



EDINGER-WESTPHAL NUCLEUS (EW)

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ALLEN
BRAIN ATLAS
MOUSE BRAIN

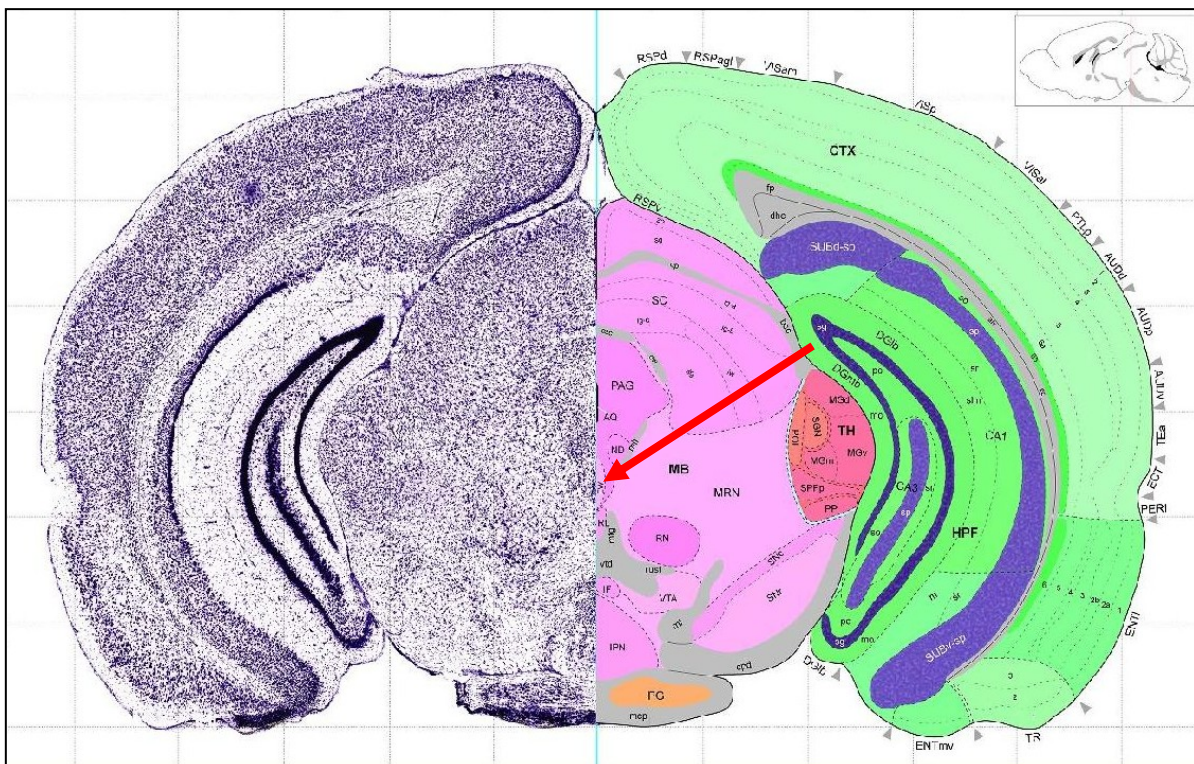
Introduction

This report contains a summary of expression patterns for genes that are enriched in the Edinger-Westphal nucleus (EW) of the midbrain. All data are derived from the [Allen Brain Atlas](#) (ABA) in situ hybridization mouse project. 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 Edinger-Westphal nucleus were compared to the values of its larger parent structure, in this case the midbrain, for the purpose of extracting regionally selective gene expression data. The highest ranking genes were manually curated and verified. 50 genes were then selected and compiled for expression analysis. 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 Edinger-Westphal 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.

Allen Reference Atlas Coronal Levels: 83-92

Allen Reference Atlas Sagittal Levels: 20-21

Shown below is a plate from the Allen Reference Atlas, depicting the EW (level [88](#)):



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 Edinger-Westphal nucleus (EW) is located at the ventro-medial border of the periaqueductal gray matter (PAG) of the midbrain. It is the accessory parasympathetic nucleus of the oculomotor nerve, and consists of mid-sized, preganglionic neurons that are darkly stained and visible in both the coronal and sagittal Nissl sections.

In the coronal plane, its long, thin appearance and its proximity to the midline make it easy to locate. At its rostral edge, the cells of the EW are separated from the large neurons of the nucleus of Darkschewitsch, which lies dorsal and lateral to the EW, by a thin portion of the PAG. The medial longitudinal fascicle (mlf) and the mammillotegmental tract also serve to separate the EW from the surrounding neurons of the midbrain reticular nucleus (MRN), which are large but scattered. More caudally, the oculomotor nucleus (III) lies lateral to, and abuts, the EW; both lie medial to the mlf. These two nuclei can easily be differentiated from one another by the larger neurons found in III, and the more columnar arrangement of neurons in the EW.

In the sagittal plane, the EW is somewhat more difficult to distinguish from surrounding structures than in the coronal plane. At the midline of the brain, it appears as a circular structure along the floor of the periaqueductal gray, located between the thalamus and the oculomotor nucleus. At its lateral aspect, it sits adjacent to the mlf, while at its medial aspect, it can be differentiated from the surrounding periaqueductal grey matter due to the striated appearance of the PAG. In this view, the oculomotor nucleus lies caudal to the EW, while the nucleus of Darkschewitsch lies dorsal and caudal.

The appearance and location of the Edinger-Westphal nucleus can be appreciated on the following two pages. Nissl-stained sections and Allen Reference Atlas (ARA) plates reveal the cytoarchitecture and extent of the Edinger-Westphal 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 [SNl]
 - 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]

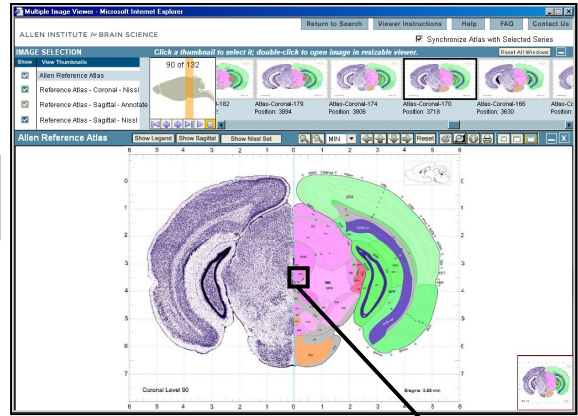
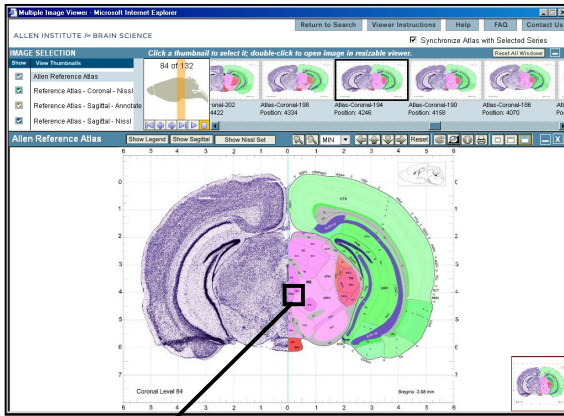
- fiber tracts
- Grooves
- ventricular systems

Atlas and Nissl:

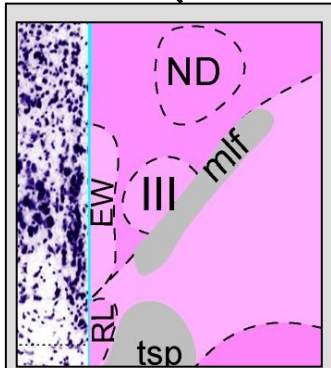
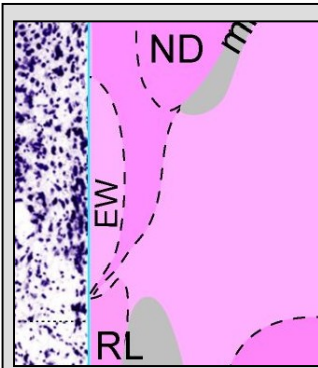
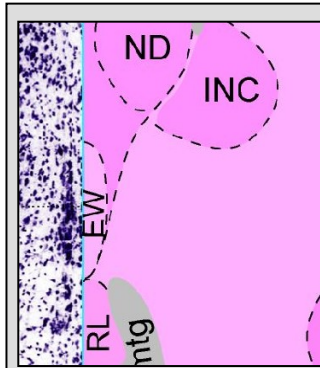
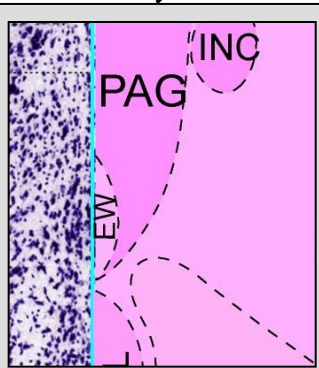
Coronal:

Rostral

Caudal



Reference Atlas

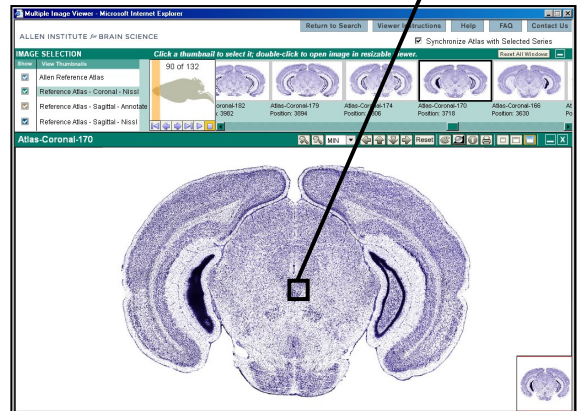
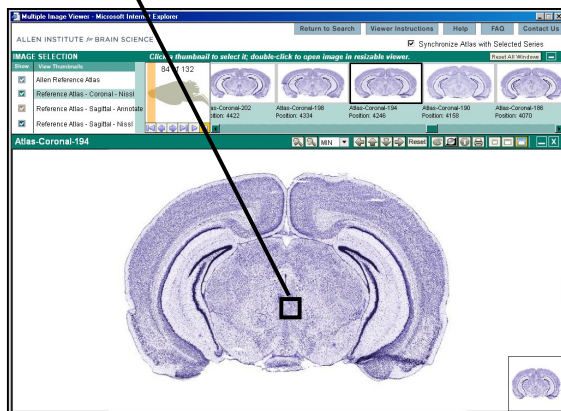
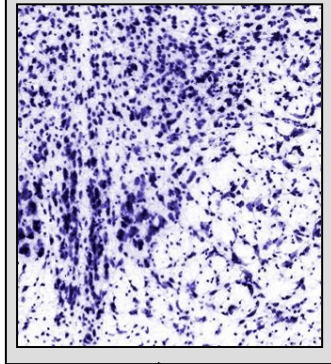
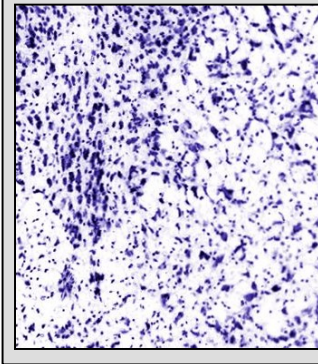
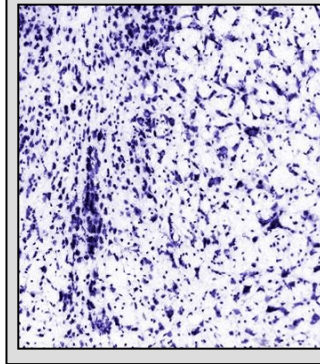
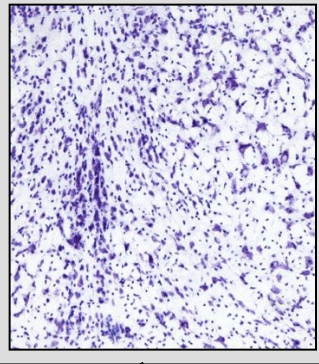


Level 84

Level 86

Level 88

Level 90

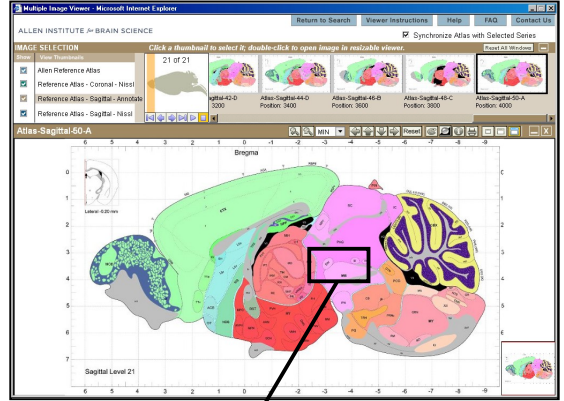
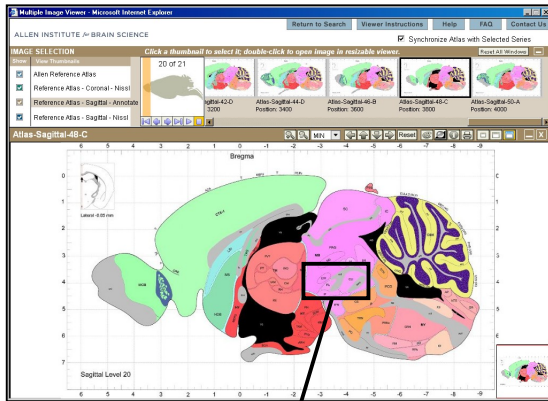


Nissl

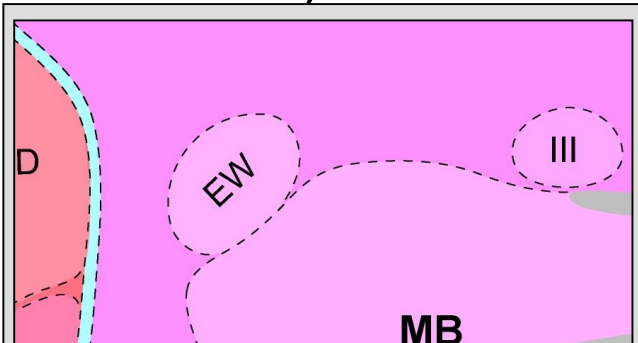
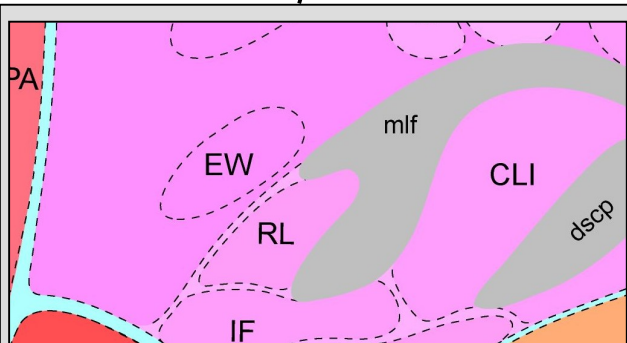
Atlas and Nissl: Sagittal:

Lateral

Medial

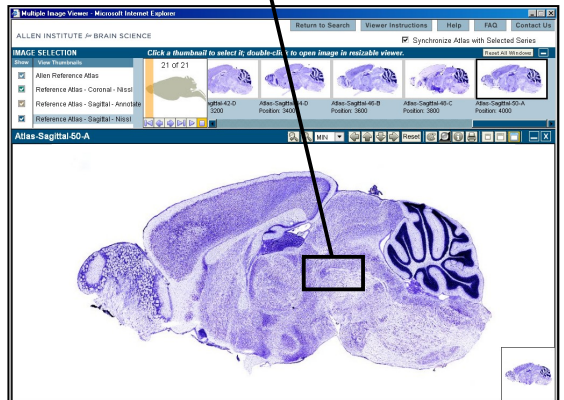
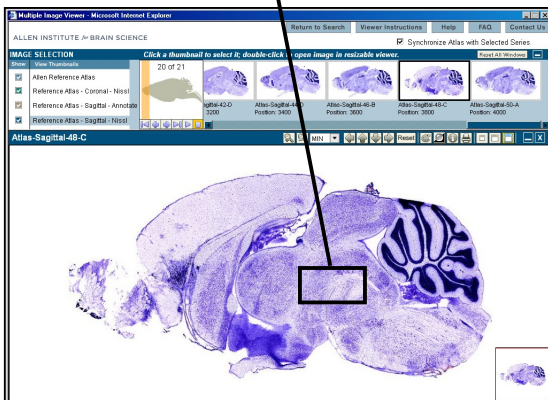
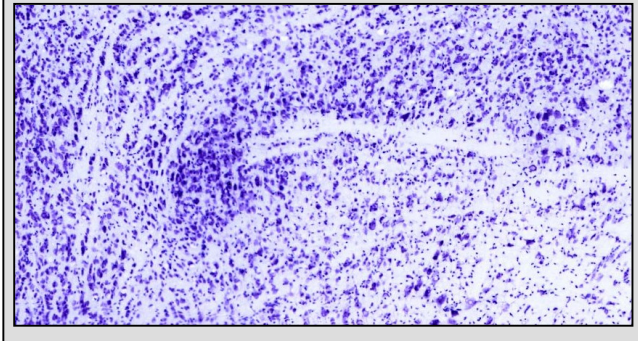
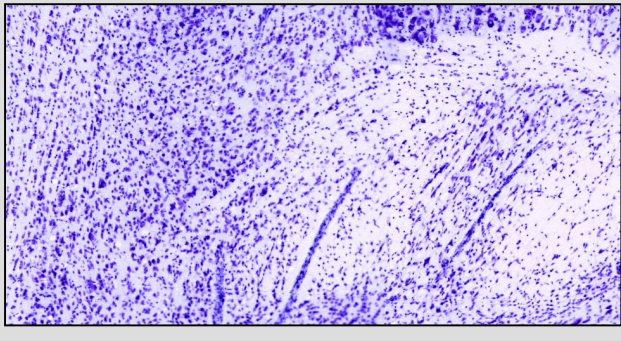


Reference
Atlas



Level 20

Level 21



Nissl

In Situ Hybridization Expression Patterns of 50 Select Genes:

The *in situ* hybridization (ISH) data below presents the Edinger-Westphal 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 Edinger-Westphal 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 presented can be further explored, in coronal and sagittal planes, at brain-map.org.

Identification of the Edinger-Westphal nucleus in ISH labeled coronal sections is straightforward due to the unique appearance of the nucleus itself. In the coronal plane, the cells appear densely packed in thin, nearly adjacent columns, two to three cells wide, on either side of the mid-line. In the sagittal plane, they form a cohesive structure seen only in the most medial sections.

The 50 selected genes presented in this report show a consistently uniform expression pattern, with expression in all or nearly all cells within the nucleus. Expression gradients are not observed, nor are distinct sub-divisions or subnuclei. However, some genes are also expressed in the surrounding PAG and midbrain reticular nucleus. The expression patterns suggest that the EW extends farther caudally than is portrayed in the ARA sagittal view.

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."

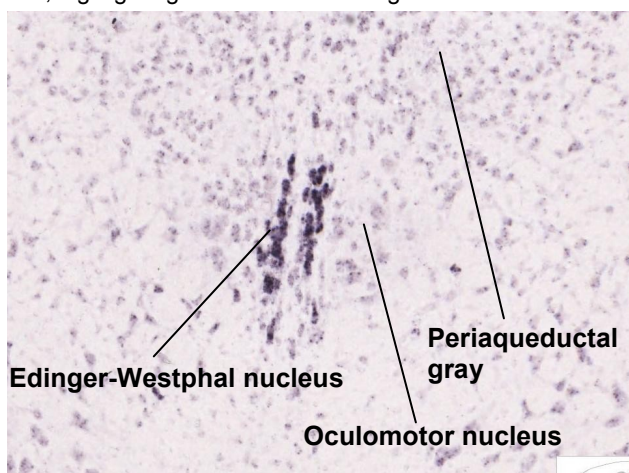
ISH DATA The images below were selected to highlight various expression patterns of the Edinger-Westphal nucleus.

ISH

[Nenf](#)

Coronal:

Nenf expression shows the characteristic expression pattern for the EW, highlighting the columnar arrangement of cells.

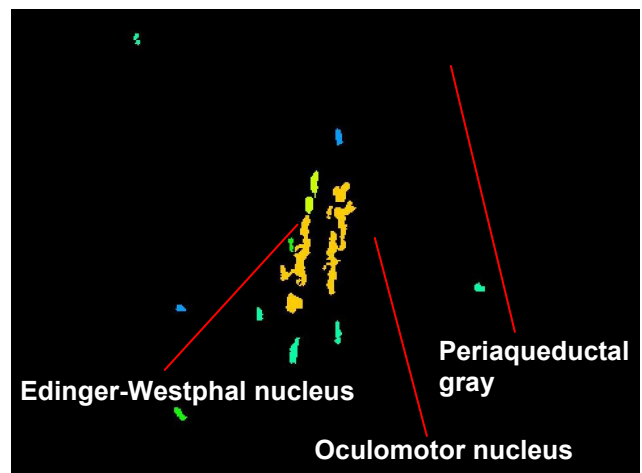


Heat map

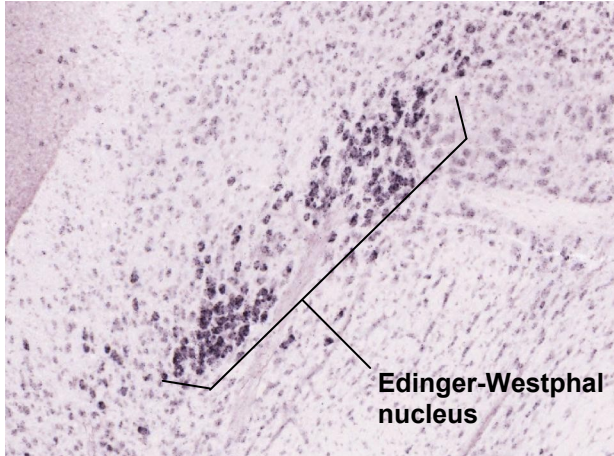
[Nenf](#)

Coronal:

The heat map image shows high density and high intensity expression of *Nenf*.

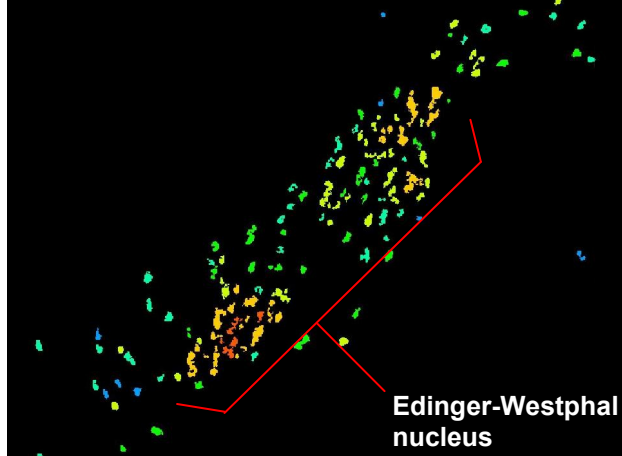


ISH
[Nenf](#)
Sagittal:
A sagittal view of *Nenf* suggests that the EW continues farther caudally than is portrayed in the sagittal views of the ARA.



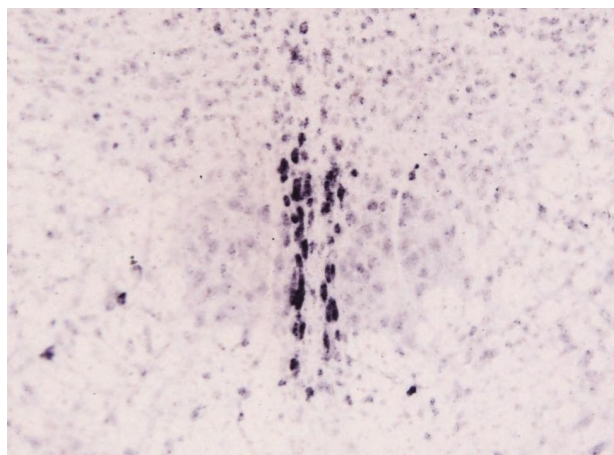
Edinger-Westphal nucleus

Heat map
[Nenf](#)
Sagittal:
Again, the high density and high intensity of *Nenf* expression is evident in the heat map image.



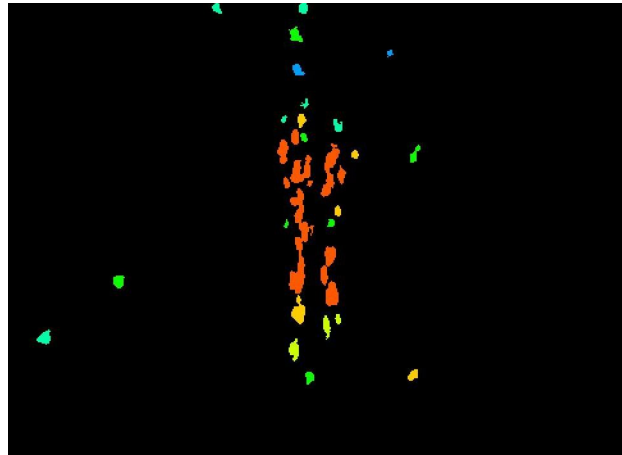
Edinger-Westphal nucleus

ISH
[Spint2](#)
Coronal:
Spint2 expression clearly differentiates EW from the neighboring oculomotor nucleus.



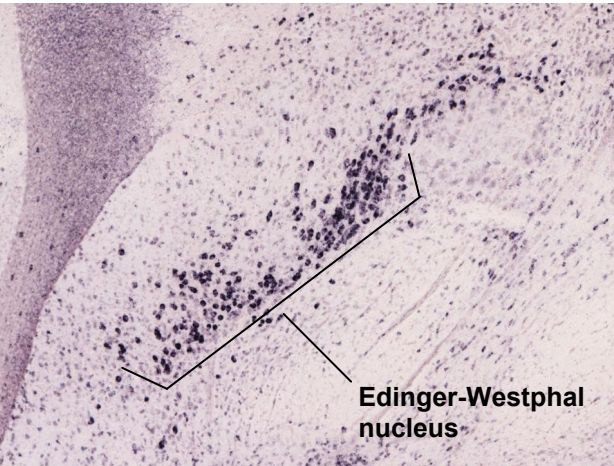
Edinger-Westphal nucleus

Heat map
[Spint2](#)
Coronal:
The columnar arrangement of the cells within the EW is clearly visualized in the heat map image.



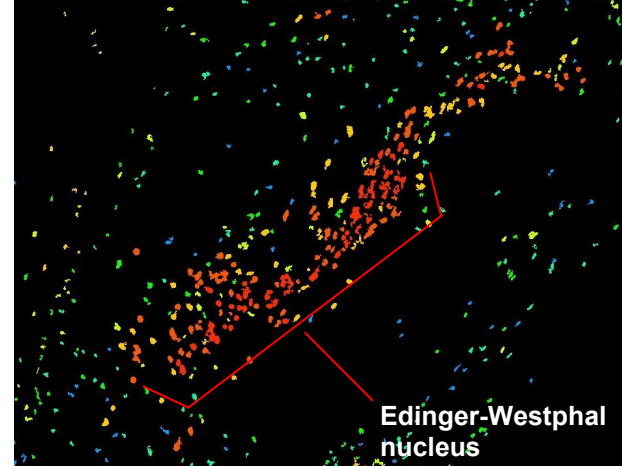
Edinger-Westphal nucleus

ISH
[Spint2](#)
Sagittal:
Spint2 expression also suggests that the EW extends farther caudally than is portrayed in the ARA.



Edinger-Westphal nucleus

Heat map
[Spint2](#)
Sagittal:
Although expressed in cells outside of the EW, the intensity of *Spint2* expression is greatest in the EW.



Edinger-Westphal nucleus

50 SELECT GENES:

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

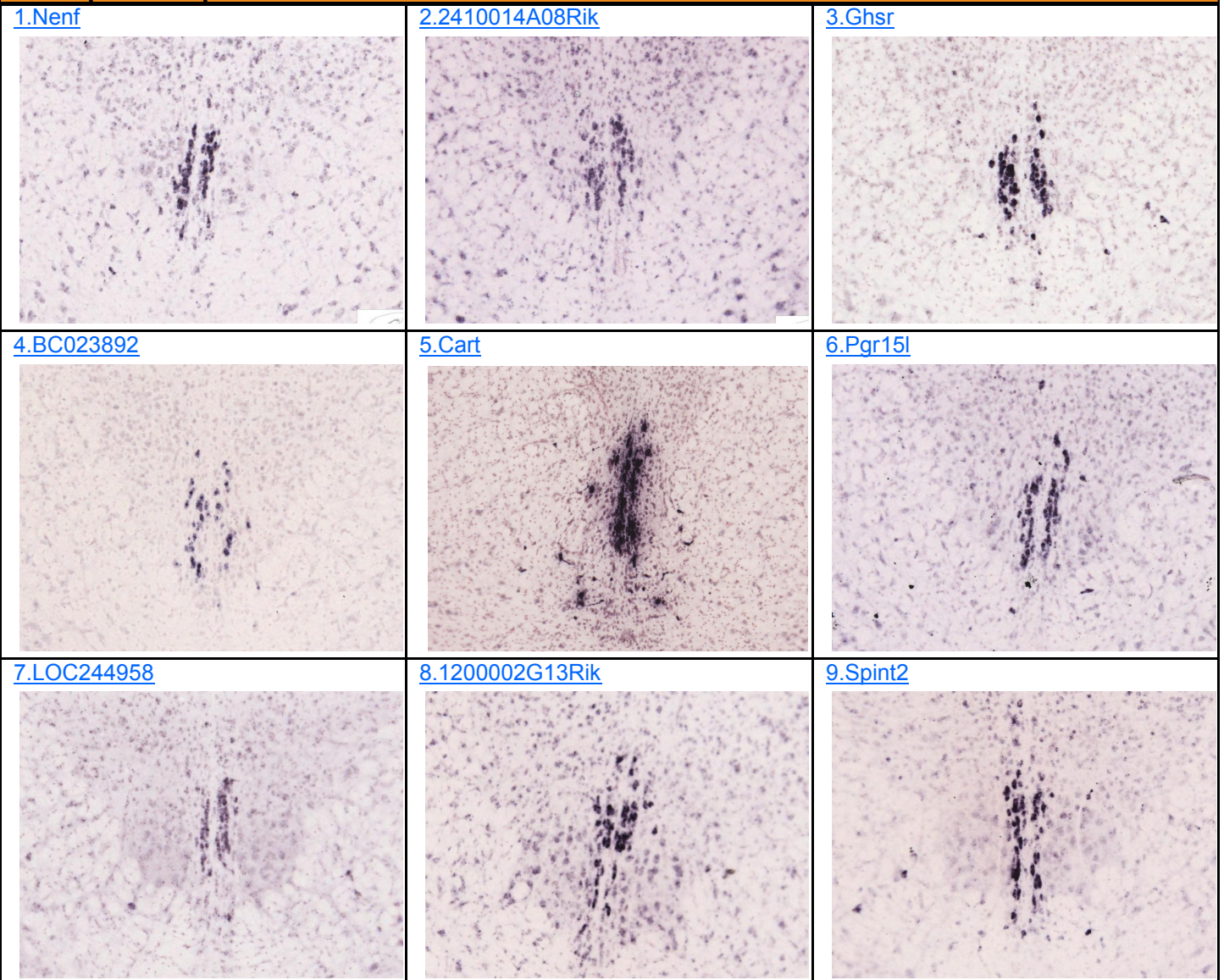
Curation of 50 Select Genes List: July, 2008

Widespread Expression Pattern

Number	Gene Symbol	Gene Name	Expression Pattern
1	Nenf	neuron derived neurotrophic factor	High density, high intensity
2	2410014A08Rik	RIKEN cDNA 2410014A08 gene	High density, medium-high intensity
3	Ghsr	growth hormone secretagogue receptor	High density, high intensity
4	BC023892	cDNA sequence BC023892	Medium density, medium high intensity
5	Cart	cocaine and amphetamine regulated transcript	High density, very high intensity
6	Pgr15l	G protein-coupled receptor 15-like	High density, high intensity
7	LOC244958	similar to Chromosome 6 open reading frame 117	High density, medium-high intensity
8	1200002G13Rik	transmembrane emp24 domain containing 3	High density, high intensity
9	Spint2	serine protease inhibitor, Kunitz type 2	High density, high intensity
10	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	High density, medium-high intensity
11	Nhlh2	nescient helix loop helix 2	Medium density, medium-low intensity
12	Cthrc1	collagen triple helix repeat containing 1	Medium density, high intensity
13	Nmb	neuromedin B	Medium density, medium-low intensity
14	Sncg	synuclein, gamma	High density, high intensity
15	Rcn1	reticulocalbin 1	High density, high intensity
16	Dgcr6	DiGeorge syndrome critical region gene 6	High density, medium intensity
17	Pcdh11x	protocadherin 11 X-linked	High density, high intensity
18	Psme2	proteasome (prosome, macropain) 28 subunit, beta	High density, medium-high intensity
19	Doc2b	double C2, beta	Medium density, medium intensity
20	Neurl	neuralized-like homolog (Drosophila)	High density, medium intensity
21	Cpeb1	cytoplasmic polyadenylation element binding protein 1	Medium density, high intensity
22	C530008M17Rik	RIKEN cDNA C530008M17 gene	Medium density, high intensity
23	Gabre	gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon	Medium density, medium-low intensity
24	Cd8b1	CD8 antigen, beta chain 1	High density, high intensity
25	Pou4f1	POU domain, class 4, transcription factor 1	Medium density, medium intensity
26	Ptpkr	protein tyrosine phosphatase, receptor type, K	Medium density, medium intensity
27	B830021E24Rik	SID1 transmembrane family, member 1	Medium density, medium-high intensity
28	Dnajc12	DnaJ (Hsp40) homolog, subfamily C, member 12	High density, high intensity
29	Lrsam1	leucine rich repeat and sterile alpha motif containing 1	Medium density, medium-high intensity
30	Txnrd1	thioredoxin reductase 1	Medium density, medium intensity
31	Btg3	B-cell translocation gene 3	Medium density, medium intensity
32	Bves	blood vessel epicardial substance	Medium density, high intensity
33	Pfdn4	prefoldin 4	Medium density, medium-high intensity
34	Sesn1	sestrin 1	High density, medium intensity
35	Hadhb	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	Medium density, medium intensity
36	Lmna	lamin A	Medium density, medium-high intensity
37	Capn2	calpain 2	High density, high intensity
38	Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	High density, high intensity

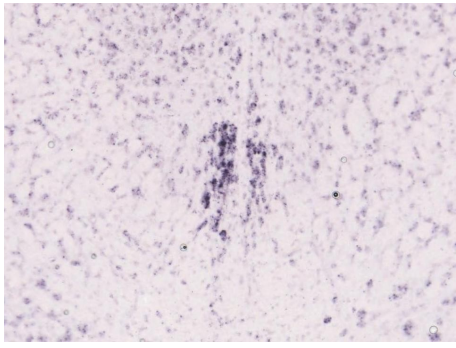
39	Mum111	melanoma associated antigen (mutated) 1-like 1	Medium density, medium intensity
40	Gm519	transmembrane protein 22	High density, high intensity
41	Neto1	neuropilin (NRP) and tolloid (TLL)-like 1	High density, high intensity
42	Fxyd6	FXYD domain-containing ion transport regulator 6	High density, high intensity
43	Brunol6	bruno-like 6, RNA binding protein (Drosophila)	High density, high intensity
44	Adcyap1	adenylate cyclase activating polypeptide 1	High density, high intensity
45	Arsa	arylsulfatase A	Medium density, medium intensity
46	Trar3	trace amine receptor 3	Medium density, medium intensity
47	P4ha2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide	High density, high intensity
48	Prdx4	peroxiredoxin 4	Medium density, medium high intensity
49	9530068E07Rik	RIKEN cDNA 9530068E07 gene	Medium density, medium intensity
50	Rpl23	ribosomal protein L23	High density, very high intensity

Widespread Expression Pattern

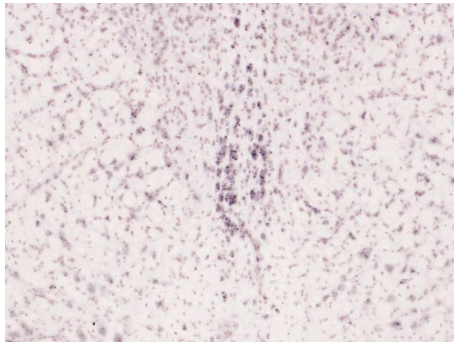


Widespread Expression Pattern

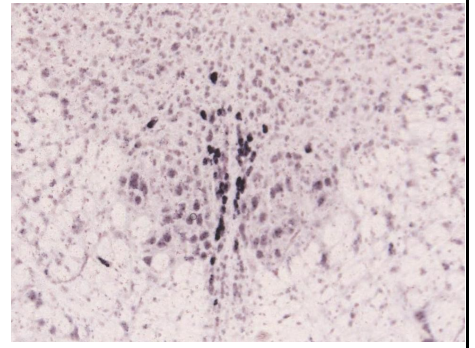
[10.Slc39a6](#)



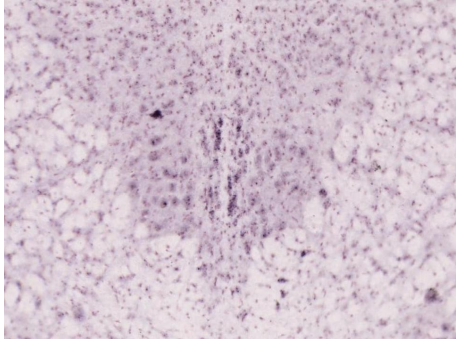
[11.Nhlh2](#)



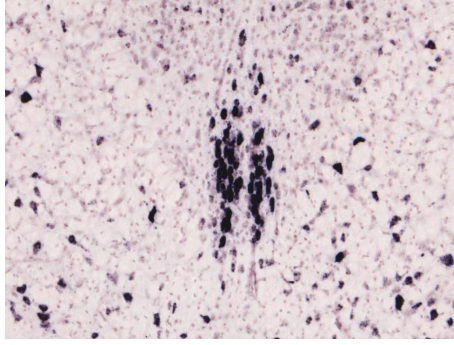
[12.Cthrc1](#)



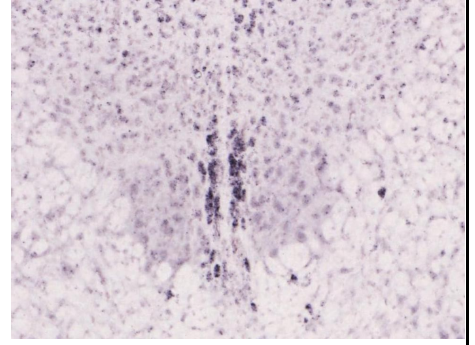
[13.Nmb](#)



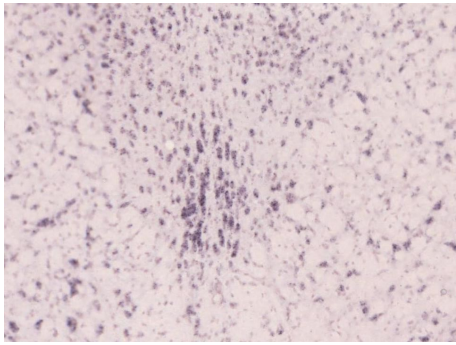
[14.Sncg](#)



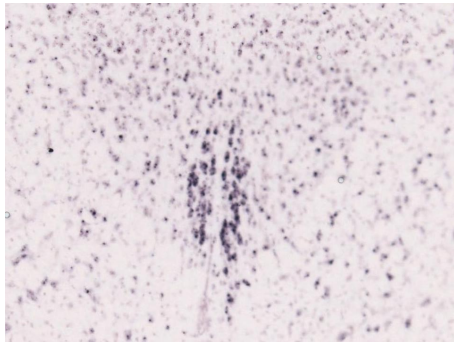
[15.Rcn1](#)



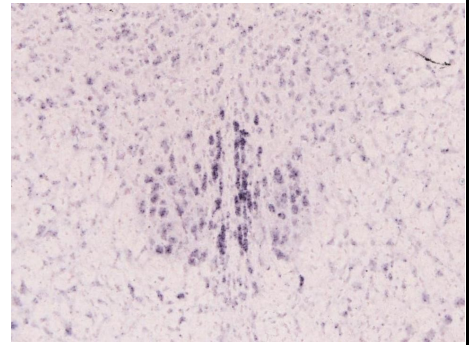
[16.Dgcr6](#)



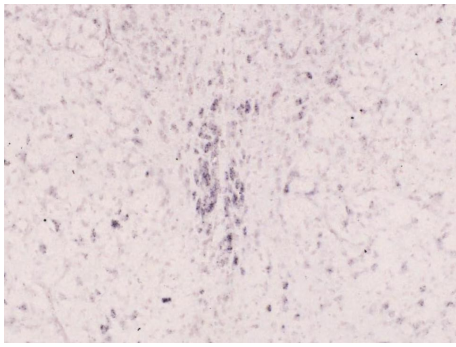
[17.Pcdh11x](#)



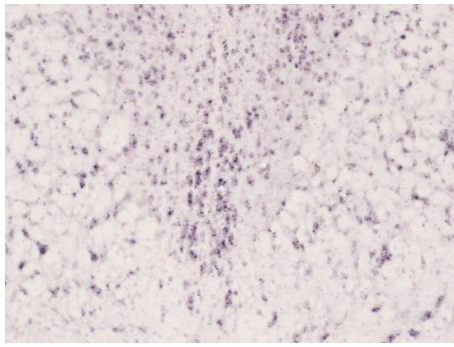
[18.Psme2](#)



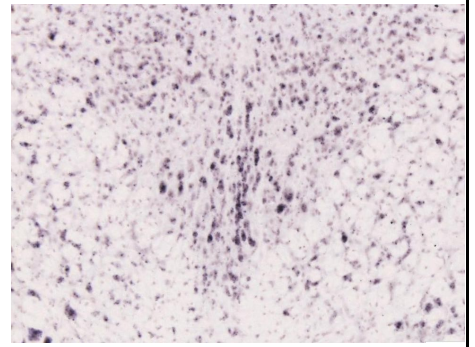
[19.Doc2b](#)



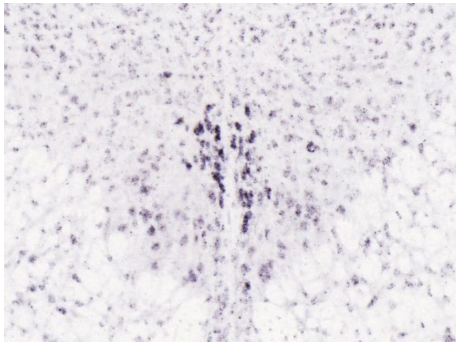
[20.Neurl](#)



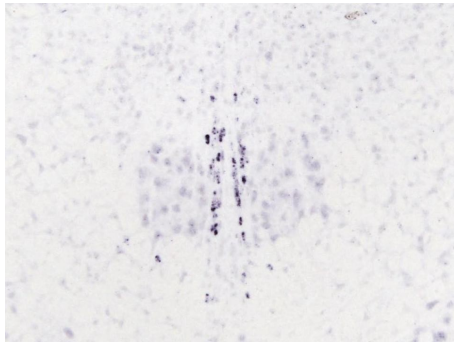
[21.Cpeb1](#)



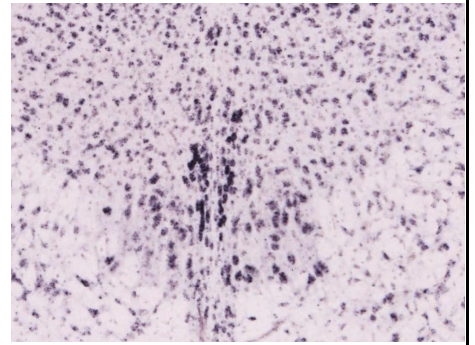
[22.C530008M17Rik](#)



[23.Gabre](#)

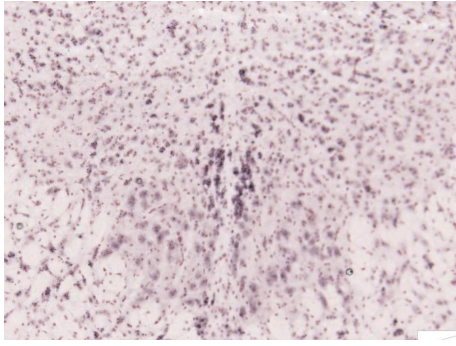


[24.Cd8b1](#)

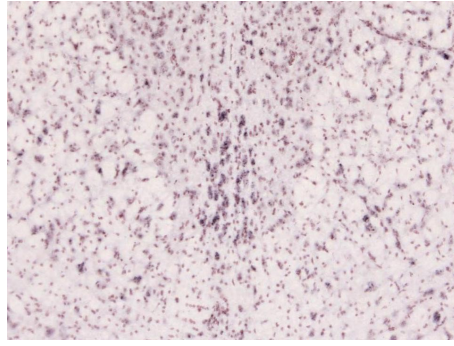


Widespread Expression Pattern

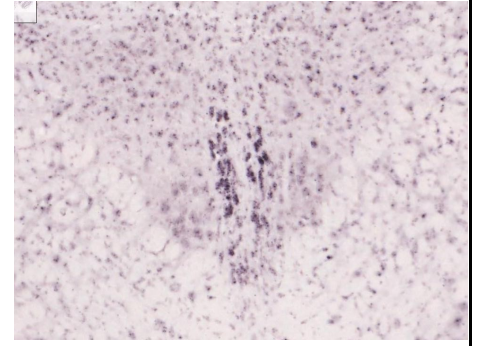
[25.Pou4f1](#)



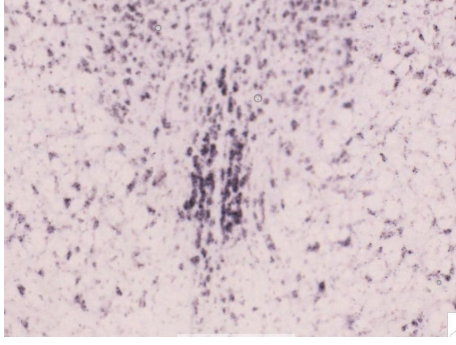
[26.Ptprk](#)



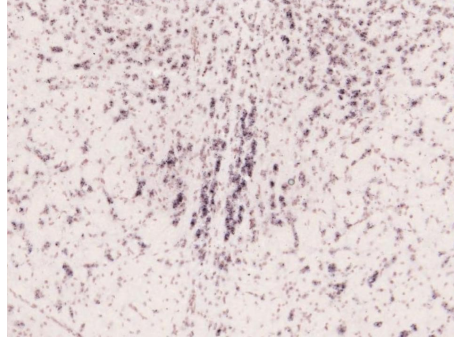
[27.B830021E24Rik](#)



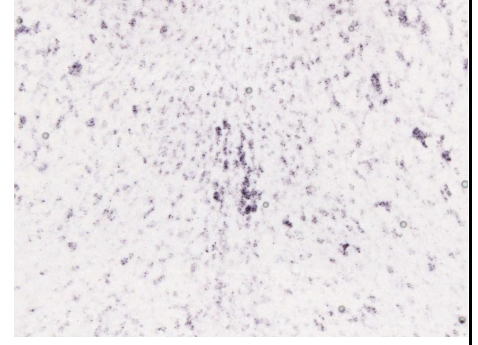
[28.Dnajc12](#)



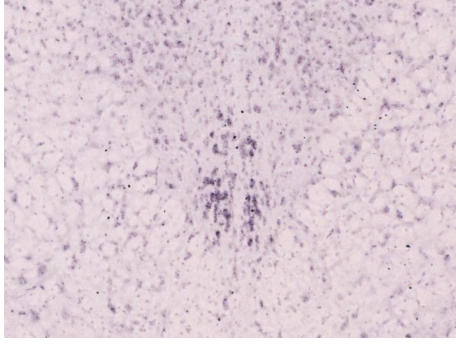
[29.Lrsam1](#)



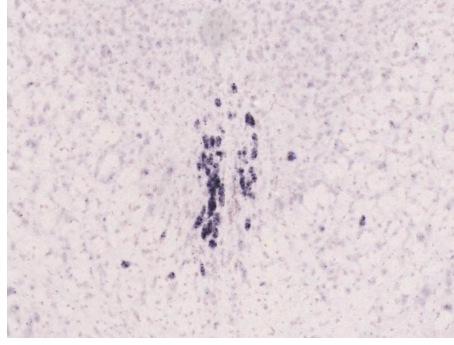
[30.Txnrd1](#)



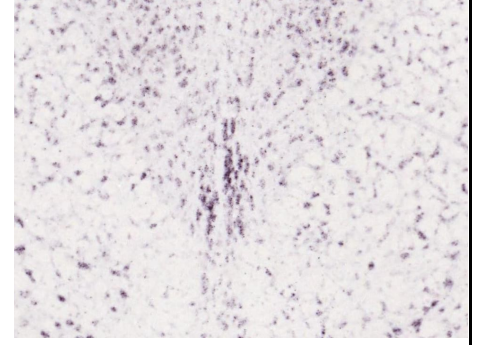
[31.Btg3](#)



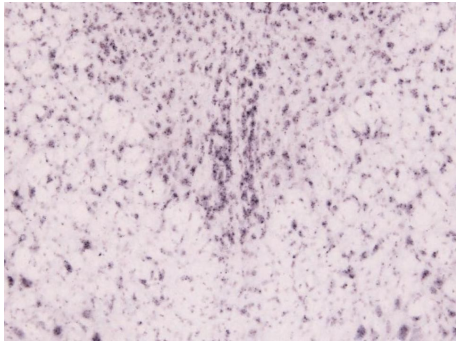
[32.Bves](#)



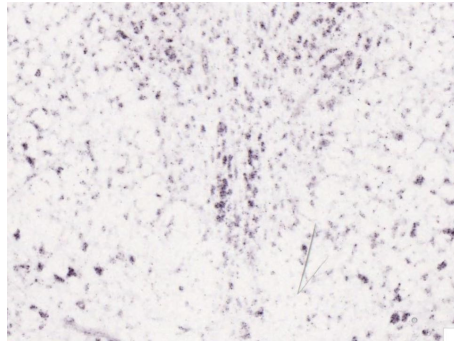
[33.Pfdn4](#)



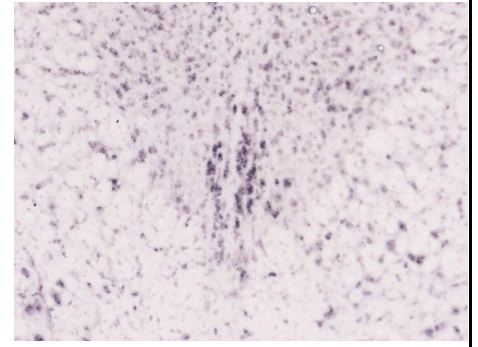
[34.Sesn1](#)



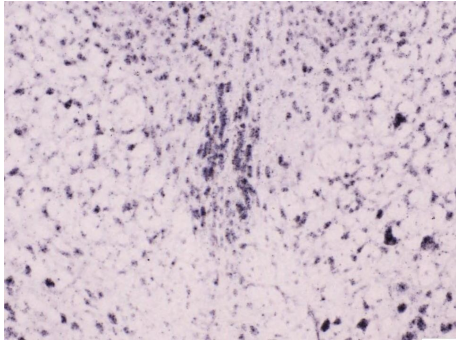
[35.Hadhb](#)



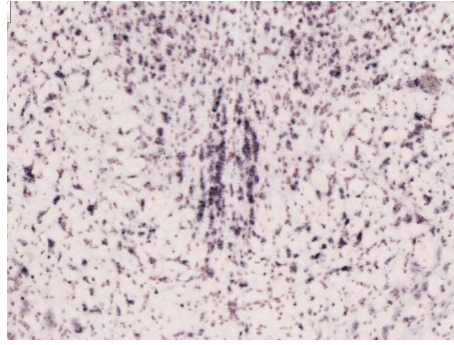
[36.Lmna](#)



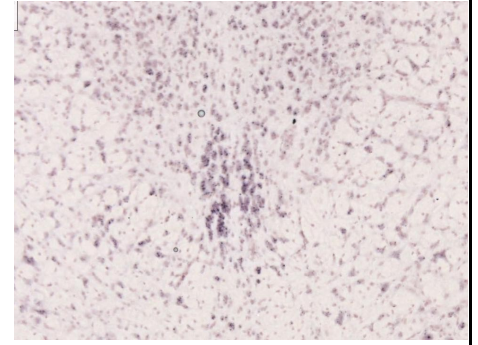
[37.Capn2](#)



[38.Sema6d](#)

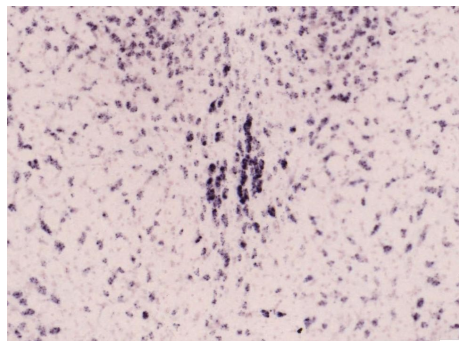


[39.Mum111](#)

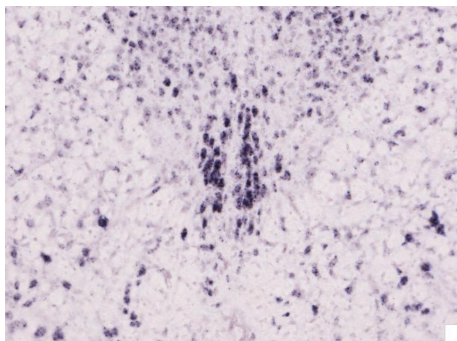


Widespread Expression Pattern

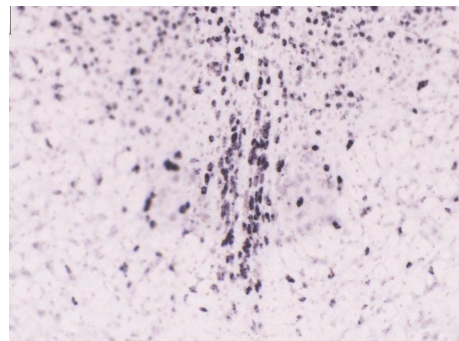
[40.Gm519](#)



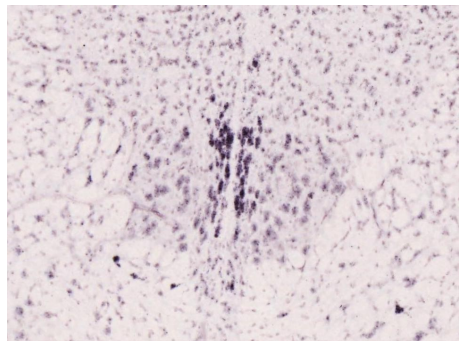
[41.Neto1](#)



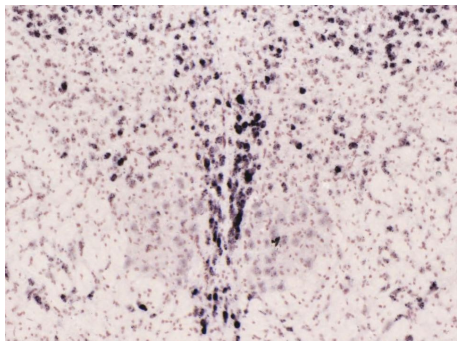
[42.Fxyd6](#)



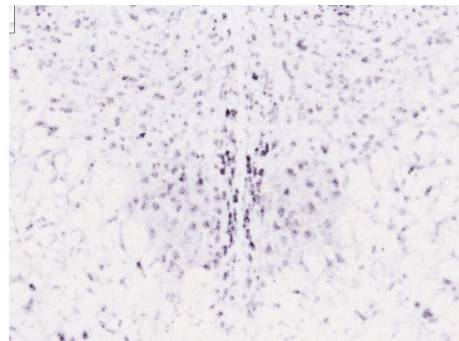
[43.Bruno16](#)



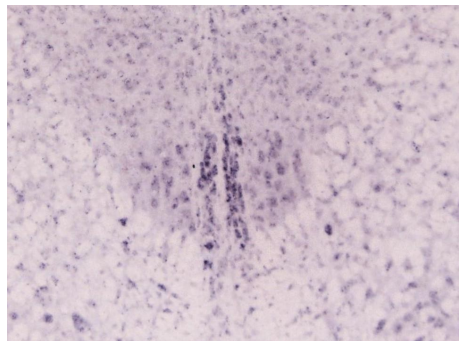
[44.Adcyap1](#)



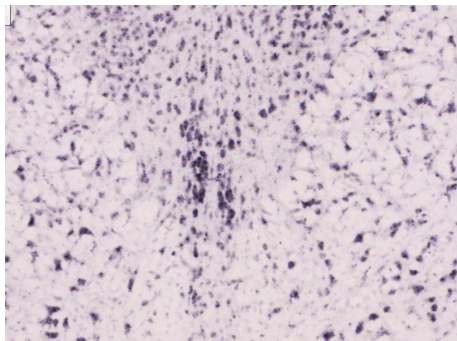
[45.Arsa](#)



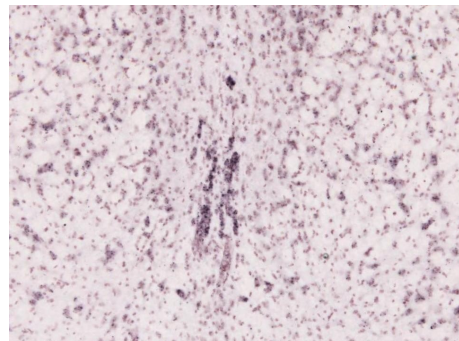
[46.Trar3](#)



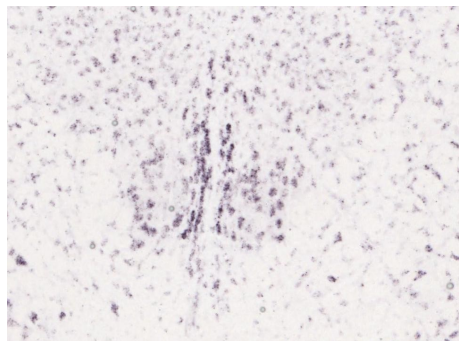
[47.P4ha2](#)



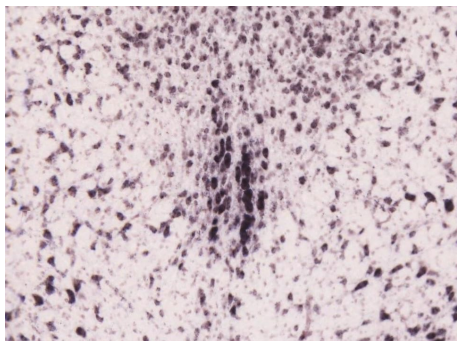
[48.Prdx4](#)



[49.9530068E07Rik](#)



[50.Rpl23](#)



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 Edinger-Westphal 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 Edinger-Westphal nucleus and other brain regions, expression values from all voxels within the Edinger-Westphal nucleus were aggregated to form a single expression value. Two types of comparisons were then made. First, the aggregate expression values of the Edinger-Westphal 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 Edinger-Westphal 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 Edinger-Westphal 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 Edinger-Westphal nucleus and macro/parent-structures are presented, as well as correlation between the Edinger-Westphal 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.

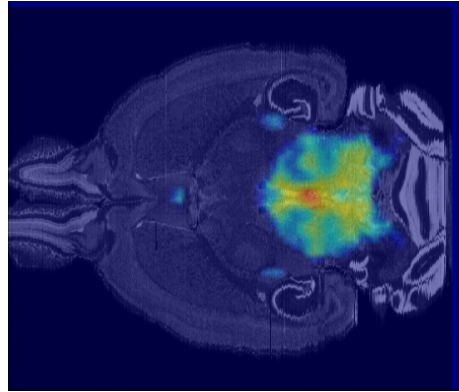
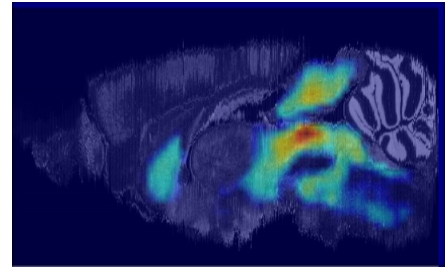
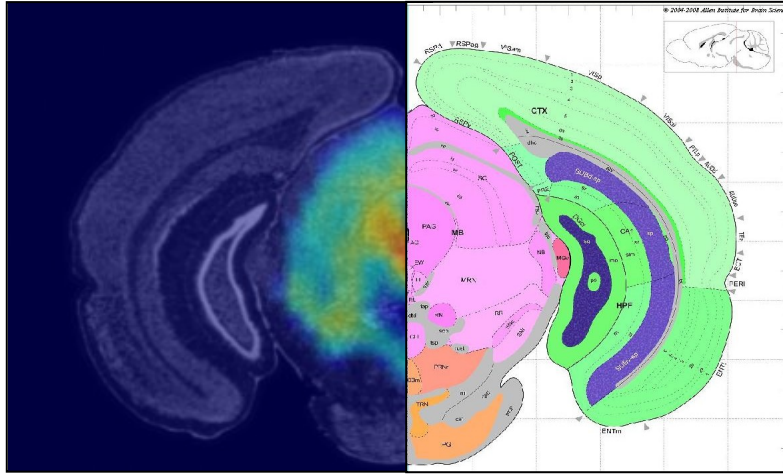
Correlation of EW with macrostructures:

Macrostructure	Correlation
OLF (Olfactory areas)	0.825238
STR (Striatum)	0.768771
PAL (Pallidum)	0.920825
CTX (Cerebral cortex)	0.818687
HY (Hypothalamus)	0.929328
TH (Thalamus)	0.871089
HIP (Hippocampal region)	0.790198
RHP (Retrohippocampal formation)	0.843374
MB (Midbrain)	0.95419
P (Pons)	0.934812
MY (Medulla)	0.924411
CB (Cerebellum)	0.693368

Substructure	Correlation
Edinger-Westphal nucleus (EW)	1
Nucleus of Darkschewitsch (ND)	0.970973
Oculomotor nucleus (III)	0.966793
Dorsal nucleus raphé (DR)	0.957505
Midbrain raphe nuclei (RAmb)	0.952729
Sublaterodorsal nucleus (SLD)	0.950825
Midbrain reticular nucleus, retrorubral area (RR)	0.947048
Superior colliculus, motor related (SCm)	0.946545
Trochlear nucleus (IV)	0.945418
Midbrain trigeminal nucleus (MEV)	0.944614
Pontine central gray (PCG)	0.94435
Pedunclopontine nucleus (PPN)	0.94418
Superior central nucleus raphé (CS)	0.944115
Nucleus incertus (NI)	0.943521
Nucleus of the solitary tract (NTS)	0.942537
Supratrigeminal nucleus (SUT)	0.941859
Cuneiform nucleus (CUN)	0.94163
Midbrain reticular nucleus, magnocellular part, general (MRNm)	0.940814
Zona incerta (ZI)	0.940607
Parabrachial nucleus (PB)	0.940496
Substantia nigra, compact part (SNc)	0.938054
Anterior tegmental nucleus (AT)	0.937299
Interstitial nucleus of Cajal (INC)	0.936768
Ventral tegmental area (VTA)	0.935792
Nucleus of the posterior commissure (NPC)	0.933972

STRUCTURE vs. VOXEL:

Correlation between the Edinger-Westphal 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 rostro-caudal levels throughout the brain.

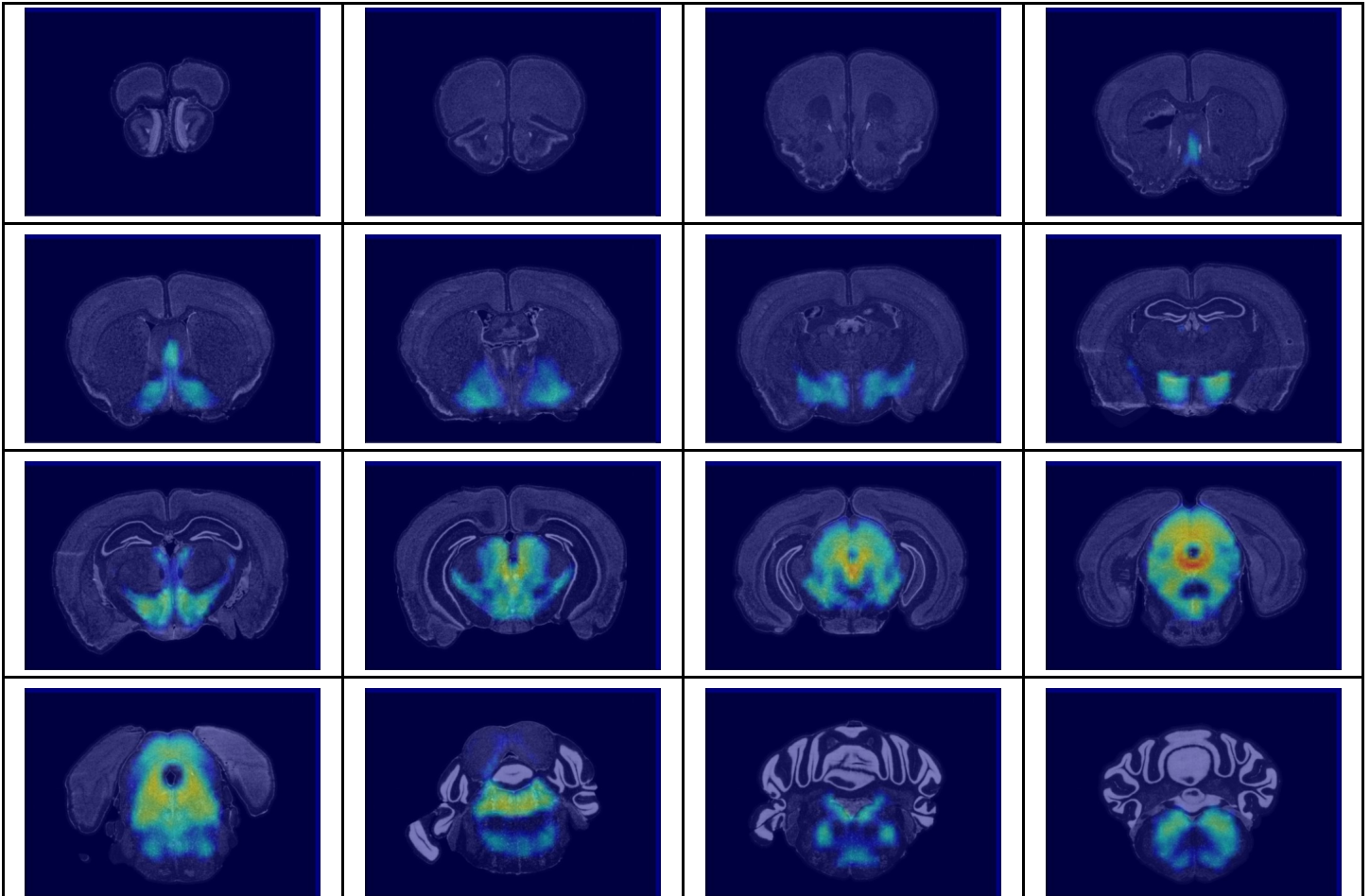


0.93



1.0

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	46 gene IDs/ 50 input genes

Date of table completion: July, 2008

GO Category	GO Term	Gene Count	% of Genes	p-value
GOTERM_CC_ALL	extracellular region part	13	28.26%	0.00634
GOTERM_BP_ALL	localization	13	28.26%	0.029029
GOTERM_CC_ALL	extracellular region	14	30.43%	0.004237
GOTERM_CC_ALL	extracellular space	12	26.09%	0.011178

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.

Edinger-Westphal nucleus Summary:

Anatomy

- The Edinger-Westphal nucleus (EW), located along the ventral border of the periaqueductal grey, is a thin, elongated structure consisting of mid-sized, parasympathetic preganglionic neurons.
- It is closely apposed to the nucleus Darkschewitsch, the oculomotor nucleus, and the rostral linear nucleus of the raphé.

Expression Patterns of the 50 Select Genes

- In this gene set, the dominant expression pattern seen is widespread expression throughout the nucleus.
- No gradients or subdivisions are observed for these fifty genes.
- Although most of the genes presented here make identification of the EW easy due to a lack of expression in structures in the immediate vicinity (for example, *Nenf* and *Ghsr*), some label the surrounding PAG, MRN, and III as well, such as *Fxyd6*, *Rpl3*, and *P4ha2*.
- Given the gene expression patterns presented here, it is probable that the EW extends farther caudally than is portrayed in the sagittal view of the ARA, although it is consistent with the coronal view.

Correlation

- Macrostructure correlation identifies the midbrain and pons as the most highly correlated structures.
- The most highly correlated structures are the adjacent nucleus of Darkschewitsch, the oculomotor nucleus, and the raphé nucleus, portions of which sit just ventral to the EW.
- The cerebellum shows the least correlation with the EW.
- The structure to voxel correlation and heat map reveals additional correlations with portions of the medial septum (MS), substantia inominata (SI), lateral habenula (LH), zona incerta (ZI) and the posterior hypothalamic nucleus (PH).

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.