (Die)
  - thalamus (THM)
  - dorsal thalamus (DTH)
  - lateral nuclear complex of thalamus (LNC)
  - ventral group of lateral nucleus (VLN)
  - ventral anterior nucleus of thalamus (VA)

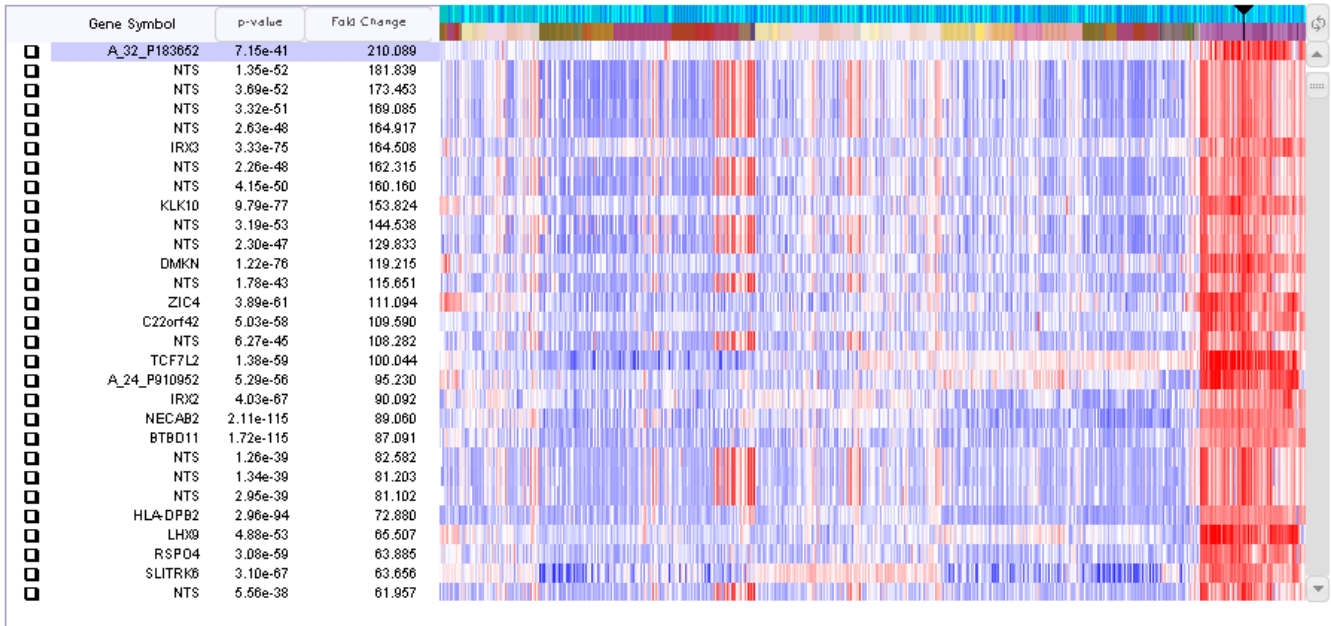
Gene Info:

Symbol: [A\\_32\\_P183652](#)  
 Name: AGILENT probe A\_32\_P183652 (non-RefSeq)  
 Probe: [A\\_32\\_P183652](#)  
 Expression - z-score: 1.93427, log2 intensity: 10.0596  
 Related Data:  
 Donor: ■ H376.IV.03, 21 pow, F, Asian

For:   
 For this probe: [A\\_32\\_P183652](#)

1 - 29 of 19273

■ Donor H376.IV.03 ■ Age: 21 pow ■ ventral anterior nucleus of thalamus (VA)



**Figure:** Screenshot of top returns of a differential search for genes with higher expression in the thalamus than in the transient structures of forebrain. The z-score heatmap shows enrichment in the thalamus relative to other brain regions.

## Correlative Search

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



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

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

### Example:

Correlative search for probes with similar expression to PVALB probe CUST\_11451\_PI416261804 over the whole neural plate

- Find Probe ID for probe "CUST\_11451\_PI416261804" (id = 1052410)

```

http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Probe,
rma::criteria,[name$eq'CUST_11451_PI416261804'],
rma::options[only$eq'probes.id']
  
```

- Find Structure ID for "neural plate" (id = 10153)

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=model::Structure,  
rma::criteria,[name$il'neural plate'],ontology[name$eq'Developing Human 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::dev_human_microarray_correlation  
[probes$eq1052410][structures$eq10153]
```

- Visualize the same search result in the Web application



**Figure:** Screenshot of top returns of a correlative search for probes with similar expression to a PVALB probe with expression values displayed as a z-score heatmap.