

Novel Small Molecule EPHB3 Inhibitors to Treat Neurodegenerative Disease by Targeting Astrocyte-Mediated Disease Mechanisms

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No, Nothing to disclose

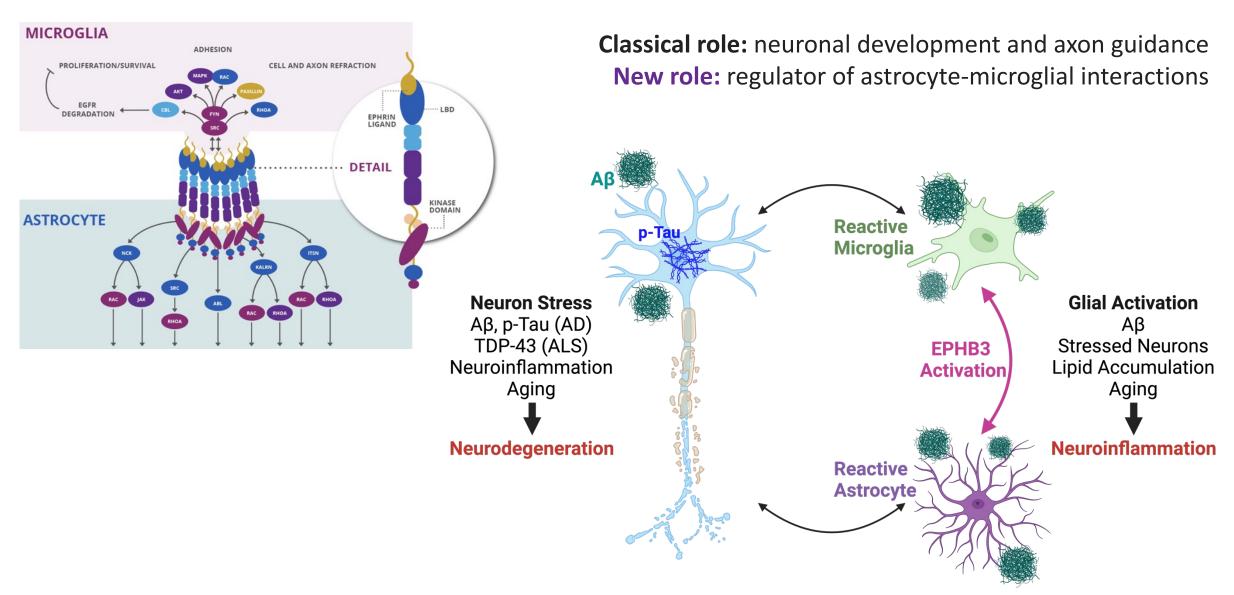
X Yes, please specify

Company / Name	Honoraria / Expense	Consulting / Advisory Board	Funded Research	Royalties / Patent	Stock Options	Ownership / Equity Position	Employee	Other (Please specify)
Evan Lebois, Violet Therapeutics					X		Х	

# EPHB3 is an astrocyte receptor tyrosine kinase that facilitates interactions with microglia to drive neuroinflammation

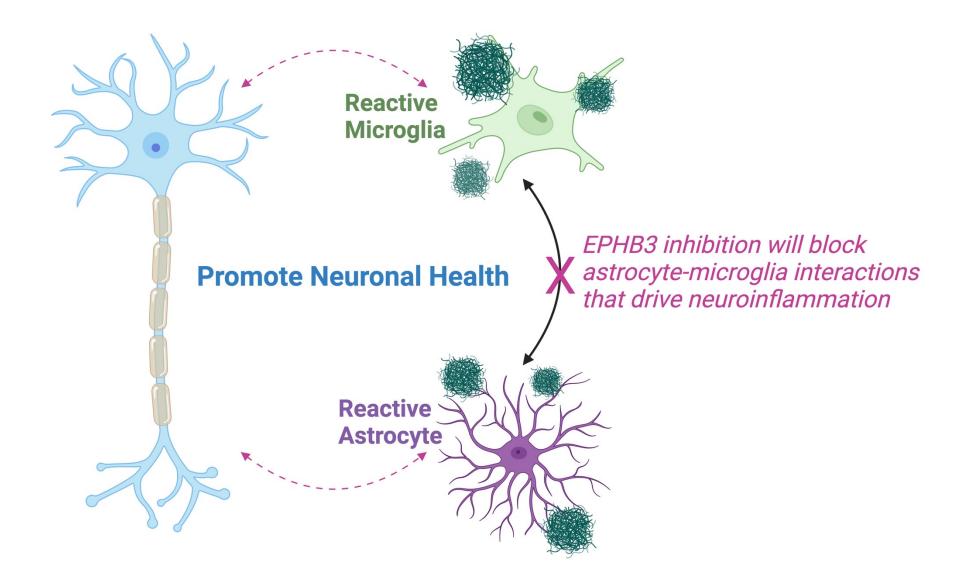






Therapeutic Hypothesis: EPHB3 inhibition will promote neuron health by blocking astrocyte-microglia interactions that drive neuroinflammation





### Construction of EPHB3 astrocyte activation score and in silico mapping to human disease and mouse model datasets



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#### **Target ID**

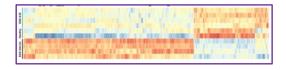
RABID-seg identified EPHB3 activation in astrocytes as neuroinflammation driver in FAF



#### **Target signature**

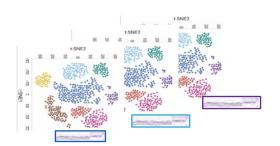
162 transcriptional changes that occur in Astrocytes when EPHB3 is activated





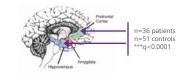
#### Mine human and mouse data sets

Bulk and scRNA-seq datasets are mined for target signature



#### Indication and mouse model selection

Target signature is found in human disease and mouse model data sets



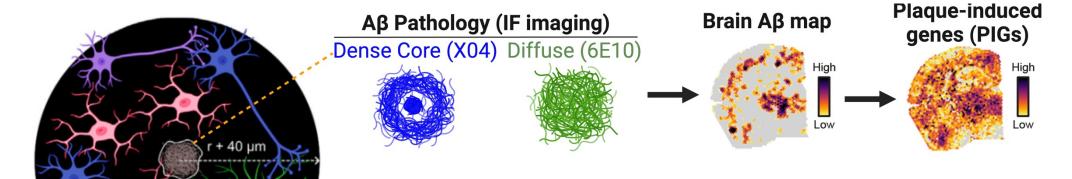


#### Aim = map EPHB3 activation to:

- human disease data sets for indication relevance
- 2. in vivo mouse model data sets for therapeutic development

## EPHB3 activation is highly co-localized and correlated with Aβ plaque-induced gene (PIG) response in AD, revealed by spatial transcriptomics





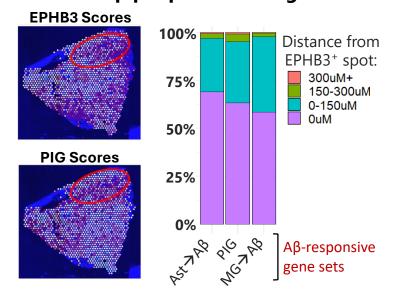
**Astrocytes** Oligodendrocytes

Microglia

**Neurons (Glu)** 

**Neurons (GABA)** 

**EPHB3** activation is highly colocalized with Aβ plaque-induced genes

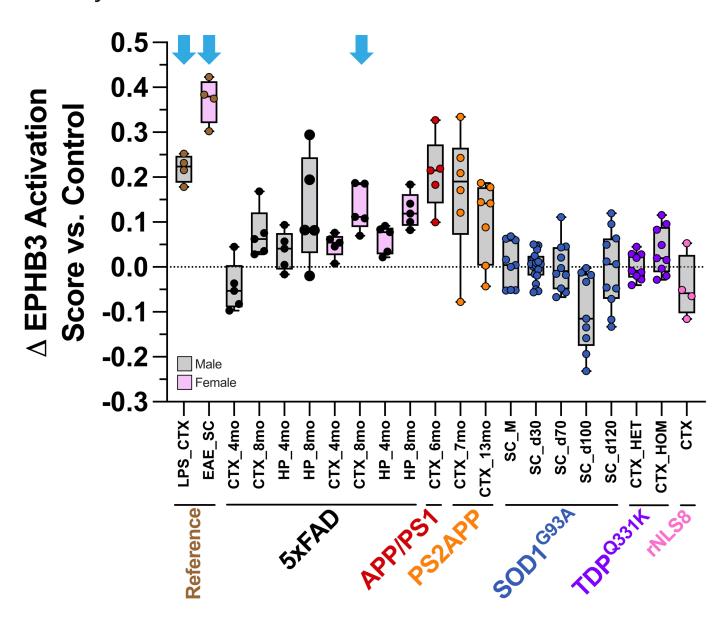


#### **Key Takeaways:**

- Astrocyte and MG gene expression altered around Aβ plaques
- This drives neuroinflammation
- EPHB3 activation happens in the same place

EPHB3 activation scores in astrocytes are markedly elevated in RNA-seq data from three amyloidosis mouse models, as well as LPS and EAE models





## Highly selective, brain penetrant tool compound VT-001 shows robust pharmacology and in vivo efficacy in ICV LPS assay



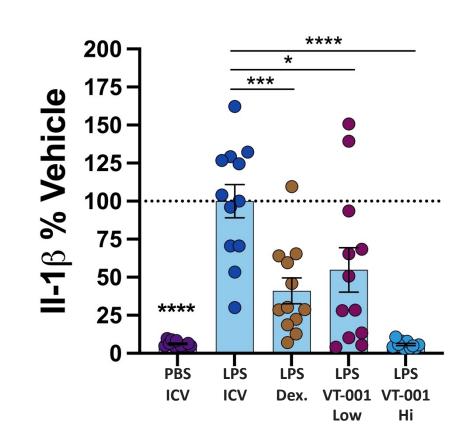
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#### Drug-like small molecule with excellent selectivity

	Selected assay/ Target	VT-001		
Properties	CNS MPO <sup>1</sup>	5		
	Kinetic solubility (7.4, uM)	192		
	MW, cLogD	<410, <1		
	PPB % unbound (m, r, d, c, h)	64, 71, 65, 61, 51		
Biochemical	EphB3 (IC50, uM)	0.048		
	Carna NanoBRET (196 kinases)	1/240 (EPHB3)		
Kpuu	Rat	40%		
In vitro tox	CYPs	< 50% @ 10uM		
	hERG	37% @ 10uM		
	SafetyScreen44	1/44 (3 μM AChE)		

<sup>1.</sup> CNS MPO: combination of cLogp/ cLogD/ MW/ TPSA/ HBD/ pKa

## Neuroinflammatory reduction in mouse LPS model greater than positive control



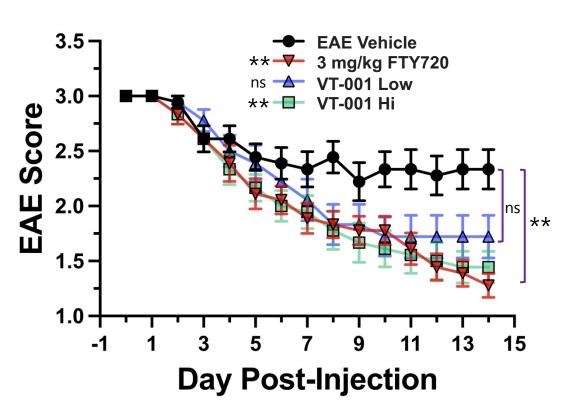
<sup>2.</sup> ER – extraction ratio. Predicted Clp/hepatic blood flow; in vivo Clp/ hepatic blood flow

### VT-001 significantly rescues clinical EAE score deficits in mice

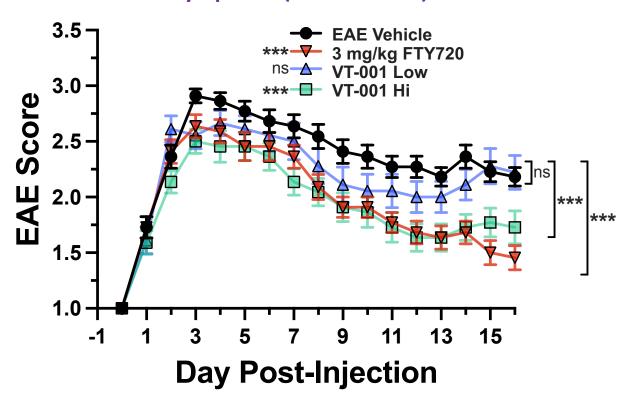


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#### **Dosing initiated at peak EAE**



## Dosing initiated at first detectable EAE symptoms (EAE score = 1)

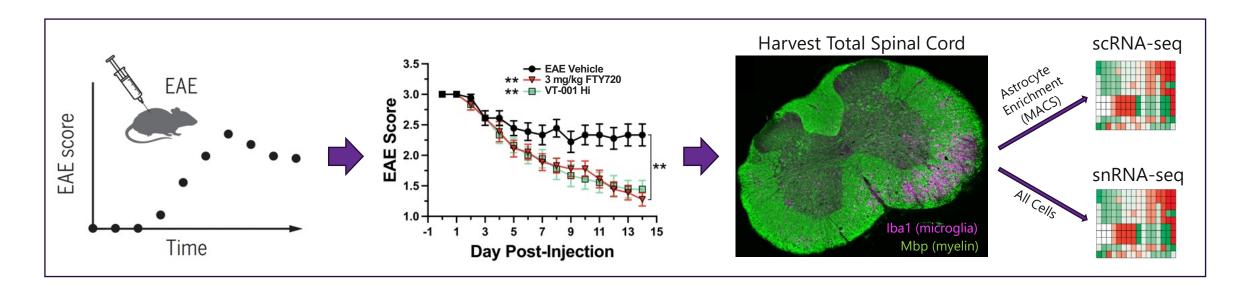


### EAE scRNA-seg studies to reveal VT-001 mechanism of action (MOA)



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**Are experimental groups** different from one another?

> **How** are experimental groups different?

Identify clusters that differentiate EAE and VT-001 groups:

Differentially expressed gene (DEG) analysis and clustering of astrocyte scRNA-seq data

Attach biological function to these clusters:

- What clusters are associated with VT-001 treatment effects?
- Of these, which clusters are associated with: EAE induction, EPHB3 activation, and neuroinflammatory gene expression?

# Clusters

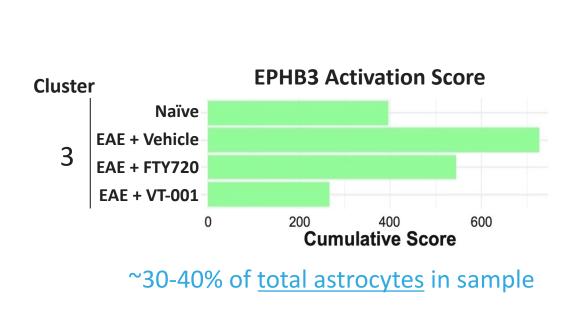
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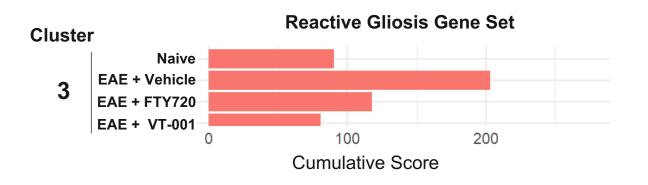


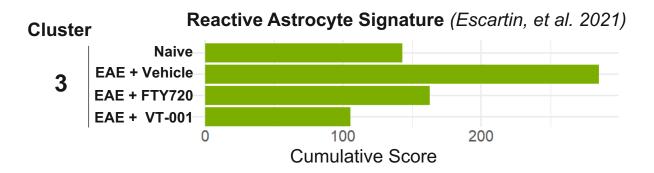
# VT-001 rescues expression of pro-inflammatory and reactive astrocyte signature gene sets in astrocytes



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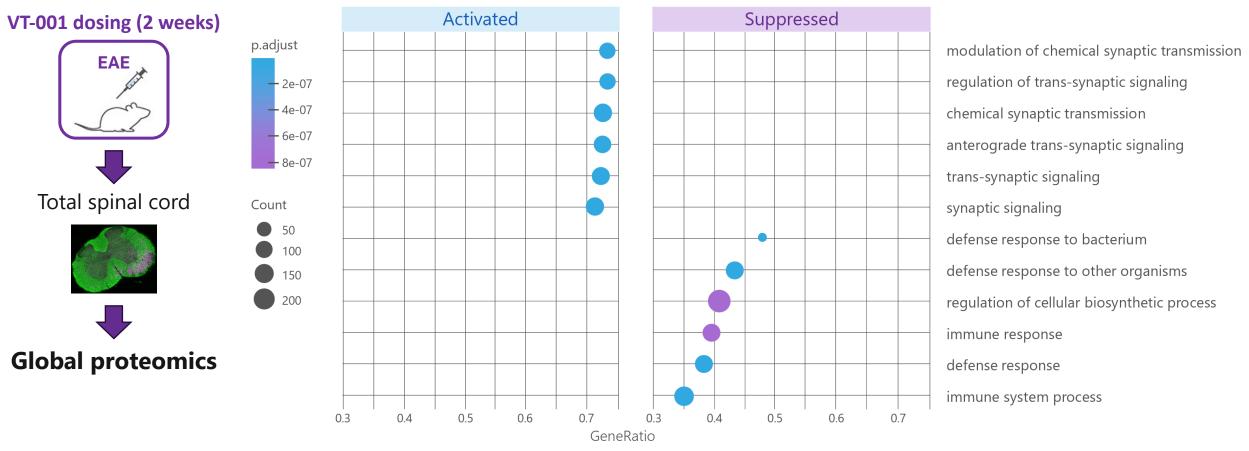
scRNA-seq in EAE spinal cord shows, in astrocytes, VT-001 decreases EPHB3 activation scores, proinflammatory, and reactive astrocyte gene expression signatures

## Global proteomic analysis of spinal cord reveals VT-001 treatment reduces inflammation and restores neuronal signaling pathways



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Using global proteomics, the top upregulated protein pathways by VT-001 treatment were synaptic signaling pathways and top suppressed pathways are immune pathways

### VT-001 rescues cognitive deficits and Aß plaque-induced gene (PIG) expression signature in cortex of 5xFAD mice



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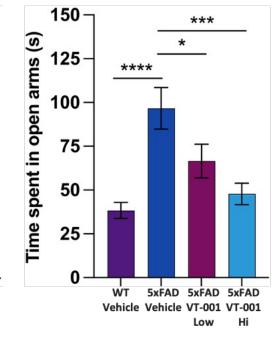


#### 2-month treatment



5xFAD 5xFAD 5xFAD

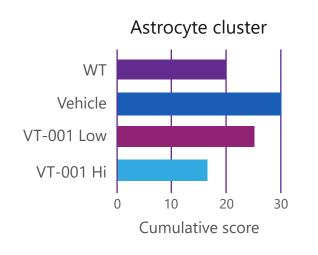
Vehicle Vehicle VT-001

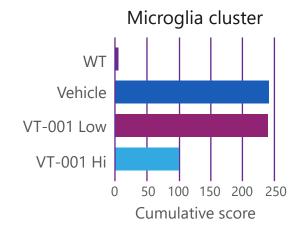




Reduced astrocyte and microglia Aß plaqueinduced gene expression in cortex (scRNA-seq)

#### Aβ plaque induced gene (PIG) response





#### **Study Timeline**

Day 6 Mean Latency

50 -

40

20

10

MWM **Drug treatment EPM Tissue** Study Time: t<sub>0</sub> 2 mos Mouse Age: 6.5 m/o 8.5 m/o

Astrocytes in 5xFAD mice have increased plaque inflammatory response

• Inflammation local to Aβ plaques damaging to neurons that represents pathogenic astrocyte-microglia crosstalk



VT-001 attenuates astrocyte and microglia inflammatory response

### Conclusions and next steps



**Overall Conclusion:** VT-001 is highly efficacious in vivo in LPS, EAE, and 5xFAD models

- 1. LPS
  - ✓ VT-001 robustly attenuates LPS-evoked IL-1β release to WT levels (MSD)
- 2. EAE
  - ✓ Spinal cord gliosis and reactive astrocyte gene signatures attenuated by VT-001 (scRNA-seq)
  - ✓ Rescue of neuronal signaling pathways and inhibition of immune response pathways (proteomics)
- 3. 5xFAD
  - ✓ Significant Aβ PIG expression in cortex astrocytes and microglia attenuated by VT-001 (scRNA-seq)

#### **Next Steps**

- 1. 5xFAD follow-up studies
  - Neurohistology to characterize VT-001 efficacy at molecular level
  - Spatial transcriptomics to establish VT-001 MOA local to Aβ plaque pathology
  - Fluid and tissue proteomics to identify VT-001 biomarkers
- 2. PS19 study to test VT-001 efficacy in setting of tauopathy



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