



OCULOMOTOR NUCLEUS (III)

ALLEN
BRAIN ATLAS
MOUSE BRAIN

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Introduction

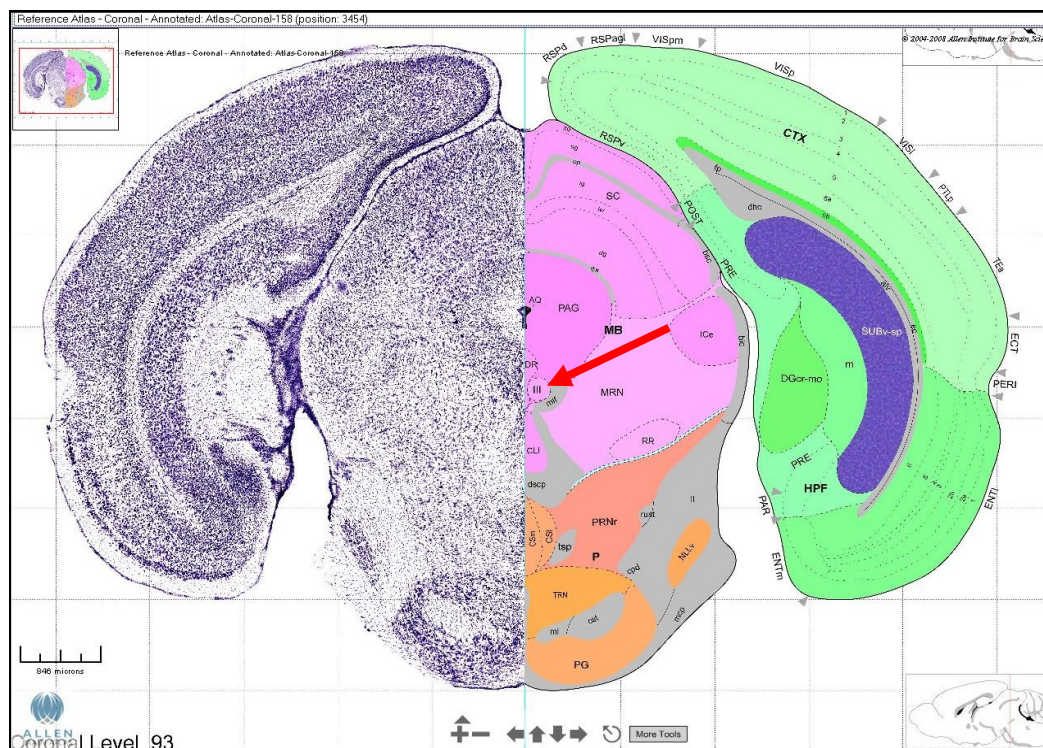
This report contains a gene expression summary of the oculomotor nucleus, derived from the [Allen Brain Atlas \(ABA\)](#) *in situ* hybridization mouse data set. The structure's location and morphological characteristics in the mouse brain are described using the Nissl data found in the [Allen Reference Atlas](#). Using an established algorithm, the expression values of the oculomotor nucleus were compared to the values of the macro/parent-structure, in this case the midbrain, for the purpose of extracting regionally selective gene expression data. The genes with the highest ranking selectivity ratios were manually curated and verified. 50 genes were then selected and compiled for expression characterization. The experimental data for each gene may be accessed via the links provided; additional data in the sagittal plane may also be accessed using the [ABA](#). Correlations between gene expression in the oculomotor nucleus and the rest of the brain, across all genes in the coronal dataset (~4300 genes), were derived computationally. A gene ontology table (derived from DAVID Bioinformatics Resources 2007) is also included, highlighting possible functions of the 50 genes selected for this report.

To read more about how our 50 Select Genes list is derived, please refer to the [Fine Structure Annotation white paper](#).

Allen Reference Atlas Coronal Levels: 90-96

Allen Reference Atlas Sagittal Levels: 18-21

Shown below is a plate from the Allen Reference Atlas, depicting the oculomotor nucleus ([level 93](#)):



Description of Structure:

LOCATION and STRUCTURAL ANATOMY:

The hierarchical relationship within the brain is depicted below in the structure [legend](#). The Allen Reference Atlas (based on Nissl-stained sections scanned at 10X) was the primary resource for the following descriptions.

For additional information please refer to the [Allen Reference Atlas white paper](#).
[BrainInfo](#) houses a search engine that allows searches for structure name aliases.

The oculomotor nucleus (III) is located in the midbrain in the ventromedial portion of the periaqueductal gray. It is bordered caudally by the trochlear nucleus (IV), medially by the Edinger-Westphal (EW) and dorsal raphe (DR) nuclei, ventrolaterally by the medial longitudinal fascicle (mlf), and laterally by the midbrain reticular nucleus (MRN).

Large motor neurons evenly distributed throughout the structure distinguish the oculomotor nucleus from the surrounding structures. This is readily apparent in both the coronal and sagittal Nissl sections, as well as in the Allen Institute ISH data.

The appearance and location of the oculomotor nucleus can be appreciated on the following two pages. Nissl-stained sections and Allen Reference Atlas plates reveal the cytoarchitecture and extent of the nucleus and its location in relation to surrounding structures.

Alphabetically | By Structure

Allen Brain Atlas: Structural Relationships

Click on a row to see what structures it contains.

[show all](#) | [hide all](#)

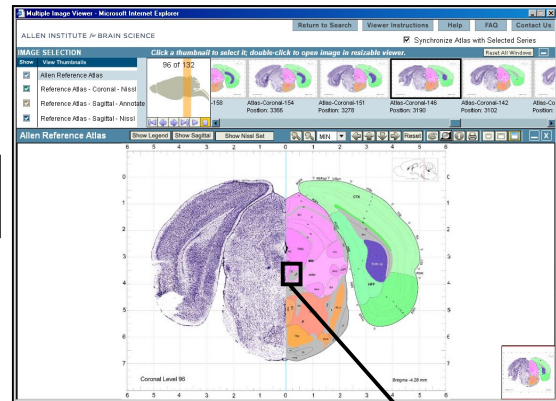
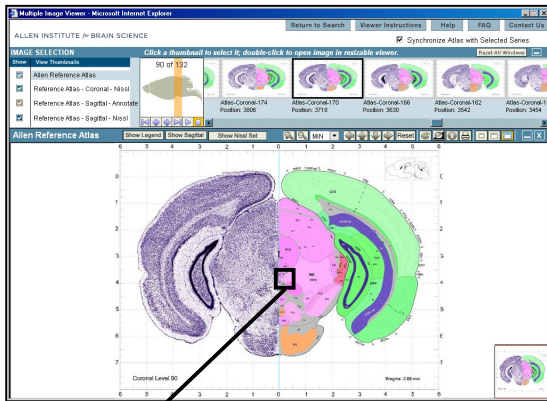
- Basic Cell Groups and Regions
 - Cerebrum [CH]
 - Cerebellum [CB]
 - Brain stem [BS]
 - Interbrain [IB]
 - Midbrain [MB]
 - Midbrain, sensory related [MBsen]
 - Midbrain, motor related [MBmot]
 - Midbrain reticular nucleus [MRN]
 - Superior colliculus, motor related [SCm]
 - Substantia nigra, lateral part [SNI]
 - Substantia nigra, reticular part [SNr]
 - Ventral tegmental area [VTA]
 - Ventral tegmental nucleus [VTN]
 - Anterior tegmental nucleus [AT]
 - Midbrain reticular nucleus, retrorubral area [RR]
 - Medial terminal nucleus of the accessory optic tract [MT]
 - Lateral terminal nucleus of the accessory optic tract [LT]
 - Dorsal terminal nucleus of the accessory optic tract [DT]
 - Periaqueductal gray [PAG]
 - Pretectal region [PRT]
 - Cuneiform nucleus [CUN]
 - Red Nucleus [RN]
 - Oculomotor nucleus [III]**
 - Edinger-Westphal nucleus [EW]
 - Trochlear nucleus [IV]
 - Midbrain, behavioral state related [MBsta]
 - Hindbrain [HB]
- fiber tracts
- Grooves
- ventricular systems

Atlas and Nissl:

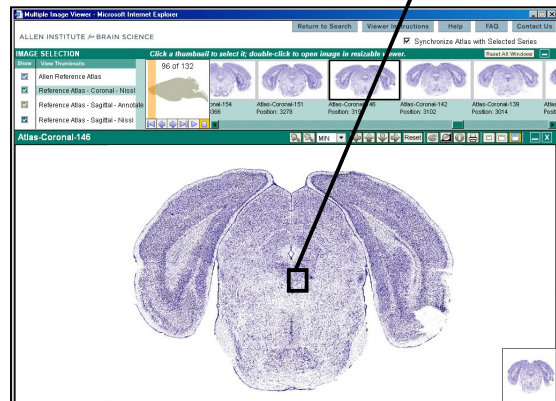
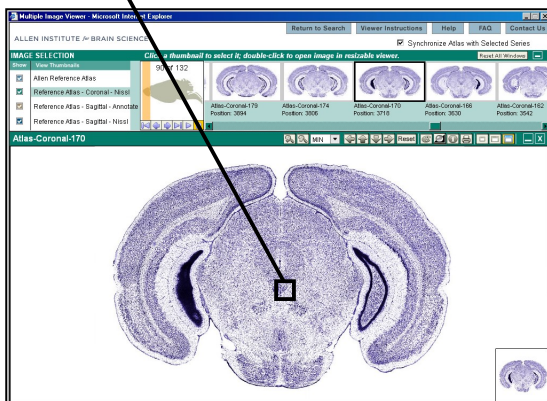
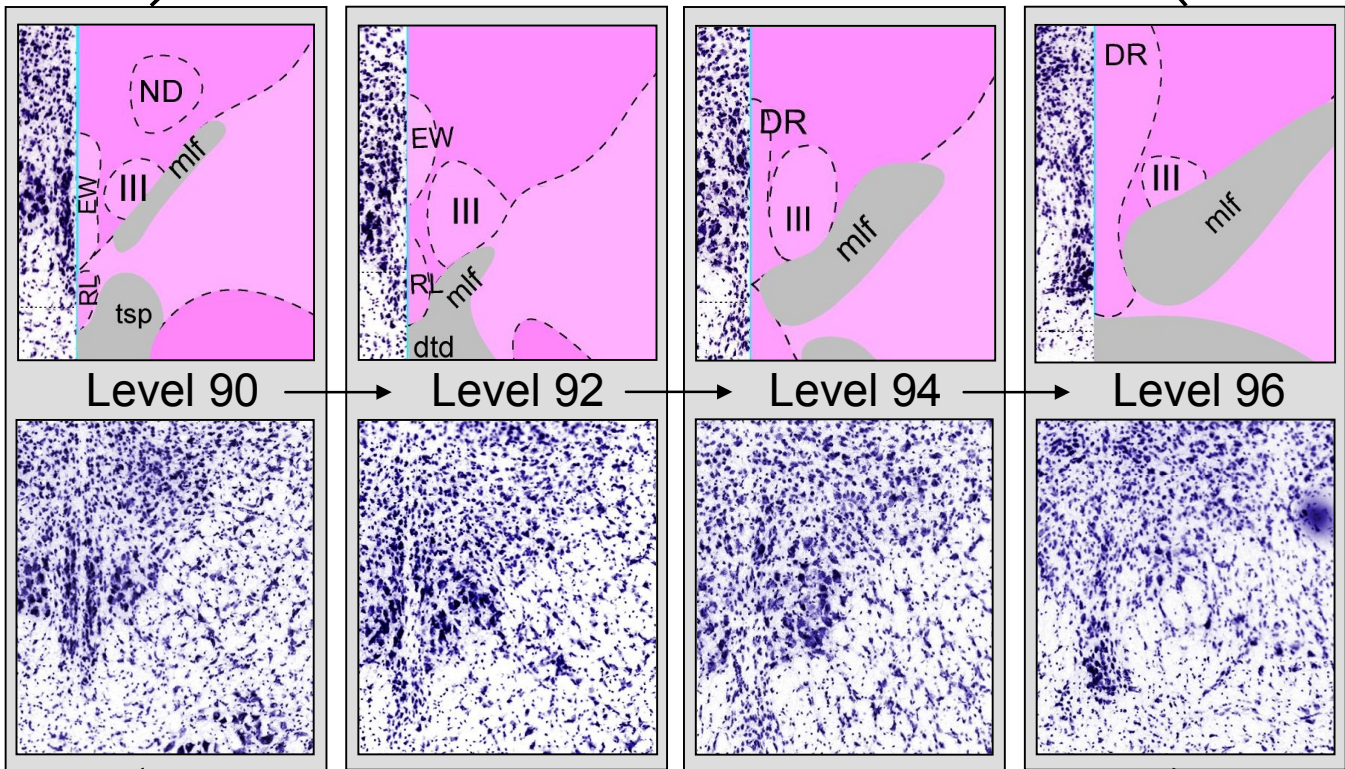
Coronal:

Rostral

Caudal



Reference Atlas

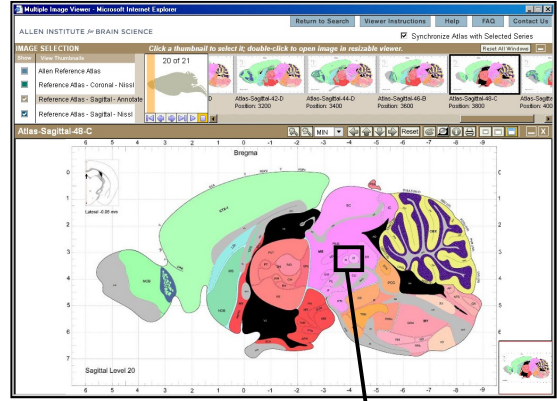
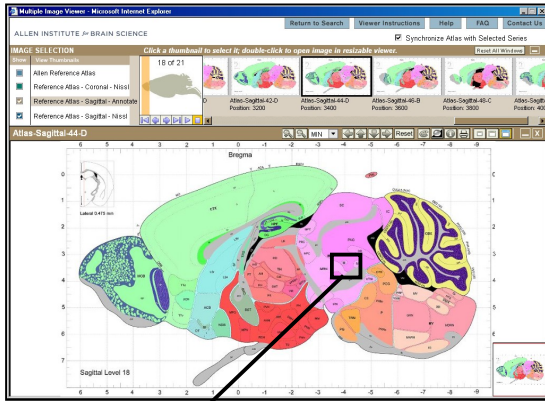


Nissl

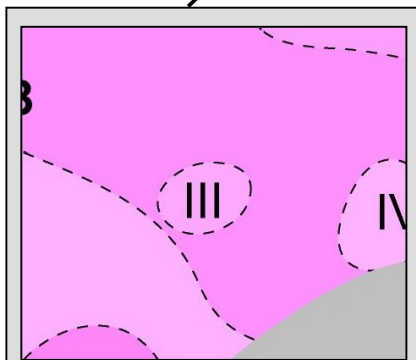
Atlas and Nissl: Sagittal

Lateral

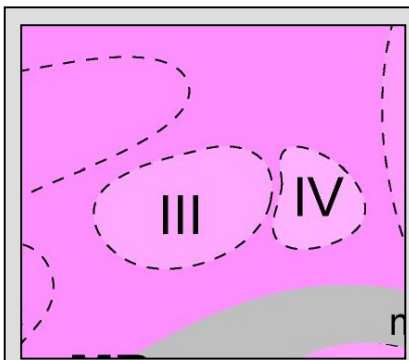
Medial



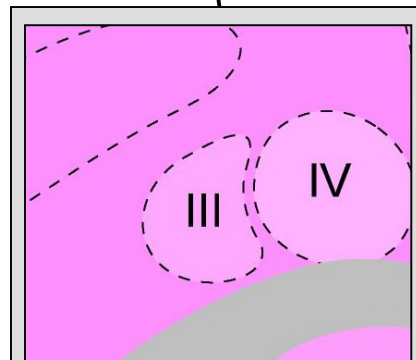
Reference
Atlas



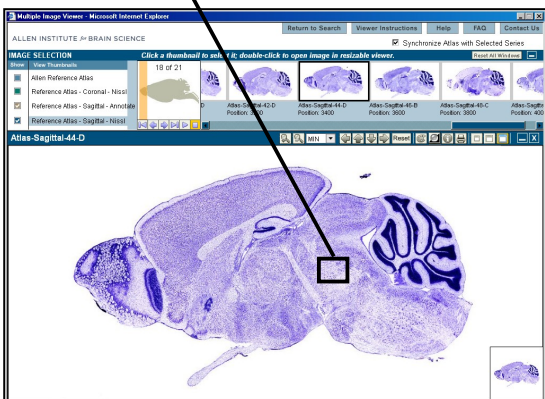
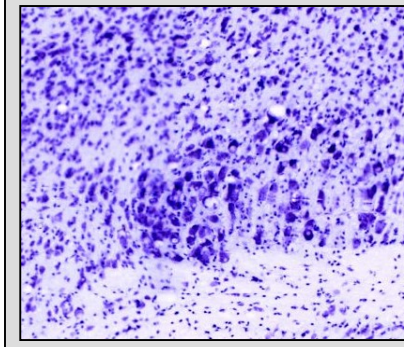
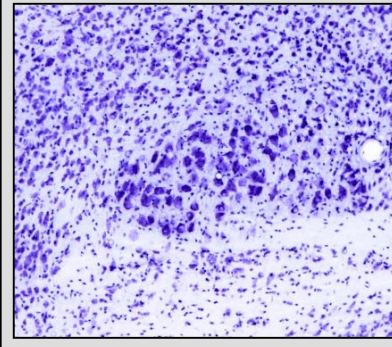
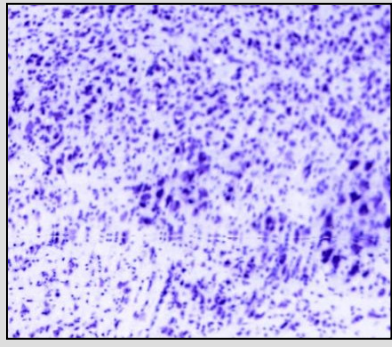
Level 18



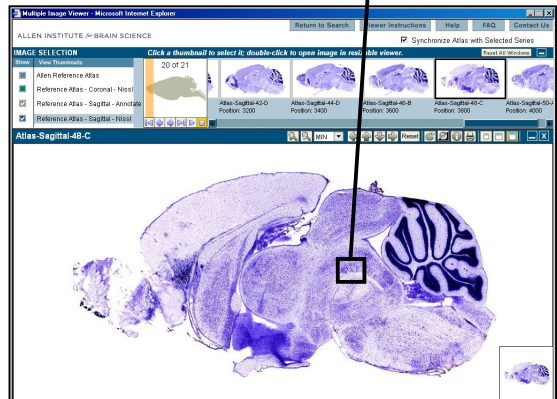
Level 19



Level 20



Nissl



In Situ Hybridization Expression Patterns of 50 Select Genes:

The in situ hybridization (ISH) data below presents the oculomotor nucleus' anatomical and cytoarchitectural characteristics in the context of actual gene expression. In addition to presenting molecularly defined borders, ISH gene expression patterns also aid in phenotyping cell populations that otherwise can not be differentiated on purely morphological grounds.

The 50 genes in this section were selected based on a mathematical algorithm to identify gene expression patterns that allow selective identification of the oculomotor nucleus. The gene expression patterns were then verified manually. As such, these genes do not represent the only genes found in this structure, genes specific to this structure, or genes expressing at the highest level within this structure.

Please refer to our protocol in the [Data Production Processes white paper](#).

To read about heat map conversion, refer to the [Informatics Data Processing white paper](#).

The expression data subsequently presented can be further explored, in coronal and sagittal planes, at brain-map.org.

Expression within the oculomotor nucleus is easily discernible due to the large size of the motor neurons as well as the high contrast between the nucleus and the medial longitudinal fascicle (mif). Motor neurons often express uniformly within the nucleus with a relatively high density.

Neither expression gradients across the nucleus nor distinct regional expression patterns within the nucleus are observed for this gene set. Widespread expression is the prevailing pattern.

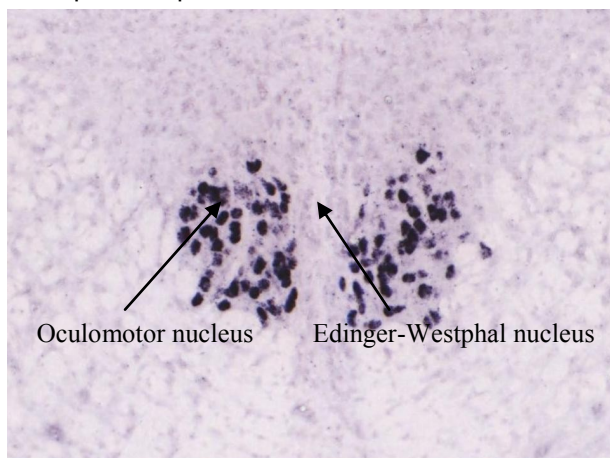
Cellular density expression key		Cellular intensity expression key	
None	No expression	No color	Very low intensity
Sparse	Very few cells expressing	Blue	Low intensity
Scattered	Less than 10% of cells expressing in scattered pattern	Green	Medium intensity
Medium	10-80% of cells expressing	Yellow	High intensity
High	Greater than 80% of cells expressing	Red	Very high intensity

To view heat map at brain-map.org, right click on the ISH image and select "Show Expression Analysis."

ISH DATA The images below were selected to highlight various expression patterns of the oculomotor nucleus.

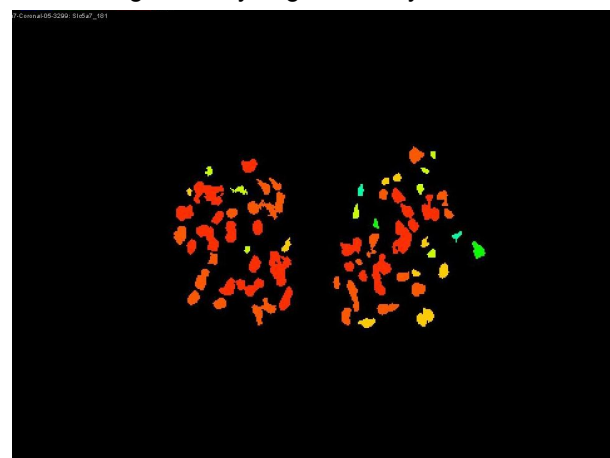
ISH [Slc5a7](#)

Coronal:
Widespread expression within the nucleus



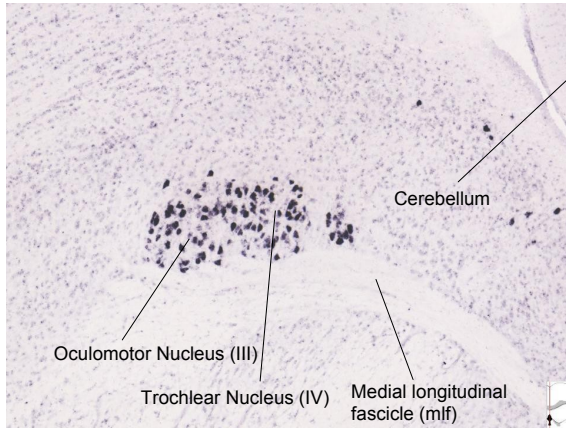
Heat map [Slc5a7](#)

Coronal:
Medium-high density, high intensity



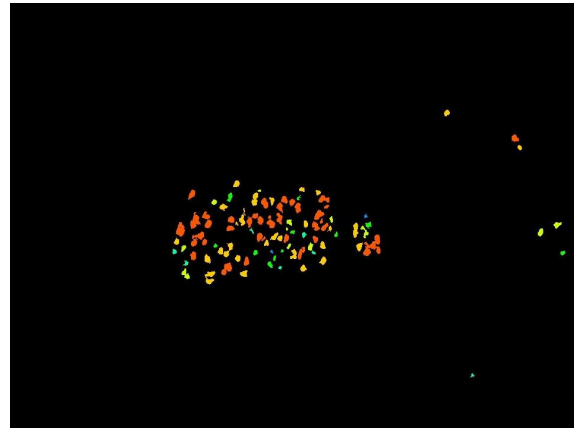
ISH
[Slc5a7](#)

Sagittal:



Heat map
[Slc5a7](#)

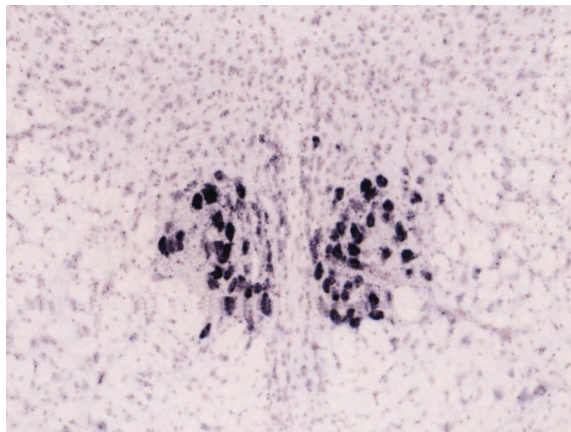
Sagittal:



ISH
[Lgals1](#)

Coronal:

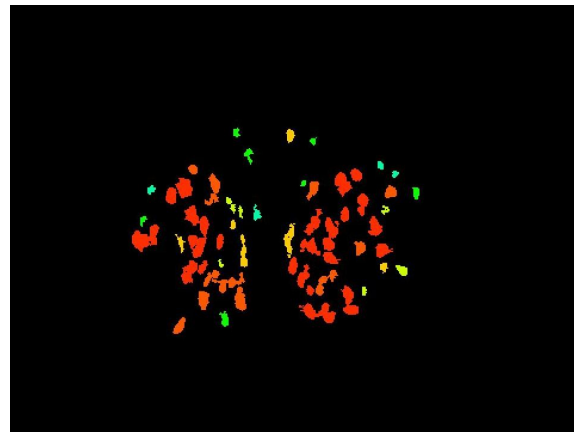
Another widespread expression pattern showing boundaries of the nucleus



Heat map
[Lgals1](#)

Coronal:

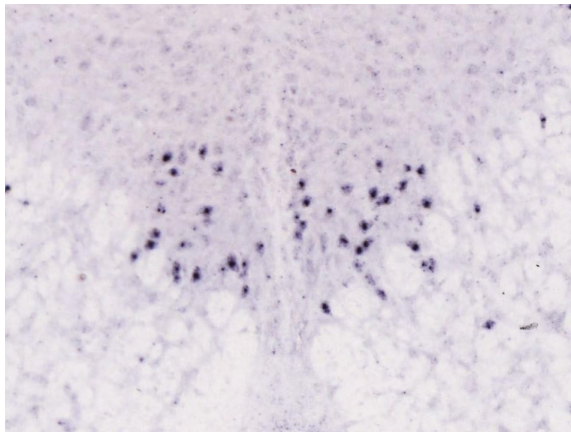
Medium-high density, high intensity



ISH
[Grid2ip](#)

Coronal:

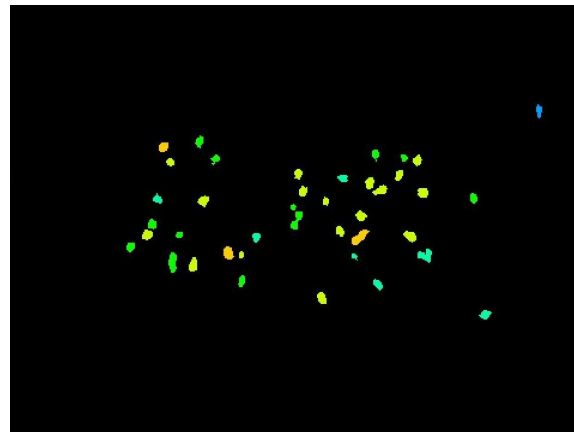
Medium intensity, medium density



Heat map
[Grid2ip](#)

Coronal:

Medium intensity, medium density



50 SELECT GENES:

This gene list was generated by manual curation of an [algorithmically](#) derived list that compared gene expression values of the oculomotor nucleus to those of the midbrain. Categories of expression are subjectively grouped by relative expression characteristics.

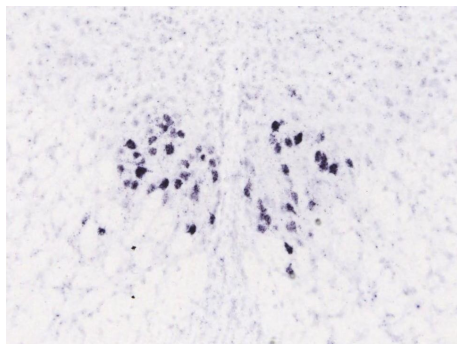
Curation of 50 Select Genes List: June 2008

General Expression Pattern

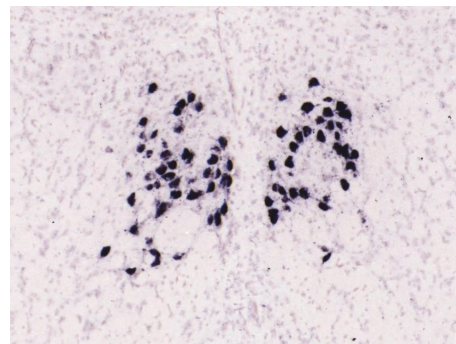
Number	Gene Symbol	Gene Name	Expression Pattern
1	Kcnj14	potassium inwardly-rectifying channel, subfamily J, member 14	medium density, medium-high intensity
2	Slc18a3	solute carrier family 18 (vesicular monoamine), member 3	medium density, medium-high intensity
3	Pacrg	Park2 co-regulated	medium density, medium intensity
4	A330102H22Rik	RIKEN cDNA A330102H22 gene	medium density, medium intensity
5	Lgals1	lectin, galactose binding, soluble 1	medium density, high intensity
6	Calcb	calcitonin-related polypeptide, beta	medium density, medium-high intensity
7	Pkp2	plakophilin 2	medium density, low intensity
8	Cd59a	CD59a antigen	medium density, medium intensity
9	Itpr3	inositol 1,4,5-triphosphate receptor 3	medium density, medium-low intensity
10	Sema3d	sema domain, imedium density, medium intensityunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D	medium density, medium-low intensity
11	Tspan12	tetraspanin 12	medium density, medium intensity
12	Prss12	protease, serine, 12 neurotrypsin (motopsin)	medium density, high intensity
13	Gem	GTP binding protein (gene overexpressed)	high density, medium intensity
14	1700010C24Rik	RIKEN cDNA 1700010C24 gene	medium density, medium intensity
15	AI450948	expressed sequence AI450948	medium density, medium-high intensity
16	Smug1	single-strand selective monofunctional	medium density, medium-low intensity
17	A330043P19Rik*	RIKEN cDNA A330043P19 gene (non-RefSeq)	medium density, medium-high intensity
18	Eya1	eyes absent 1 homolog (Drosophila)	medium density, medium-high intensity
19	Anxa2	annexin A2	medium density, medium intensity
20	Lrrc38	leucine rich repeat containing 38	medium density, medium intensity
21	Trim16	tripartite motif protein 16	medium density, medium intensity
22	Calca	calcitonin/calcitonin-related polypeptide,	medium density, medium intensity
23	Slc5a7	solute carrier family 5 (choline transporter),	high density, high intensity
24	Cabp7	calcium binding protein 7	high density, high intensity
25	Anxa4	annexin A4	medium density, medium intensity
26	Htr3a	5-hydroxytryptamine (serotonin) receptor 3A	medium density, low intensity
27	Pde6g	phosphodiesterase 6G, cGMP-specific, rod, gamedium density, medium intensity	medium density, medium-low intensity
28	Fstl4	follistatin-like 4	medium density, medium intensity
29	Dffa	DNA fragmentation factor, alpha subunit	medium density, high intensity
30	Adam19	a disintegrin and metallopeptidase domain	medium density, medium intensity
31	Dmp1	dentin matrix protein 1	medium density, medium intensity
32	Grb14	growth factor receptor bound protein 14	medium density, medium intensity
33	Pcbp3	poly(rC) binding protein 3	medium density, medium intensity
34	Tsc22d3	TSC22 domain family 3	medium density, medium intensity
35	Ddef1	development and differentiation enhancing	medium density, medium intensity
36	Isoc1	isochorismatase domain containing 1	medium density, high intensity
37	Ern2	endoplasmic reticulum (ER) to nucleus sig-	medium density, medium-high intensity
38	Cast	calpastatin	medium density, medium intensity

39	Ephx2	epoxide hydrolase 2, cytoplasmic	medium density, medium intensity
40	Manba	mannosidase, beta A, lysosomal	medium density, medium-low intensity
41	Grid2ip	glutamate receptor, ionotropic, delta 2 (Grid2) interacting protein 1	medium density, medium-high intensity
42	Arl4d	ADP-ribosylation factor-like 4D	medium density, medium intensity
43	D130073L02Rik	RIKEN cDNA D130073L02 gene	medium density, medium intensity
44	Lypla1	lysophospholipase 1	medium density, medium-high intensity
45	TC1460681	TIGR MGI TC1460681	medium density, medium-high intensity
46	Acyp2	acylphosphatase 2, muscle type	medium density, medium-high intensity
47	Nrg1	neuregulin 1	high density, high intensity
48	Dexi	dexamethasone-induced transcript	medium density, medium-high intensity
49	Txnrd1	thioredoxin reductase 1	medium density, medium intensity
50	P2rx11	purinergic receptor P2X-like 1, orphan receptor	medium density, medium-high intensity

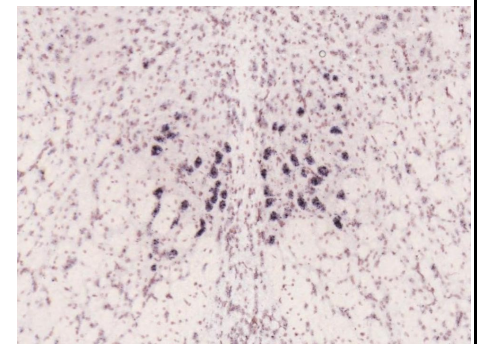
[1.Kcnj14](#)



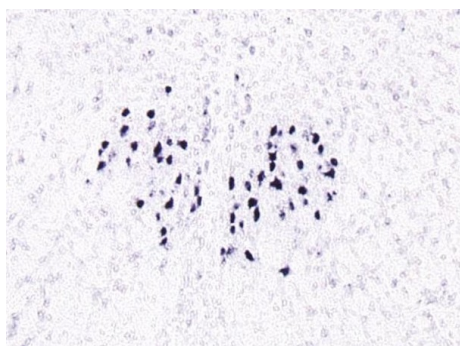
[2.Slc18a3](#)



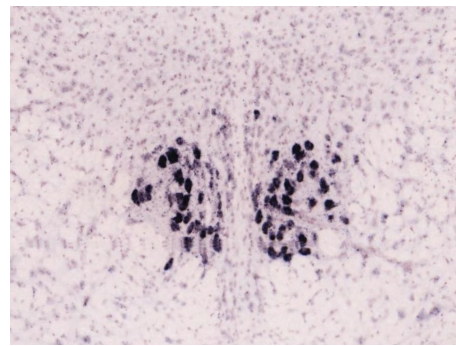
[3.Pacrg](#)



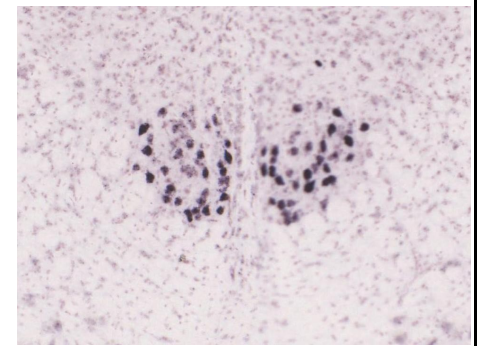
[4.A330102H22Rik](#)



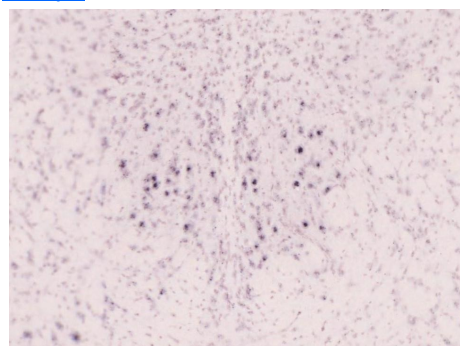
[5.Lgals1](#)



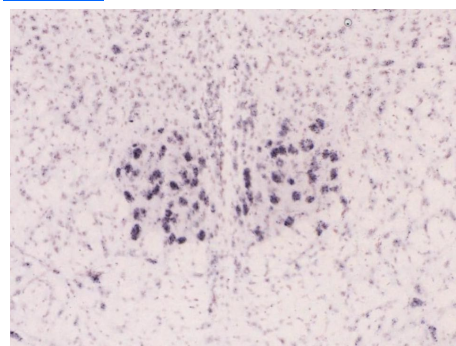
[6.Calcb](#)



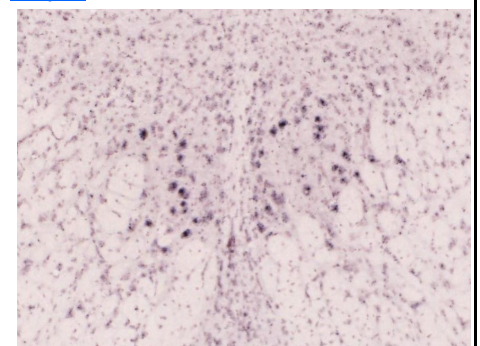
[7.Pkp2](#)

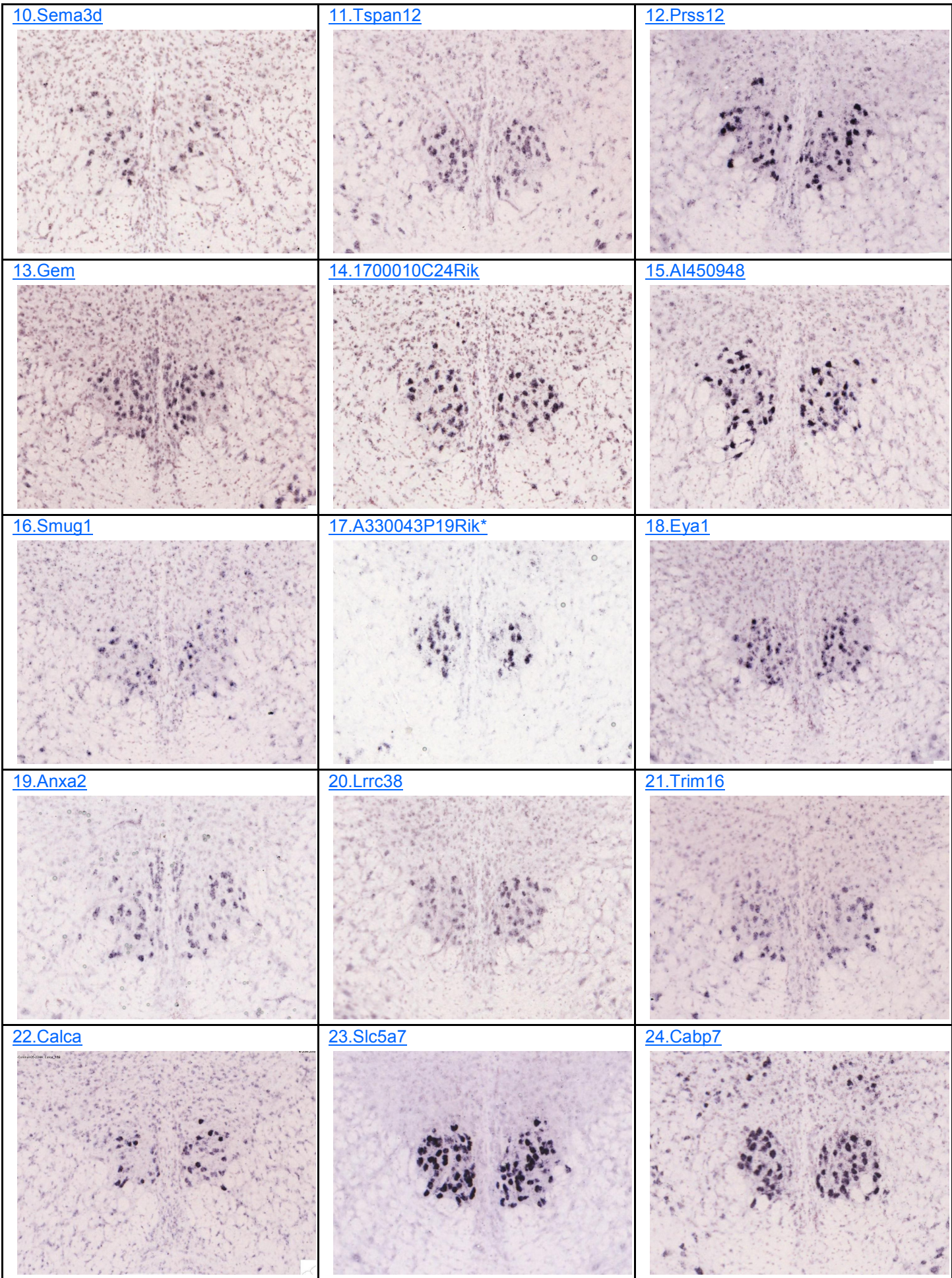


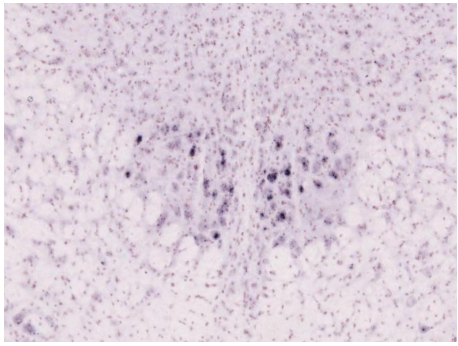
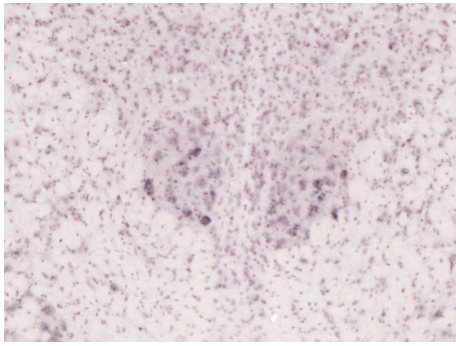
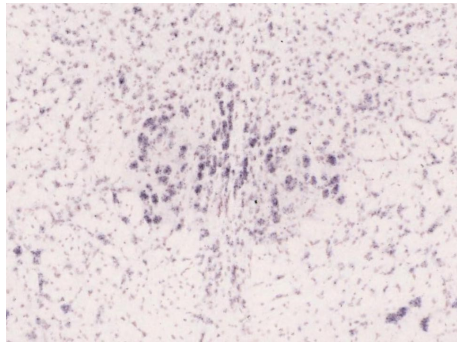
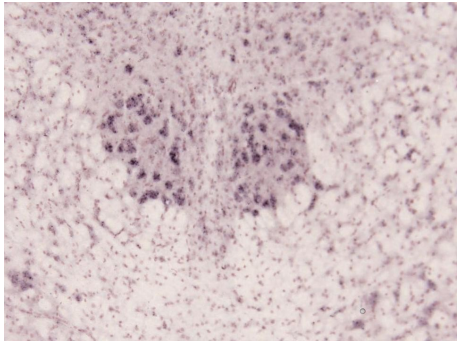
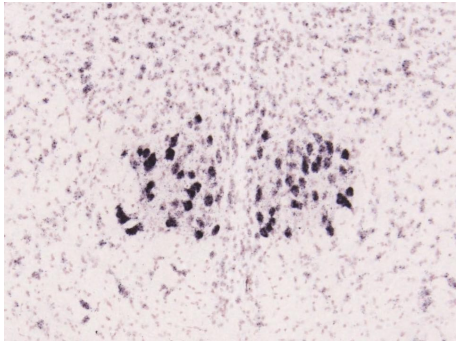
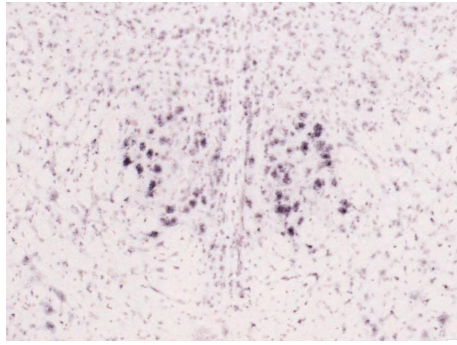
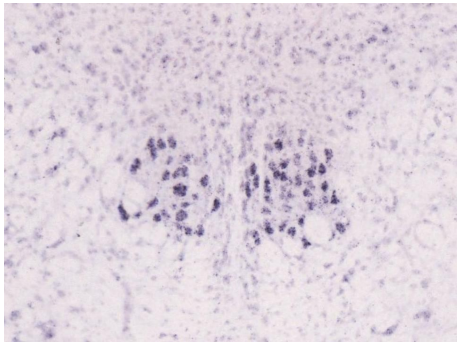
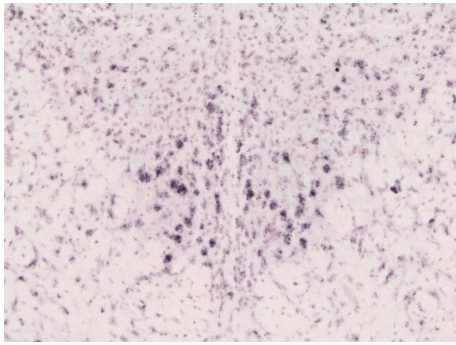
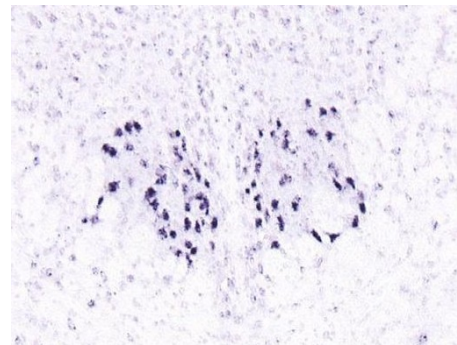
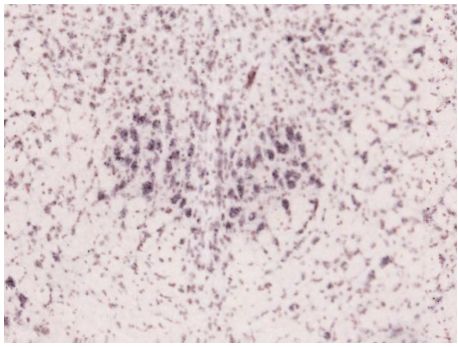
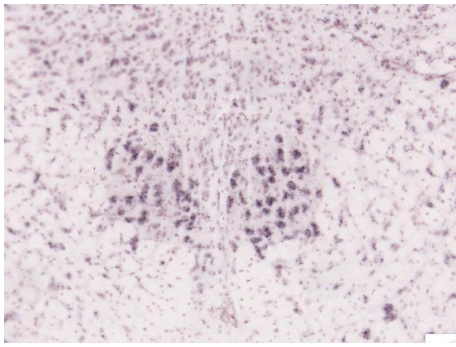
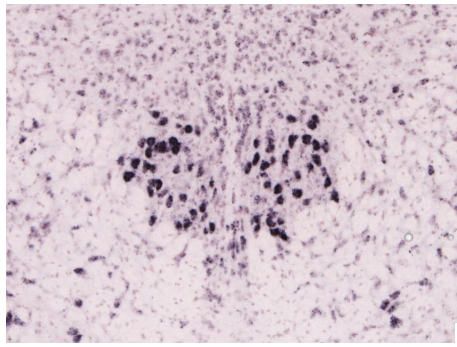
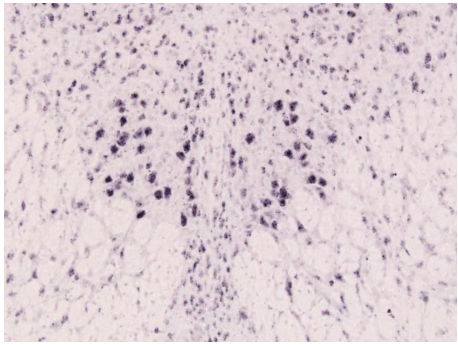
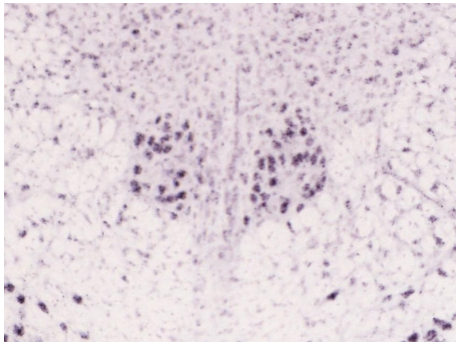
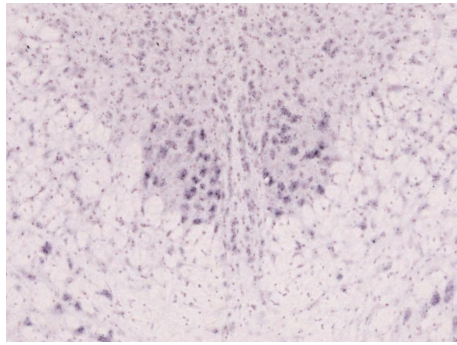
[8.Cd59a](#)



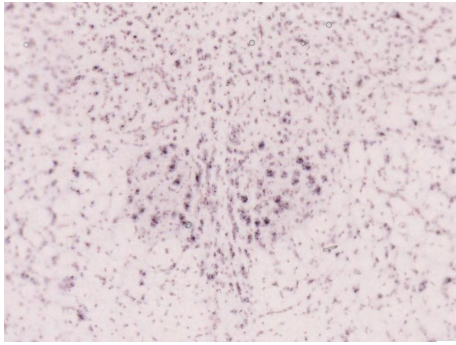
[9.Itpr3](#)



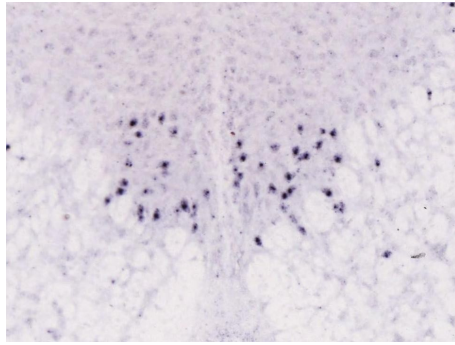


25.Anxa4 	26.Htr3a 	27.Pde6g 
28.Fstl4 	29.Dffa 	30.Adam19 
31.Dmp1 	32.Grb14 	33.Pcbp3 
34.Tsc22d3 	35.Ddef1 	36.Isoc1 
37.Ern2 	38.Cast 	39.Ephx2 

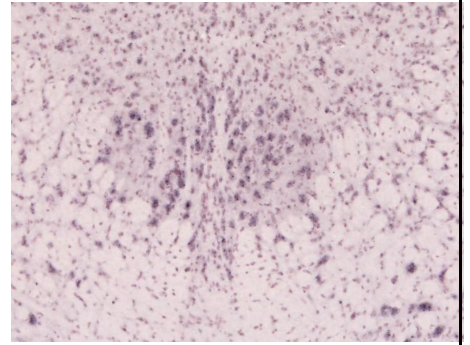
[40.Manba](#)



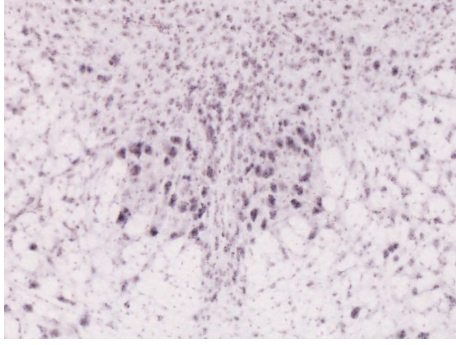
[41.Grid2ip](#)



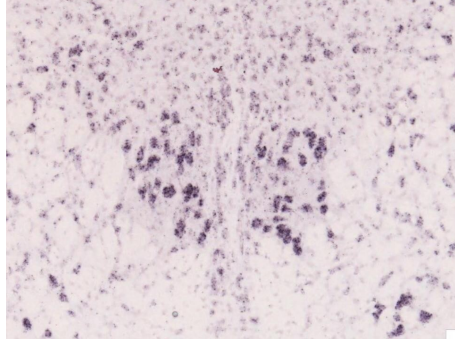
[42.Arff4l](#)



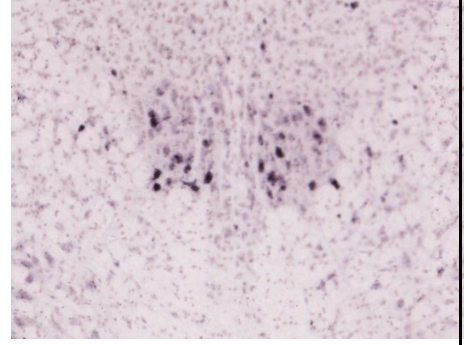
[43.D130073L02Rik](#)



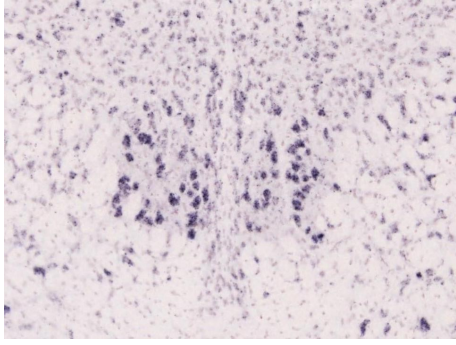
[44.Lypla1](#)



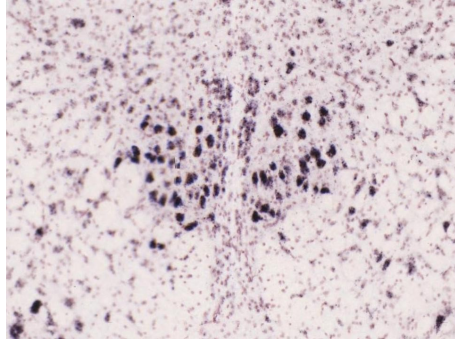
[45.TC1460681](#)



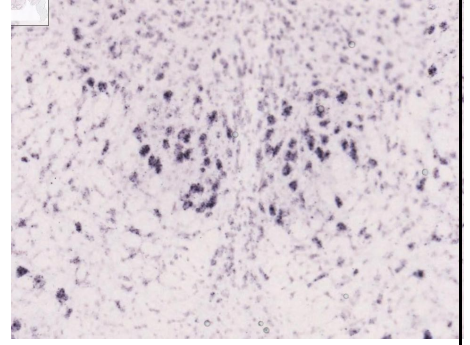
[46.Acyp2](#)



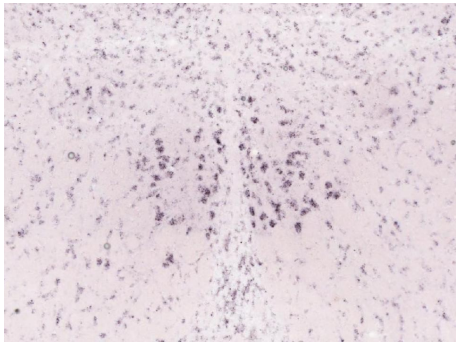
[47.Nrg1](#)



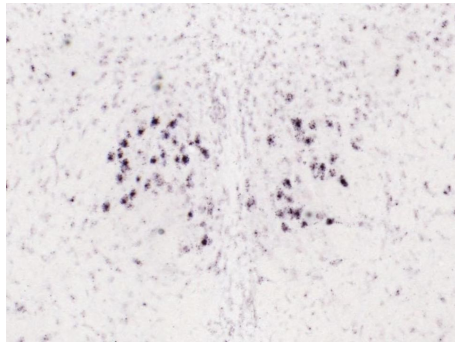
[48.Dexi](#)



[49.Txnrd1](#)



[50.P2rx1l](#)



Correlated Expression:

The ABA coronal set contains many genes of known scientific interest as well as genes exhibiting combinatorial or unique expression patterns. A correlation analysis of all available ABA coronal experiments (4376) was performed by comparing the expression value of the oculomotor nucleus to expression values in other regions of the brain. Following [image analysis](#), the data values for each experiment were mapped to a 3-D reference brain at $(200\mu\text{m})^3$ voxel resolution. Then, each voxel was assigned a single expression value based on the product of density and intensity of expression. Values from all 4376 experiments were computed, and the likelihood of co-expression between any two voxels or regions are reported as a Pearson's correlation coefficient.

For the purposes of determining correlated expression between the oculomotor nucleus and other brain regions, expression values from all voxels within the nucleus were aggregated to form a single expression value. Two types of comparisons were then made. First, the aggregate expression values of the nucleus and those of other anatomically defined regions (~200 structures) were compared within the 3-D reference brain (structure vs. structure; table below). Second, a color map was then generated to display the correlation between the oculomotor nucleus and each of the ~53,000 voxels of the reference volume (structure vs. voxel; correlation map on the following page).

STRUCTURE vs. STRUCTURE

The expression value of the oculomotor nucleus was compared to expression values for all other defined atlas regions. Degree of correlation is displayed as a comparative fraction, with self-correlation = 1.000. Correlation between the nucleus and macro/parent-structures are presented, as well as correlation between the oculomotor nucleus and the 25 highest ranking substructures. The most highly correlated macro/parent-structures don't always contain the 25 top most correlated substructures. Columns match the Allen Reference Atlas palette.

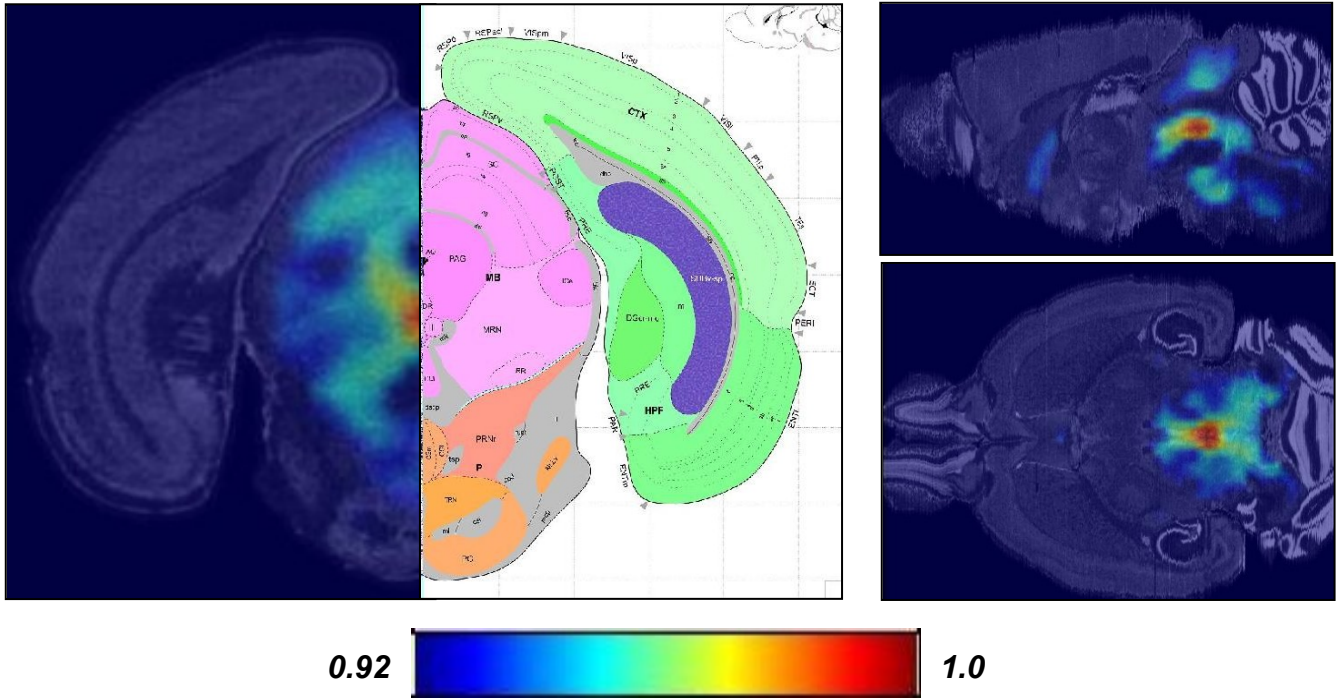
Correlation of oculomotor nucleus with macro structures:

Macro Structure	Correlation
OLF (Olfactory areas)	0.804748
STR (Striatum)	0.746395
PAL (Pallidum)	0.893593
CTX (Cerebral cortex)	0.804628
HY (Hypothalamus)	0.890531
TH (Thalamus)	0.859554
HIP (Hippocampal region)	0.78077
RHP (Retrohippocampal formation)	0.822014
MB (Midbrain)	0.930337
P (Pons)	0.92756
MY (Medulla)	0.922566
CB (Cerebellum)	0.689892

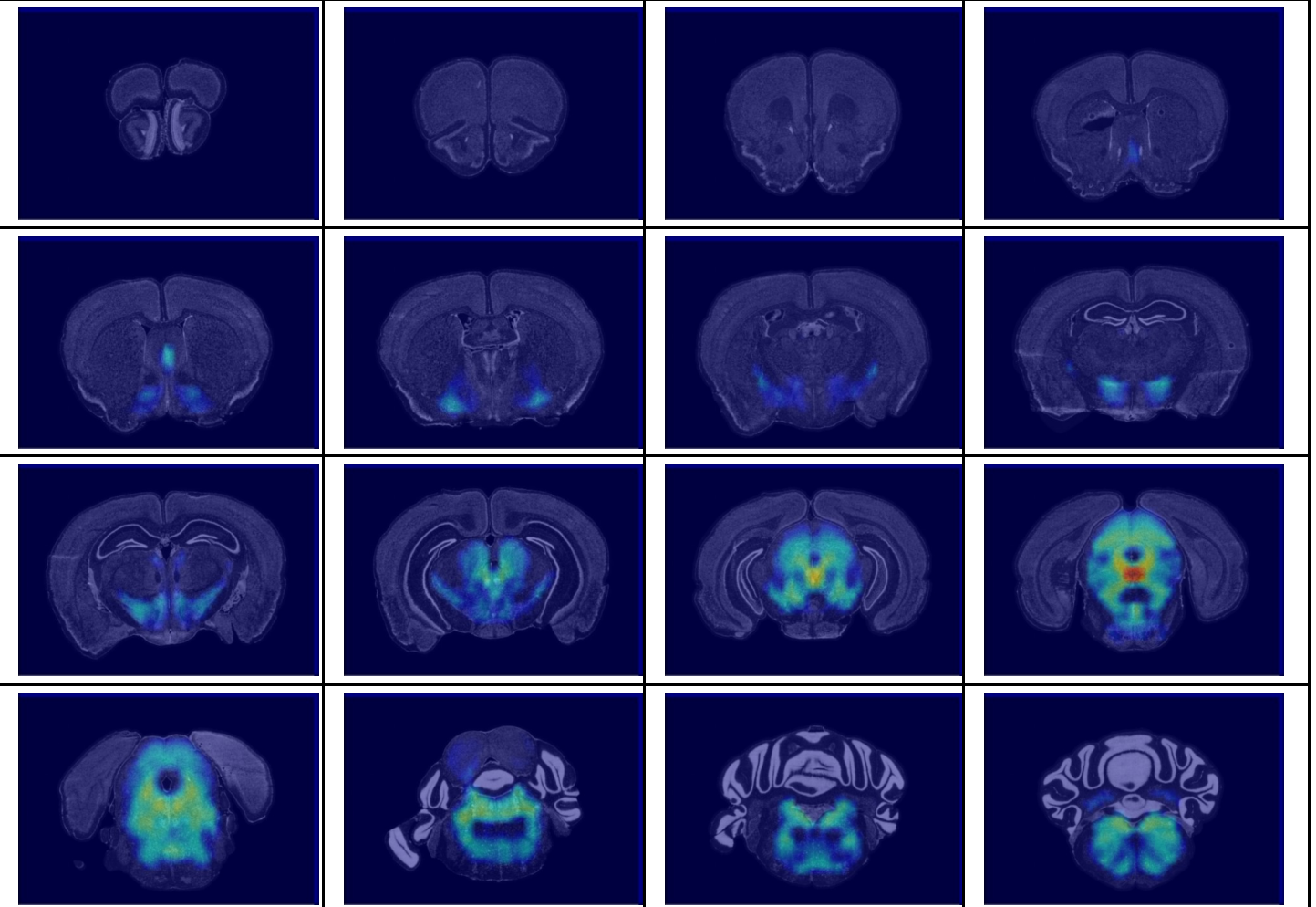
Substructure	Correlation
Oculomotor nucleus (III)	1
Edinger-Westphal nucleus (EW)	0.966793
Nucleus of Darkschewitsch (ND)	0.948229
Trochlear nucleus (IV)	0.946526
Anterior tegmental nucleus (AT)	0.937446
Dorsal nucleus raphé (DR)	0.935489
Sublaterodorsal nucleus (SLD)	0.934469
Supratrigeminal nucleus (SUT)	0.934114
Medial vestibular nucleus (MV)	0.933078
Midbrain reticular nucleus (MRN)	0.932033
Midbrain trigeminal nucleus (MEV)	0.93126
Vestibular nuclei (VNC)	0.929652
Periaqueductal gray (PAG)	0.929383
Red Nucleus (RN)	0.928749
Hypoglossal nucleus (XII)	0.927132
Midbrain reticular nucleus, retrorubral area (RR)	0.924254
Pontine central gray (PCG)	0.923842
Nucleus of the solitary tract (NTS)	0.923811
Pedunculopontine nucleus (PPN)	0.923639
Midbrain raphé nuclei (Ramb)	0.92356
Nucleus ambiguus (AMB)	0.923248
Interstitial nucleus of Cajal (INC)	0.922905
Cuneiform nucleus (CUN)	0.922903
Tegmental reticular nucleus (TRN)	0.921145
Superior central nucleus raphé (CS)	0.920389

STRUCTURE vs. VOXEL:

Correlation between the oculomotor nucleus and all other $(200\mu\text{m})^3$ voxels in the brain. Degree of correlation assessed for each voxel is provided visually (lower value = the correlation value of the 25th ranked substructure reported on the previous page) using the "jet" color scale at rostrocaudal levels throughout the brain.



Coronal series through brain:



Gene Ontology (GO) Analysis:

GO TABLE:

Below is an ontological analysis of the 50 Select Genes, using [DAVID](#) Bioinformatics Resources. The functional terms that follow were returned using these constraints:

Category	Definition	Constraints
P-value	Probability that the term is over-represented in this 50 Select Genes list relative to the mouse genome	when $p \leq 0.05$
Gene Count	The minimum number of genes that must fall into an ontological category to be considered a group	5 genes per term group
GO Level	The level of functional specificity for GO functional categories: Molecular Function (mf), Biological Process (bp) and Cellular Components (cc)	Level GO_All
# of DAVID IDs	Number of unique DAVID gene IDs from user's input list	44 DAVID gene IDs / 50 input genes

Date of table completion: April 2008

GO Category	GO Term	Gene Count	% of Genes	p-value
GOTERM_BP_ALL	organ development	8	16.67%	0.004254803
GOTERM_MF_ALL	hydrolase activity	12	25.00%	0.006099631
GOTERM_MF_ALL	ion binding	15	31.25%	0.007166104
GOTERM_MF_ALL	metal ion binding	15	31.25%	0.007166104
GOTERM_BP_ALL	negative regulation of physiological process	6	12.50%	0.010666325
GOTERM_BP_ALL	intracellular signaling cascade	7	14.58%	0.016307342
GOTERM_BP_ALL	organ morphogenesis	5	10.42%	0.023218331
GOTERM_BP_ALL	negative regulation of biological process	6	12.50%	0.023436045
GOTERM_MF_ALL	binding	32	66.67%	0.023916074
GOTERM_CC_ALL	extracellular space	11	22.92%	0.027951375
GOTERM_MF_ALL	calcium ion binding	6	12.50%	0.033320027
GOTERM_MF_ALL	transporter activity	8	16.67%	0.048197384

Glynn Dennis Jr., Brad T. Sherman, Douglas A. Hosack, Jun Yang, Michael W. Baseler, H. Clifford Lane, Richard A. Lempicki. "DAVID: Database for Annotation, Visualization, and Integrated Discovery." *Genome Biology*. 2003 4(5): P3.

OCULOMOTOR NUCLEUS Summary:

Anatomy

- From rostral to caudal, the oculomotor nucleus (III) appears medially at the level of the red nucleus, persists as the dorsal nucleus raphé (DR) emerges, and gives way to the trochlear nucleus (IV). The close positional relationship between the trochlear and oculomotor nucleus is especially evident in the sagittal plane.
- The distinguishing cells of the oculomotor are the large motor neurons distributed evenly throughout the nucleus. Despite the small size of the nucleus, these cells make it relatively easy to discern from surrounding structures.

Expression Patterns of the 50 Select Genes

- The most common expression seen in the oculomotor nucleus is widespread expression throughout the entire nucleus.
- Occasionally expression is seen at a lower density (i.e. scattered population of cells); however, no gradients or subdivisions within the nucleus are revealed by this gene set.

Correlation

- Gene expression patterns in the oculomotor nucleus correlated most strongly with expression patterns in other nuclei of the midbrain, pons, and medulla.
- Additionally, structure to voxel correlation analysis reveals correlation with portions of the forebrain, including the medial septum, substantia inominata, zona incerta, and the bed nucleus of the stria terminalis, as well as with portions of the hypothalamus, thalamus, and the subthalamic nucleus.

We encourage you to reply with any comments or questions by email to [!Annotation@alleninstitute.org](mailto:Annotation@alleninstitute.org). To further explore the gene expression data and analytical tools referred to in this report, please access our genome-wide data set at brain-map.org.

Other Tools:

NEUROBLAST:

Many of the 50 genes listed in this report can be used to explore the NeuroBlast tool. This unique mining tool works seamlessly from within brain-map.org to produce a list of genes that share similar expression patterns to any gene in the coronal data set. Search for and select any gene, then select one of several brain regions from the NeuroBlast drop-tab to explore a ranked list of similarly expressed genes for that region.

To learn more about this function, please refer to the [NeuroBlast white paper](#).

BRAIN EXPLORER:

To compare gene expression levels across anatomical structures in 3-D detail, download the [Brain Explorer](#) desktop application. This program is used to view gene expression in 3-D view (coronal, sagittal, horizontal and everywhere in between) across all brain structures and allows for simultaneous viewing of multiple expression profiles.

The NeuroBlast spatial homology function and an anatomic search tool are also available from within Brain Explorer to allow the user to search for and visualize genes with similar expression patterns.