Aedes whole brain README

This document contains useful resources and links for working with the *Aedes aegypti* whole brain dataset acquired in Wei Lee's Lab (Harvard Medical School). More will be added in due course.

Code of Conduct

The goal of this community is to advance circuit neuroscience in the mosquito by collaboratively producing and analysing the connectome of an adult female non-blood-fed *Aedes aegypti* brain. Please read our Code of Conduct.

Accessing the dataset

Neuroglancer for viewing and proofreading neurons

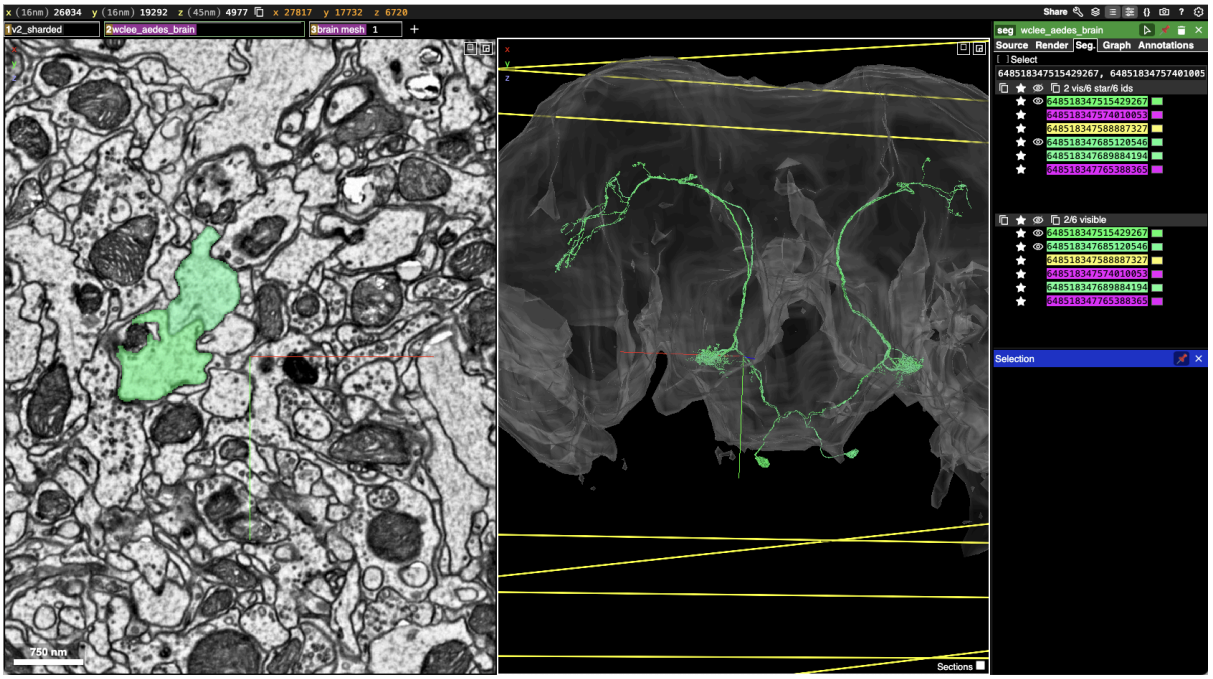
We use a dedicated platform called Neuroglancer to visualise and proofread the neurons in this dataset. Please complete the Flywire tutorial materials (courtesy of Jasper Phelps) and practice merging, finding paths, and cleaving in the Flywire sandbox if you have not done proofreading of EM datasets before. Then contact Farzaan or Mohd/Freeze via Slack for an interview to assess your readiness for working in the Aedes dataset. Once you have passed this interview, please contact Wei Lee for editing access to the production instance.

Original instance with tissue mesh

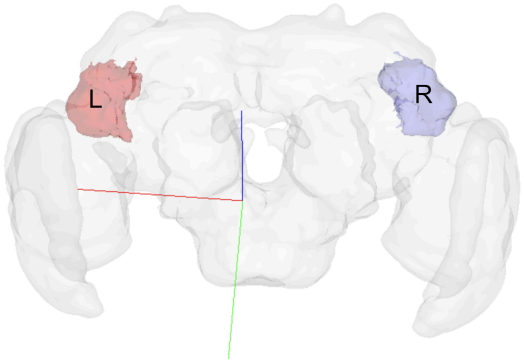
Link to Latest Production Instance

Latest Instance (updated 26/06/2026 with new antennal lobe meshes and ARC meshes)

Navigating the Aedes Neuroglancer



IMPORTANT: the brain volume (like FAFB) was flipped during imaging. Viewed from the front, the fly's actual left is on YOUR left.



Layers

v2_sharded: 2D view of the EM volume

wclee_aedes_brain: automated segmentation for proofreading (neuron meshes)

brain_mesh: mesh surrounding whole brain volume

aedes_neuropil: mesh surrounding synaptic neuropils. Several versions available in Seg. tab

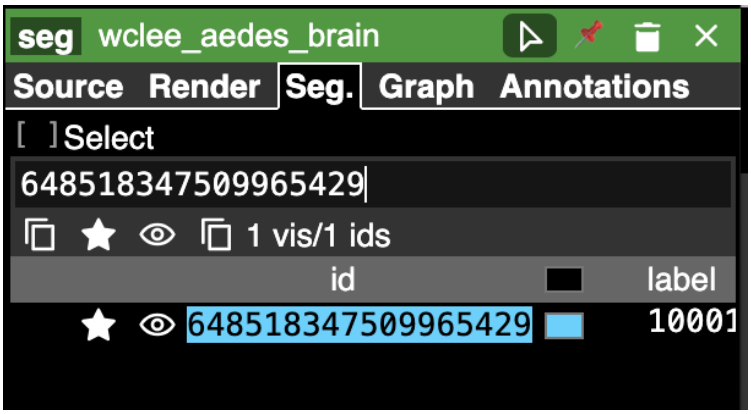
al_meshes: meshes for each glomerulus and for the whole antennal lobes (AL) as of 07/05/2026

lh_meshes: meshes surrounding lateral horns based on ALPN outputs

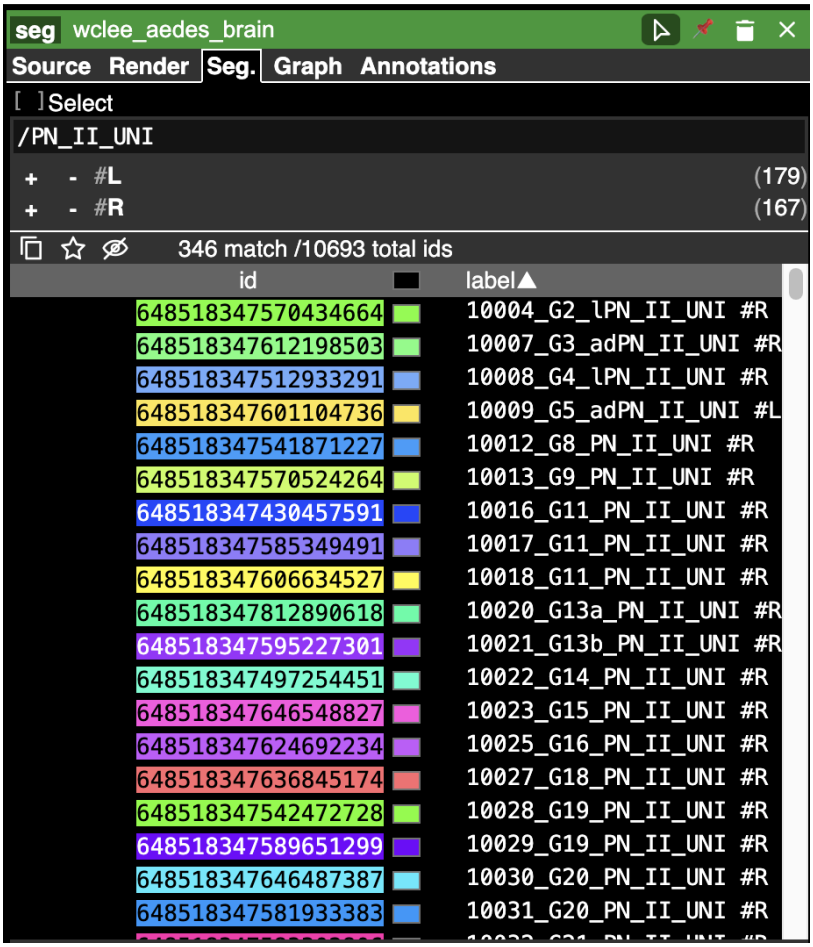
mb_meshes: meshes surrounding mushroom bodies

CX_mesh: meshes for the Fan Shaped Body (Fx_c, hDelta), Ellipsoid Body (EPG,EPGt,PEG,PGE), Protocerebral Bridge(EPG,EPGt,PEG,PGE), Noduli(LNO-output), Asymmetric Body(SA-output), Bulb(TuBu), Gall(EPG,EPGt,PEG,PGE), and assorted Lateral Complex(Fx) Neuropil

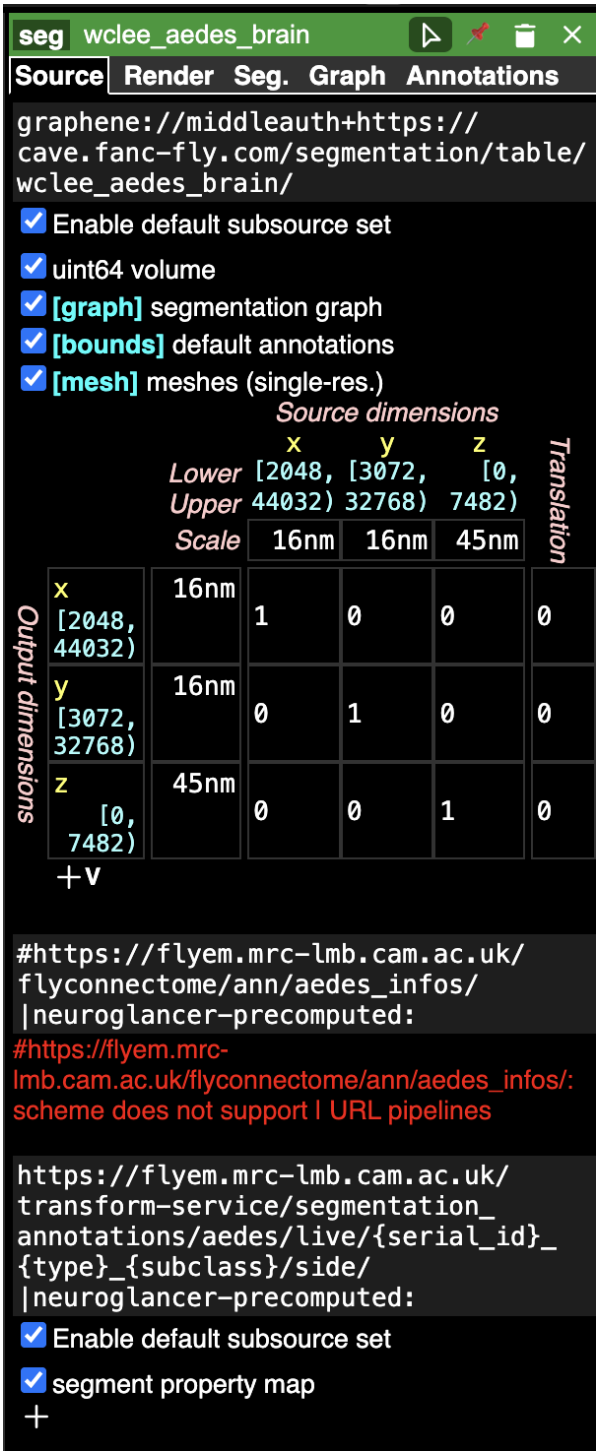
Adding neurons to the Neuroglancer view



You can copy-paste the root_id number(s) into the Seg tab of the wclee_aedes_brain layer to display them with their annotations.



You can also retrieve sets of neurons by filtering for desired annotations.



In the Source tab, near the bottom, you can edit the specific annotations being displayed (in curly brackets).

Proofreading functions

Merge when you find pieces belonging to the same neuron

Hit "m" to bring up the merge function in the lower left. Use control-click in the 2D view to add one point on either side of the desired join (in other words, one in each of the two pieces you want to merge). Then select "submit" to perform the merge. It is possible to queue several merges in this way before submitting.

Cleave when you find a merge error

Hit "c" to bring up the cleave function in the lower left. Use control-click in the 2D or 3D view to add several points on one side of the desired split (one per supervoxel). Hit "g" to swap colours and add several points on the other side. Then select "submit" to perform the cleave.

Find the most likely site of a merge error

In cases where you believe there is a merge error but are not sure where it is located, you can ask Neuroglancer to find a path. Hit "f" to bring up the "find path" function in the lower left. Use control-click in the 3D view to mark two points that you believe belong to different neurons. Then select "submit" to see a path connecting those points.

Regenerate an edited neuron

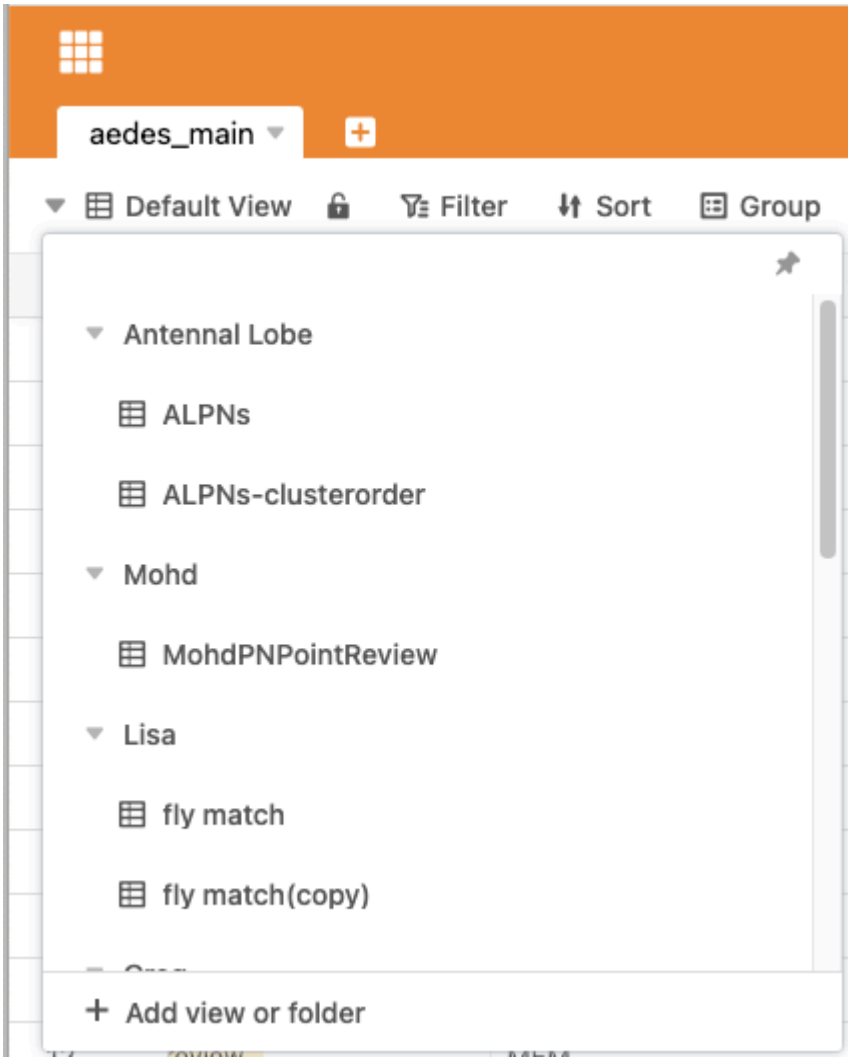
After you have performed merges or cleaves, you may need to refresh the neuron's mesh to see all changed parts. Use control-shift-click to refresh.

Aedes symmetric space

Code from Sebastian Cachero
Files for transforms

Seatable for neuron annotation

We use a dedicated spreadsheet/database for real-time recording of neurons and annotations called SeaTable. **We strongly encourage you to add neurons you are working on to this database as soon as feasible**, to avoid duplication of effort and maintain consistency of annotations. Even recording a few simple features such as point_xyz location, side, and superclass is useful. Please contact Greg Jefferis for access.



There is a default view that should NOT be used while manipulating the dataset by sorting, adding/changing filters, etc. In the top left, please **add a folder** with your name and **add a view** with your desired filters, hidden columns, etc within that folder.

Each reconstructed neuron should ideally occupy one row, although there are a few status=”duplicate” denoting bodies that were recorded more than once.

When adding a new neuron to the table, PLEASE first check whether the Neuroglancer ID number already appears in the sheet, and if not, **add a new row** at the bottom of the unfiltered table and **record the coordinates** centered in a large profile **(point_xyz, below)**. Do NOT add values to the root_id, serial_id, or supervoxel_id columns - these will be filled in automatically, as described below.

Columns from left to right

supervoxel_id: an invariant supervoxel belonging to each neuron. It will be updated every 30 minutes from a given point_xyz (see below).

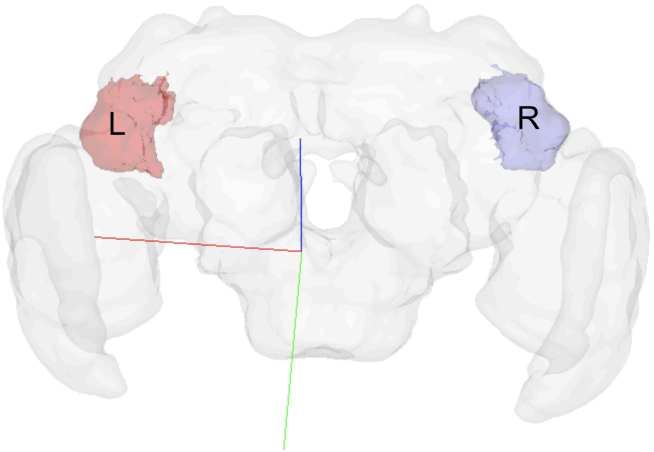
root_id: a dynamic identification number that will change each time a neuron is modified. It will be updated every 30 minutes from a given point_xyz (see below).

serial_id: a short, sequential identification number assigned automatically to each neuron that is easier to parse both manually and programmatically than the supervoxel_id.

point_xyz: coordinates of an invariant position belonging to each neuron. Ideally this should be centered in a large profile/the main backbone (near the branch leading to the soma tract if known). It can be copied directly from Neuroglancer (top left corner) and pasted here.

root_duplicated: a check mark indicates that the same neuron appears more than once in Seatable

side: the side of the neuron's soma (if known) or of the entry point (for sensory and ascending neurons). **IMPORTANT:** the brain volume (like FAFB) was flipped during imaging. Viewed from the front, the fly's actual left is on YOUR left.



group: the lowest serial_id belonging to a pair or larger set of homologous neurons. Neurons matched across the left and right sides should be given the same group number.

type: the "name" of the neuron in this dataset. All neurons in the same group should have the same type.

superclass: the broadest anatomical classification of a neuron, with defined options (cb_intrinsic, ol_intrinsic, ascending_neuron, descending_neuron, cb_sensory, ol_sensory, cb_motor))

neuropils: the main neuropil(s) innervated by the neuron (AMMC, AL, CX, GNG, LH, LO, ME, MB, SLP, SMP, TBD) see

https://www.sciencedirect.com/science/article/pii/S0896627313011781?via%3Dihub for neuropil abbreviations.

axon_tract: the main axon tract taken by the neuron, e.g. “mALT” or “lALT”

hemilineage: the developmental origin of the neuron, where known or inferred

class: the second level of anatomical classification, e.g., "ALPN" or "ALLN"

subclass: the third level of anatomical classification; rules vary by superclass.
Descending neurons: DNa, DNb, etc
Central brain intrinsic neurons: IR (ipsilateral to soma, restricted to one neuropil), BR (bilateral, restricted to one neuropil), CR (contralateral to soma, restricted to one neuropil), II (ipsilateral, interconnecting two distinct neuropils), BI (bilateral, interconnecting two neuropils), CI (contralateral, interconnecting two neuropils).

For specific classes of interest we can add more information as needed, for example whether an ALPN is uniglomerular (II_UNI) or multiglomerular (II_MUL).

notes: miscellaneous comments from annotators and proofreaders of the neuron

annotator: individual(s) who have reviewed and annotated this neuron

status: proofreading status. "duplicate" neurons should be ignored. "to_review" is the default before proofreading promotes them to "adequate." Neurons requiring extension can be labelled as "needs_extending" and those requiring a cleave can be labelled as "merge_error." Only neurons judged to be entirely finished should be assigned "complete."

proofreader: individual(s) who have merged or cleaved the neuron in Neuroglancer.

soma_xyz: coordinates of the neuron's soma, for cases in which said soma cannot be connected.

birthtime: "early" born neurons with larger somas and more elaborate processes are likely to be unique (one on each side) whereas "late" born neurons are more likely to belong to populations of similar neurons.

nerve: nerve through which sensory neuron enters or efferent/motor neuron exits

synonyms: names given to this type of neuron in the literature, with reference(s)

flywire_type: the type assigned in the flywire FAFB dataset (used for neurons that have been matched to homologues in Drosophila)

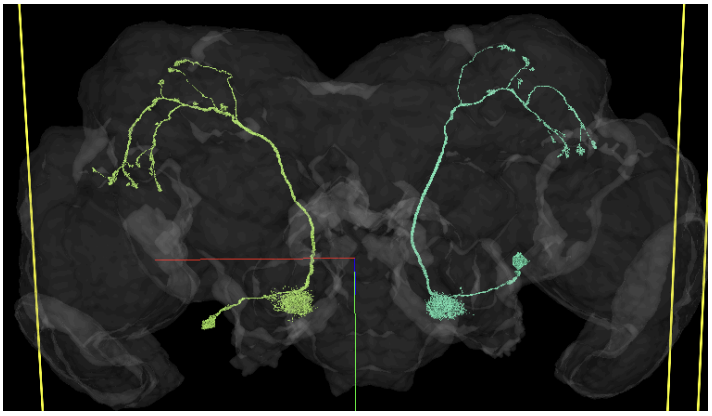
subsubclass: currently used to record glomerulus number(s) but can be used for other purposes for other neurons.

receptor: e.g., the olfactory or gustatory receptor expressed by the neuron, where known

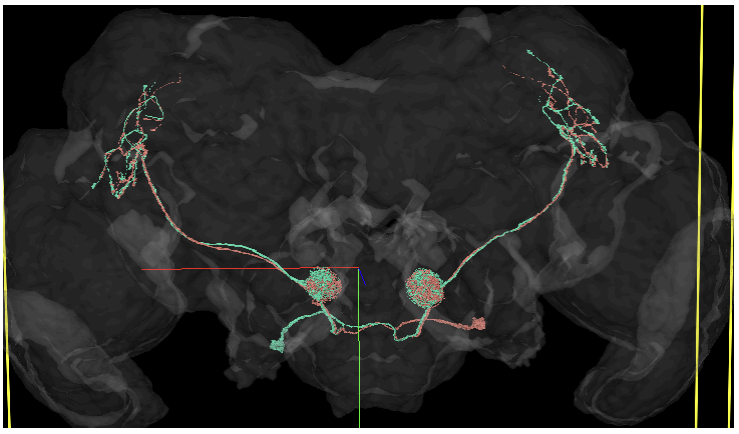
instance: please ignore for now

lrcid: left-right clustering id, e.g. for matching uniglomerular projection neurons across sides. Multiple clustering runs may be present for different groups of neurons with entries like:
C002:001 (the 1st neuron from the 2nd clustering run - LR NBLAST for PNs)
C010:1000 (the 1000th neuron for the 10th clustering run, in this case by connectivity for ORN)

Examples of annotation for ALPNs



root_id	si...	group	type	superclass	neuropils	axon_tract	hemilineage	class	subclass
648518347638197219	R	10004	G2_PN	central	AL LH MB	mALT	lPN	ALPN	lI_UNI
648518347532087542	L	10004	G2_PN	central	AL LH MB	mALT	lPN	ALPN	lI_UNI



root_id	si...	group	type	superclass	neuropils	axon_tract	hemilineage	class	subclass
648518347495878104	R	10005	G0_MD1_ilPN	central	AL LH MB	lALT	ilPN	ALPN	BI_UNI
648518347622797334	L	10005	G0_MD1_ilPN	central	AL LH MB	lALT	ilPN	ALPN	BI_UNI

Proofreader's Guide to Neurons

Here is a guide (in progress) to identifying specific classes of neurons. Please contact Lisa Marin if you would like to contribute a section.

Programmatic access

There is a private GitHub repository for scripts, functions, and other artefacts for use in analysis and eventual publication of this dataset. Please contact Greg Jefferis for access.

https://global.daf-apis.com/auth/api/v1/user/token

Dataset Collaborators

Aedes Users

Other Resources

BANC Proofreading 101

A Systematic Nomenclature for the Insect Brain