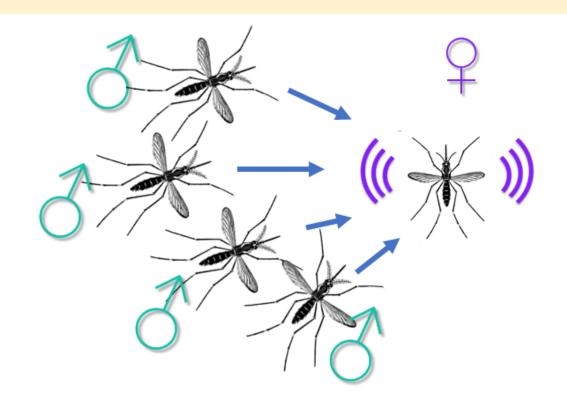
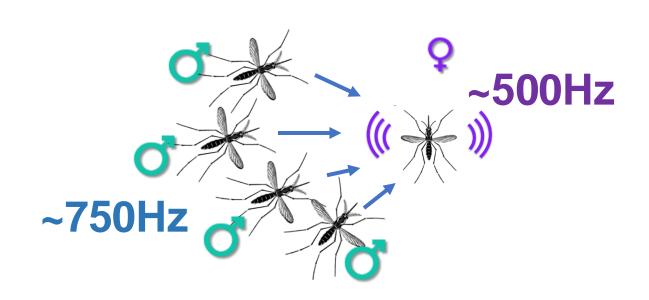
Investigating the molecular bases of differences in hearing function across species

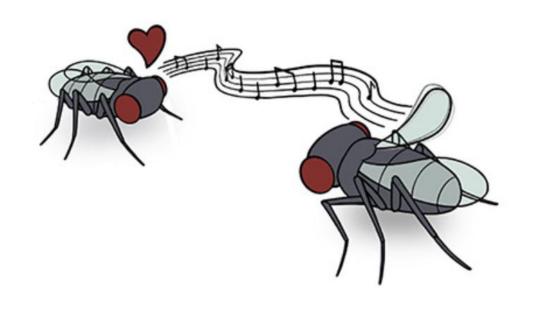


THORNTON Alberto

School of Science B3 albertothornton@outlook.com

Hearing plays a role in mating in some insect species



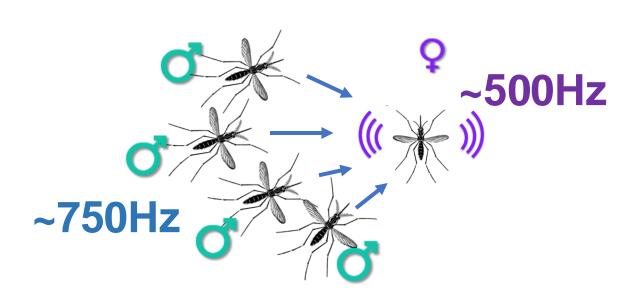


Male mosquitoes use hearing to find females

Male *Drosophila*produce courtship
songs during courtship

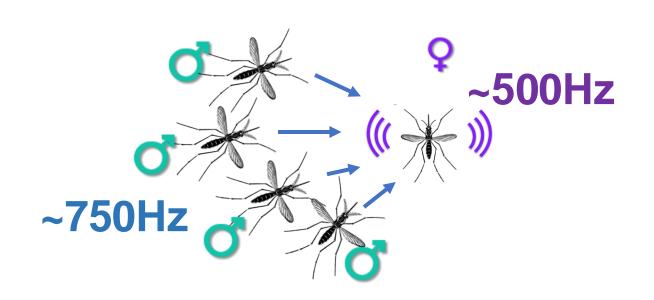
Male mosquitoes find females using hearing

Males find females by hearing flight sounds ('phonotaxis')
- Females do not show phonotaxis



Male mosquitoes find females using hearing

Male ears are tuned to sound of wingbeats

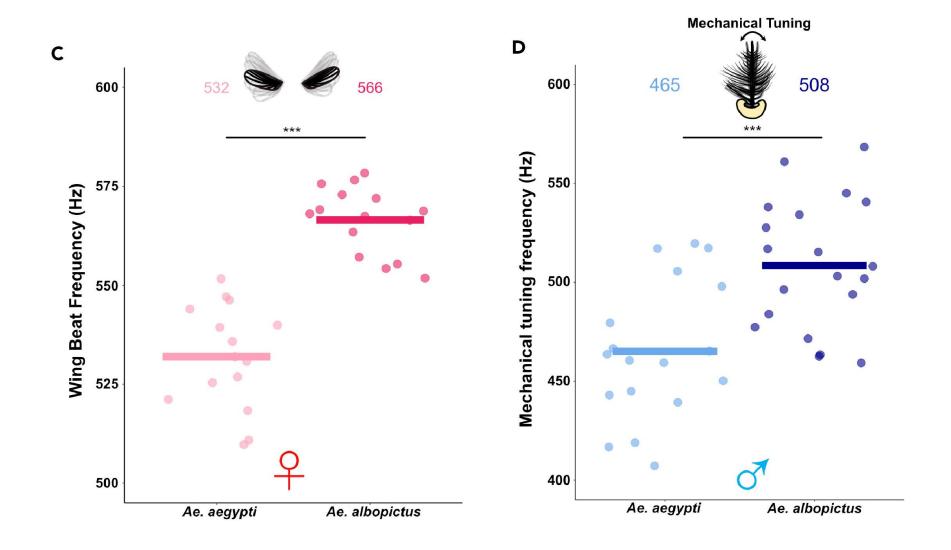


Understanding hearing is therefore key to understanding mating

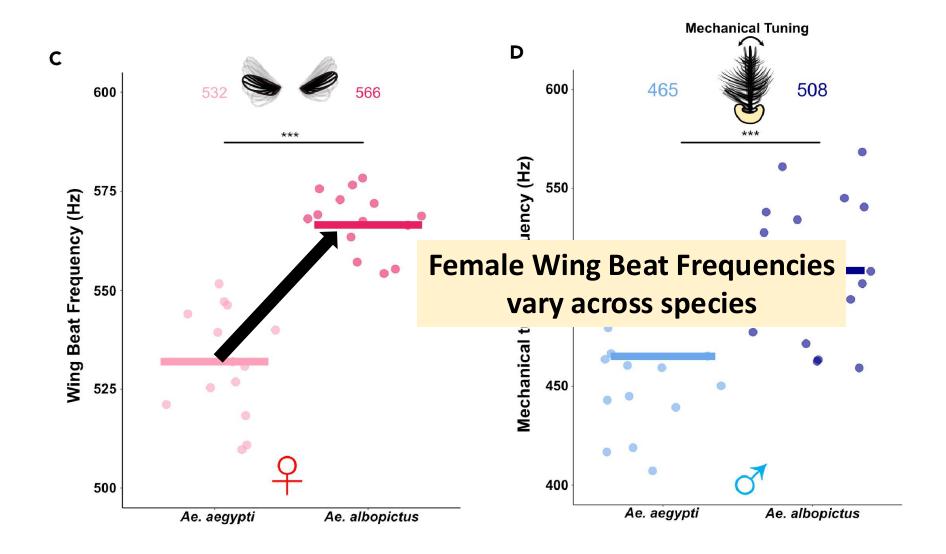
Targeting hearing option for control programs

=> Need to know more about bases of hearing

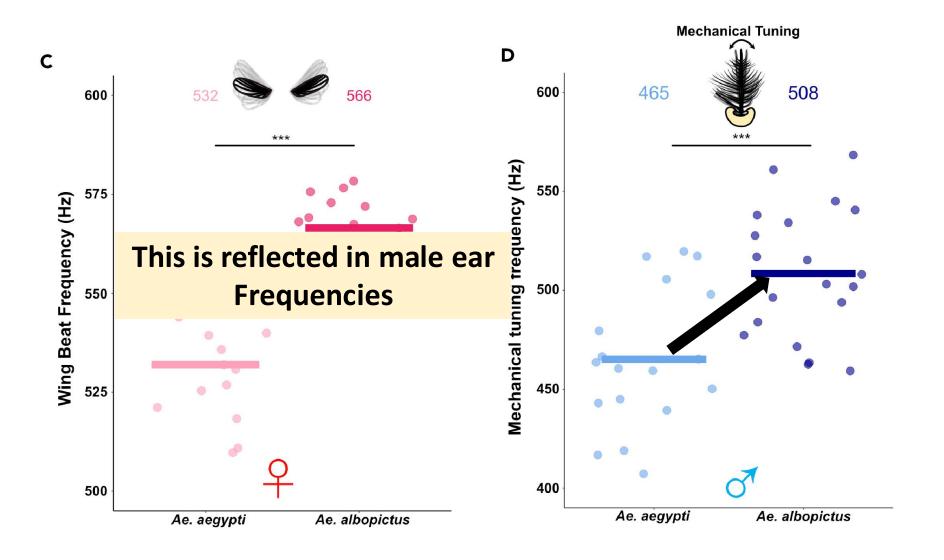
Interspecific differences in WBFs and Tuning



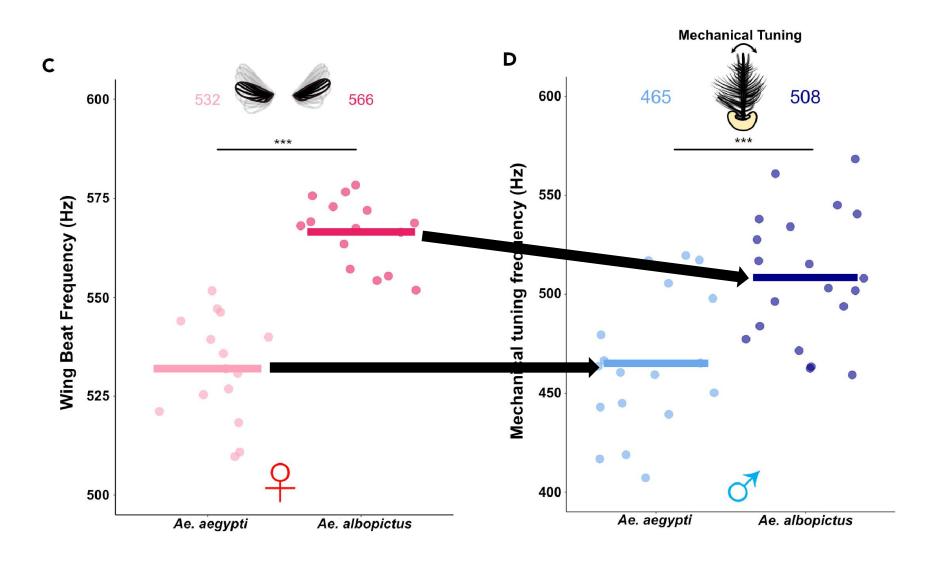
Interspecific differences in WBFs and Tuning



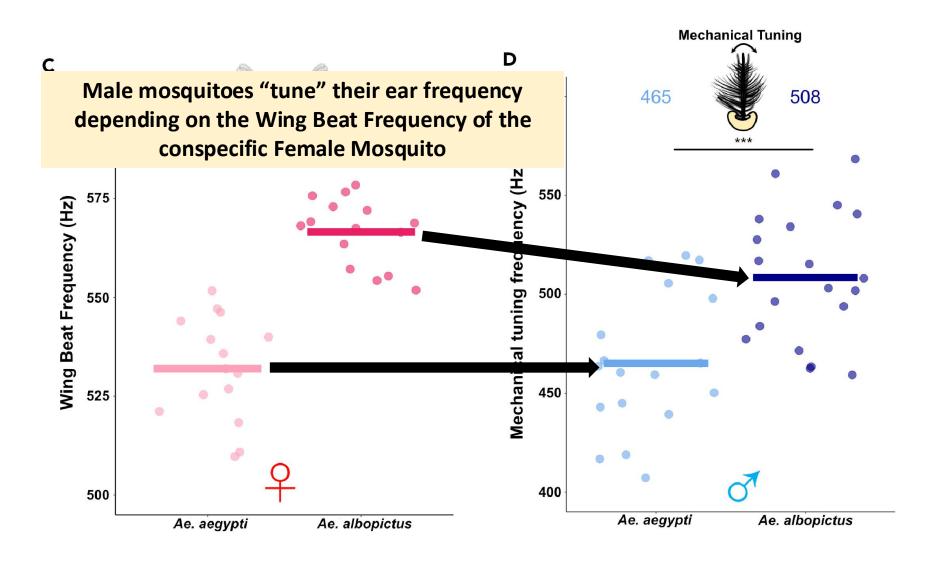
Interspecific differences in WBFs



In-tuning in mosquitos

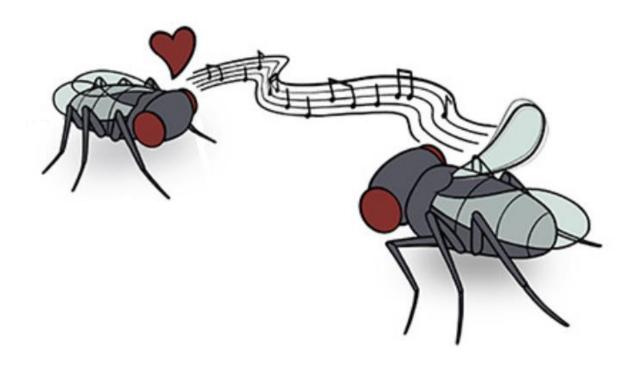


In-tuning in mosquitos



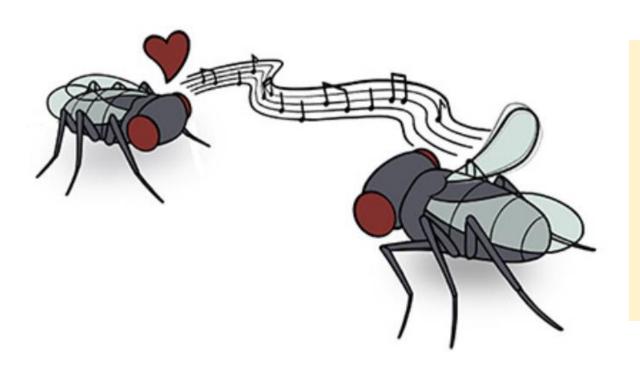
In-tuning in *Drosophila*

We know this is also the case in *Drosophila*



In-tuning in *Drosophila*

We know this is also the case in *Drosophila*



Not much data on the molecular basis of hearing in mosquitoes

However, some data in *Drosophila*=> can use it as a model to look at
the molecular basis in-tuning

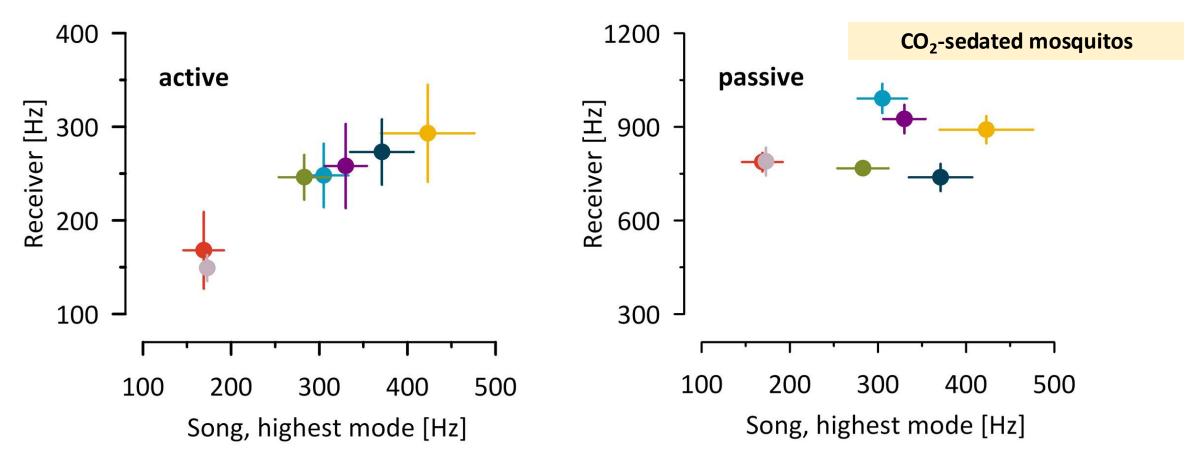
In-tuning in *Drosophila*

We know this is also the case in *Drosophila*



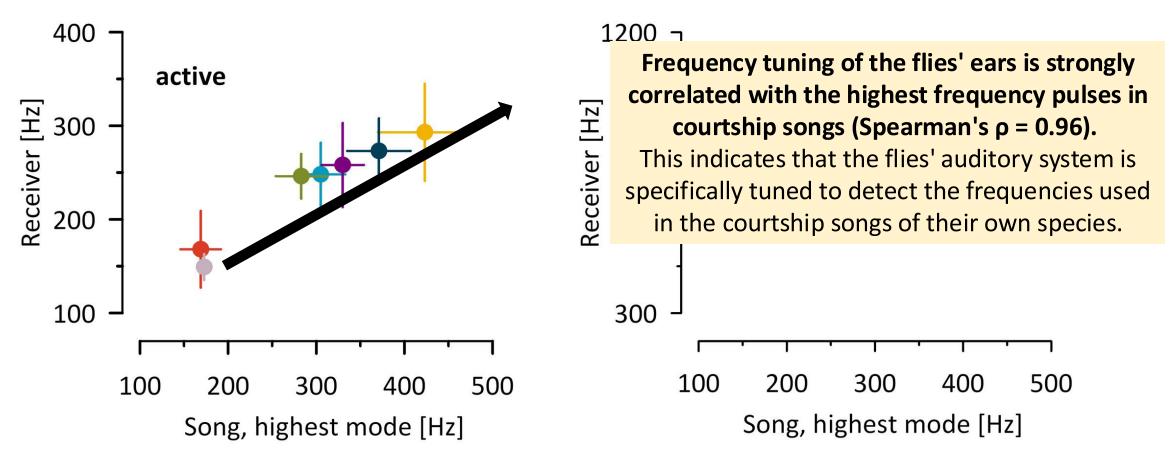
There isn't much data on the molecular basis of tuning in mosquitoes, but it is well understood in *Drosophila*, so we can use it as a model to look at in-tuning on the molecular basis

Hearing is an active process



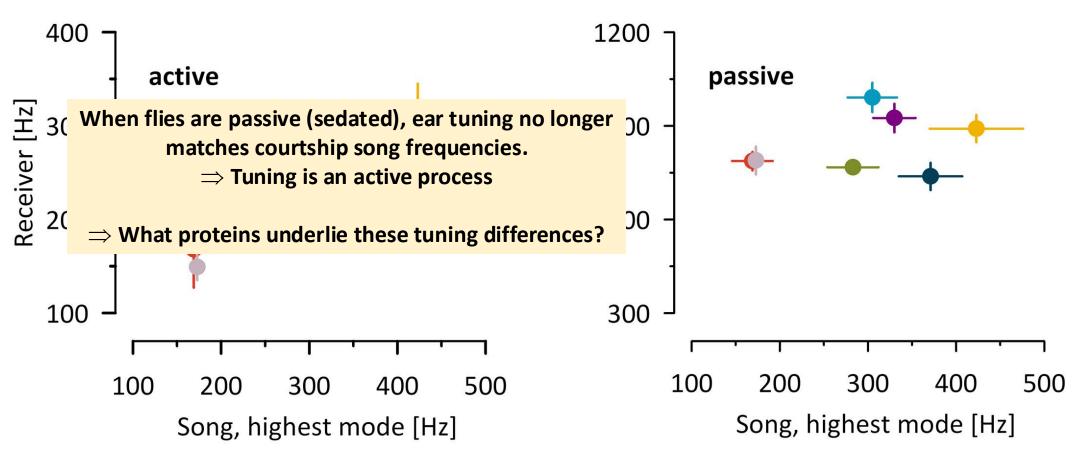
D. simulans D. mauritania D. melanogaster D. teissieri D.yakuba D. erecta D. ananassae

Hearing is an active process



D. simulans D. mauritania D. melanogaster D. teissieri D.yakuba D. erecta D. ananassae

Hearing is an active process



D. simulans D. mauritania D. melanogaster D. teissieri D.yakuba D. erecta D. ananassae

Known proteins related to hearing

No	Gene symbol	Gene name	Auditory phenotypes	Receiver best frequency	References
1	ato	atonal	Sound-receiver immobilized Sound-evoked nerve potentials lost	none	Eberl <i>et al.</i> , 2000; Göpfert <i>et al.</i> , 2002
2	btv	beethoven	Sound evoked nerve potentials reduced Active amplification lost	528 ± 24 Hz	Eberl et al., 2000; Göpfert and Robert, 2003; Göpfert et al., 2005
3	ck	crinkled	 Sound-evoked nerve potentials lost 		Todi <i>et al.</i> , 2005
4	cp309		Sound-evoked nerve potentials reduced or lost		Martinez-Campos et al., 2004
5	ct	cut	 Sound-evoked nerve potentials lost 		Ebacher et al., 2007
6	DCX-EMAP	Doublecortin-domain- containing echinoderm- microtubule-associated protein ortholog	Sound-evoked nerve potentials lost Active amplification and transducer gating impaired		Bechstedt et al., 2010
7	dia	diaphanous	 Sound-evoked nerve potentials reduced 		Cosetti et al., 2008; Schoen et al., 2010
8	Eb1		Sound-evoked nerve potentials reduced		Elliott et al., 2005
9	f	forked	Sound-evoked nerve potentials reduced		Cosetti et al., 2008
10	iav	inactive	Sound-evoked nerve potentials abolished Active amplification enhanced	~100 – 250 Hz	Gong et al., 2004; Göpfert et al., 2005; Sun et al., 2009
11	Кар3	Kinesin associated protein 3	Sound-evoked nerve potentials lost		Sarpal et al., 2003
12	Klp64D	Kinesin-like protein at 64D	Sound-evoked nerve potentials reduced		
13	nan	nanchung	Sound-evoked nerve potentials lost Active amplification enhanced	nd-evoked nerve potentials lost ~100 - 250 Hz	
14	nompA	no mechanoreceptor potential A	Sound evoked nerve potentials reduced Active amplification lost	406 ± 25 Hz	Eberl et al., 2000, Chung et al., 2001 Göpfert and Robert, 2003; Göpfert et al., 2005
15	потрВ	no mechanoreceptor potential B			Eberl <i>et al.</i> , 2000; Han <i>et al.</i> , 2003
16	nompC	no mechanoreceptor potential C	Sound-evoked nerve potentials reduced Sound-sensitivity diminished Active amplification lost	~550 Hz	Eberl <i>et al.</i> , 2000; Göpfert et al., 2005; Sun <i>et al.</i> , 2009; Effertz <i>et al.</i> , 2011

47		and and another			Fb = d = 4 = 4 0000
17	rempA	reduced mechano- receptor potential A	Sound-evoked nerve potentials lost		Eberl <i>et al.</i> , 2000
18	Rfx		 Sound-evoked nerve potentials lost 		Dubruille et al. 2002
19	salm	spalt major	Sound-evoked nerve potentials lost		Dong et al., 2002, 2003
20	salr	spalt related	Sound-evoked nerve potentials lost		Dong et al., 2002, 2003
21	tilB	touch insensitive larva B	Sound-evoked nerve potentials lost Active amplification lost	766 ± 21	Eberl et al., 2000, 2001; Göpfert and Robert, 2003; Göpfert et al., 2005; Kavlie et al., 2010
22	tko	technical knockout	Behavioral response to courtship songs diminished		Toivonen et al., 2001
23	Tmhs	Tetraspan membrane protein in hair cell stereocilia ortholog	Sound-evoked nerve potentials reduced		Cosetti et al., 2008
24	unc	uncoordinated	Sound-evoked nerve potentials lost		Eberl <i>et al.</i> , 2000; Baker <i>et al.</i> , 2004
25	eys	eyes shut	Sound-evoked nerve potentials reduced		Cook et al., 2008
26	Ank2	Ankyrin2	Sound-evoked nerve potentials reduced Active amplification reduced	364 ± 69	
27	Arr2	Arrestin2	Sound-evoked nerve potentials reduced Active amplification reduced	454 ± 42	
28	Втср	Втср	Sound-sensitivity diminished Active amplification reduced	269 ± 46	
29	bw	brown	Active amplification enhanced	123 ±16	
30	Cam	Calmodulin	Sound-evoked nerve potentials reduced Active amplification enhanced	264 ± 37	
31	CG4329		Sound-sensitivity diminished Active amplification reduced	324 ± 30	
32	CG6053		Sound-evoked nerve potentials reduced Sound-sensitivity diminished Active amplification lost	617 ± 24	
33	CG8086		Active amplification reduced	266 ± 20	

Known proteins related to hearing

No	Gene symbol	Gene name	Auditory phenotypes	Receiver best frequency	References				
1	ato	atonal	Sound-receiver immobilized Sound-evoked nerve potentials lost	none	Eberl et al., 2000; Göpfert et al., 2002	17	rempA	reduced mechano- receptor potential A	•
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3	ck cp309	crinkled	Sound-evoked nerve pote Sound-evoked nerve pote	e hav	e a list of	f ge	nes	that are	•
5	ct DCX-EMAP	cut Doublecortin-domain- containing echinoderm- microtubule-associated protein ortholog	Active amplification and transfer		to be link osophila			_	3
7	dia Eb1	diaphanous	reduced Sound-evoked nerve pote		Jopina	IIICI	arro	gaster	
9	f	forked	Sound-evoked nerve pote reduced			_ •	41		
10	iav	inactive	Sound-evoked nerve pote abolished Active amplification enhale		fference			_	S
11	Кар3	Kinesin associated protein 3	Sound-evoked nerve pote	acro	oss spec	ies	und	erlie	
12	Klp64D	Kinesin-like protein at 64D	Sound-evoked nerve pote reduced		-				•
13	nan	nanchung	Sound-evoked nerve pote Active amplification enhal	rreren	ces in he	earii	ng tu	inction	•
14	nompA	no mechanoreceptor potential A	Sound evoked nerve potentials reduced Active amplification lost	406 ± 25 Hz	Eberl et al., 2000, Chung et al., 2001 Göpfert and Robert, 2003; Göpfert et al., 2005	31	CG4329 CG6053		:
15	потрВ	no mechanoreceptor potential B	Sound-evoked nerve potentials lost		Eberl et al., 2000; Han et al., 2003	32	000000		
16	nompC	no mechanoreceptor potential C	Sound-evoked nerve potentials reduced Sound-sensitivity diminished Active amplification lost	~550 Hz	Eberl <i>et al.</i> , 2000; Göpfert et al., 2005; Sun <i>et al.</i> , 2009; Effertz <i>et al.</i> , 2011	33	CG8086		•

	Sound-evoked nerve potentials lost		Dong et al., 2002, 2003
	Sound-evoked nerve potentials lost Active amplification lost	766 ± 21	Eberl et al., 2000, 2001; Göpfert and Robert, 2003; Göpfert et al., 2005; Kavlie et al., 2010
	Behavioral response to courtship songs diminished		Toivonen et al., 2001
	Sound-evoked nerve potentials reduced		Cosetti et al., 2008
	Sound-evoked nerve potentials lost		Eberl <i>et al.</i> , 2000; Baker <i>et al.</i> , 2004
	Sound-evoked nerve potentials reduced		Cook <i>et al.</i> , 2008
;	Sound-evoked nerve potentials reduced Active amplification reduced	364 ± 69	
	Sound-evoked nerve potentials reduced Active amplification reduced	454 ± 42	
	Sound-sensitivity diminished Active amplification reduced	269 ± 46	
	Active amplification enhanced	123 ±16	
•	Sound-evoked nerve potentials reduced Active amplification enhanced	264 ± 37	
:	Sound-sensitivity diminished Active amplification reduced	324 ± 30	
•	Sound-evoked nerve potentials reduced	617 ± 24	
:	Sound-sensitivity diminished Active amplification lost		
•	Active amplification reduced	266 ± 20	

Sound-evoked nerve potentials lost

Sound-evoked nerve potentials lost

Sound-evoked nerve potentials lost

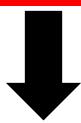
Eberl et al., 2000

Dubruille et al. 2002

Dong et al., 2002, 2003

But what about other Species?

We can find gene orthologs across species experimentally



Test for differences in amino acid sequence that result in differences in protein structure, and potentially function

However

Large number of genes and species = very time consuming

Sequence Alignment

Histone H1 (residues 120-180)



Sequence Alignment

Histone H1 (residues 120-180)



- •Sequence alignment is a method of comparing two or more biological sequences (such as DNA, RNA, or protein sequences) to find regions of similarity.
- Similarity often indicates evolutionary relationships or shared functions.

Sequence Alignment

Histone H1 (residues 120-180)

HUMAN KKASKPKKAASKAPTKKPKATPVKKAKKKLAATPKKAKKPKTVKAKPVKASKPKKAKPVK CHIMP KKASKPKKAASKAPTKKPKATPVKKAKKKLAATPKKAKKPKTVKAKPVKASKPKKAKPVK MOUSE KKAAKP KASKPKKAKTVK

RAT KKAAKP COW KKAAKP

NON-CONSERVED **AMINO ACIDS**

We can therefore look for amino sequence alignments for the same proteins across different species to find conserved proteins which are important for hearing function

Sequence alignm

sequences (such as DNA, RNA, or protein sequences) to find regions of similarity.

 Similarity often indicates evolutionary relationships or shared functions.

KASKPKKAKPVK

ore biological

So how can we do this?

We can use BLAST

What is BLAST?

BLAST

Basic Local Alignment Search Tool



Types of BLAST

- 1. BLASTN: Compares nucleotide query sequences to nucleotide databases.
- 2. BLASTP: Compares protein query sequences to protein databases.
- **3. BLASTX:** Translates a nucleotide query into six reading frames and compares it to a protein database.
- **4. TBLASTN:** Compares a protein query to a nucleotide database by translating the nucleotide sequences into six reading frames.
- **5. TBLASTX:** Translates a nucleotide query into six reading frames and compares it to a nucleotide database.

Types of BLAST

- 1. BLASTN: Compares nucleotide query sequences to nucleotide databases.
- 2. BLASTP: Compares protein query sequences to protein databases.
- **3. BLASTX:** Translates a nucleotide query into six reading frames and compares it to a protein database.
- **4. TBLASTN:** Compares a protein query to a nucleotide database by translating the nucleotide sequences into six reading frames.
- **5. TBLASTX:** Translates a nucleotide query into six reading frames and compares it to a nucleotide database.

Types of BLAST

1. BLASTN: Compares nucleotide query sequences to nucleotide databases.

2. BLASTP: Cor

3. BLASTX: Tra

compares it

4. TBLASTN: Co

translating t

5. TBLASTX: Tr

We can use proteins known to be related to hearing function (e.g., the 'ato' gene in *D. melanogaster*) as a query sequence and compare them against sequences from other species to identify similarities or conserved functions.

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5.

nes and

compares it to a nucleotide database.

How does BLAST work?

BLAST works by comparing a query sequence to a sequence database to identify regions of similarity. It uses a heuristic method to speed up the search for matching sequences, making the process faster and more efficient.

Heuristic: A problem-solving method that uses practical, approximate rules to find solutions more quickly, rather than searching for the perfect or optimal solution. For example, using a trial-and-error method. (発見的な, 試行錯誤による)

Step 1: Seeding

The first step involves creating a lookup table or word list from the query sequence. BLAST breaks the query into short segments, called words. For protein sequences, each word is typically three amino acids long.

```
Words (Protein)
                    Setup
       GTQITVEDLFYNIATRRKALKN
Query:
       GTQ
        TQI
          QIT
                      Neighborhood Words
                      LTV, MTV, ISV, LSV, etc.
           ITV
            TVE
              VED
               EDL
                DLF
```

Step 2: The second step is to search a database of known sequences to find any sequences that contain the same words as the query sequence. This is done to identify database sequences containing the matching words.

Database sequence:

Neighborhood words:

SEI

YYN

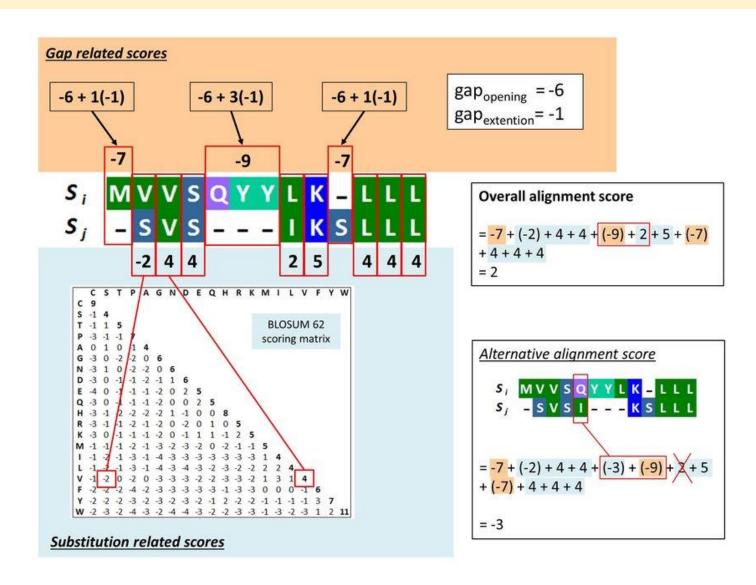
two matches - within 40 residues

Step 3: BLAST assigns a score to the similarity of the matching words using a substitution matrix. This matrix helps determine how closely the words match. If the score exceeds a certain threshold, the match is considered valid.

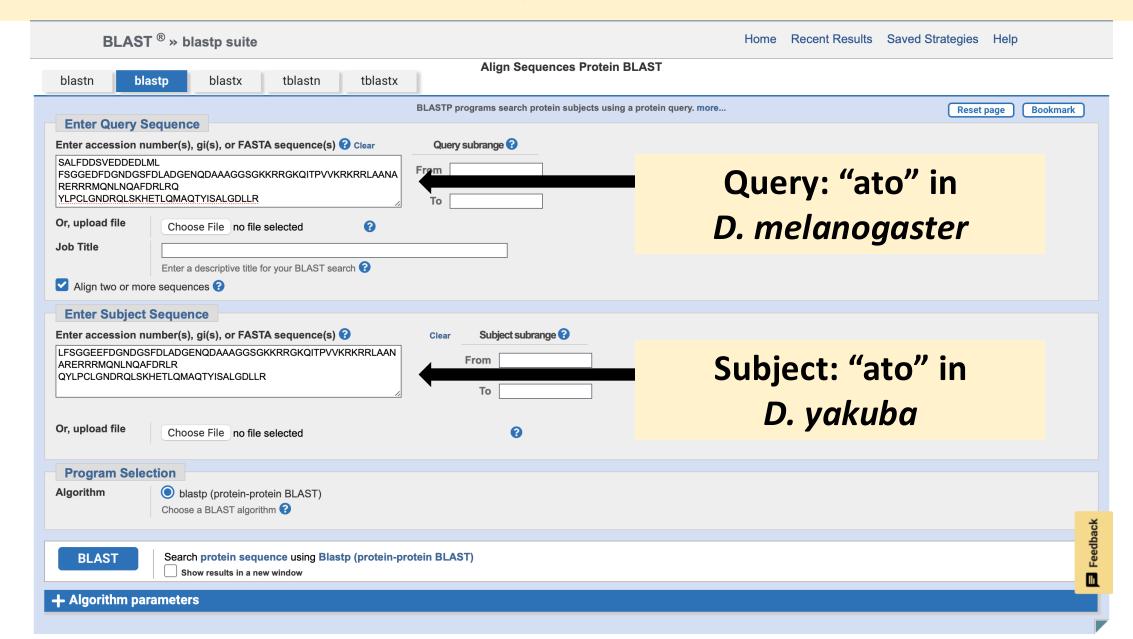
A **substitution matrix** scores how well two sequences match at each position, assigning higher scores for similar characters. In BLAST, it helps determine if matching words are significant enough to extend for further alignment.

	С	S	Т	Α	G	Р	D	Е	Q	N	Н	R	K	M	I	L	ν	W	Υ	F	
C	9																				C
S	-1	4																			S
т	-1	1	5																		Т
Α	Θ	1	0	4																	Α
G	-3	0	-2	Θ	6																G
P	-3	-1	-1	-1	-2	7															P
D	-3	0	-1	-2	-1	-1	6														D
Е	-4	0	-1	-1	-2	-1	2	5													Е
Q	-3	Θ	-1	-1	-2	-1	Θ	2	5												Q
N	-3	1	0	-2	0	-2	1	0	Θ	6											N
Н	-3	-1	-2	-2	-2	-2	-1	0	Θ	1	8										Н
R	-3	-1	-1	-1	-2	-2	-2	0	1	Θ	0	5									R
R K	-3	Θ	-1	-1	-2	-1	-1	1	1	Θ	-1	2	5								K
M	-1	-1	-1	-1	-3	-2	-3	-2	Θ	-2	-2	-1	-1	5							М
I	-1	-2	-1	-1	-4	-3	-3	-3	-3	-3	-3	-3	-3	1	4						I
L	-1	-2	-1	-1	-4	-3	-4	-3	-2	-3	-3	-2	-2	2	2	4					L
٧	-1	-2	0	θ	-3	-2	-3	-2	-2	-3	-3	-3	-2	1	3	1	4				٧
W	-2	-3	-2	-3	-2	-4	-4	-3	-2	-4	-2	-3	-3	-1	-3	-2	-3	11			W
Υ	-2	-2	-2	-2	-3	-3	-3	-2	-1	-2	2	-2	-2	-1	-1	-1	-1	2	7		Υ
F	-2	-2	-2	-2	-3	-4	-3	-3	-3	-3	-1	-3	-3	0	Θ	0	-1	1	3	6	F
	С	S	Т	Α	G	P	D	Е	Q	N	Н	R	K	М	I	L	٧	W	Υ	F	\sqcap

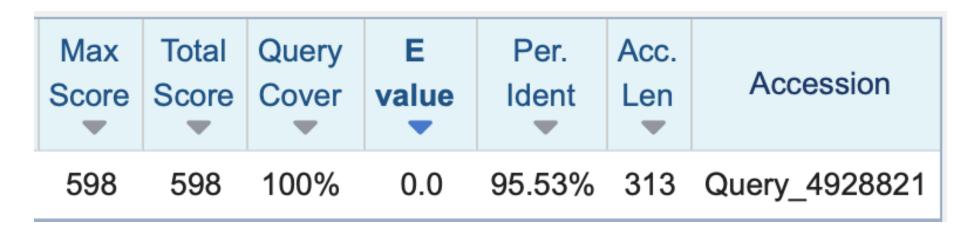
Step 4: Next, BLAST performs a pairwise alignment by extending the matching words in both directions, calculating the alignment score with the same substitution matrix. If the score falls below a certain threshold due to differences or mismatches, the alignment stops. The resulting aligned region, with no gaps, is called the high-scoring segment pair (HSP).



Using BLASTp



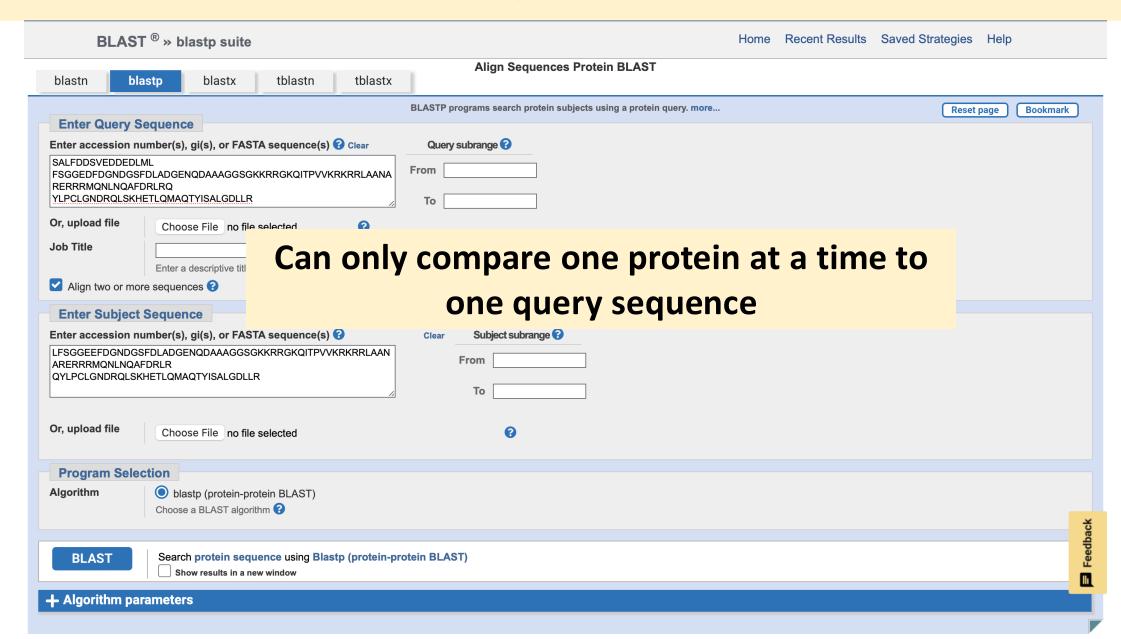
BLASTp output



E-value: The Expectation Value represents the number of hits with a similar or better score that would be expected by chance in a database of a given size. A lower E-value (e.g., 0.0) indicates a highly significant match, while a higher E-value suggests the match could be due to random chance.

Percent Identity (Per. Identity): This is the percentage of positions where the query sequence and the subject sequence have identical residues (amino acids). A higher percent identity indicates a stronger, more exact match, suggesting closer evolutionary or functional similarity between the sequences.

Using BLASTp



Genes related to hearing in *D. melanogaster*

Drosophila gene name	Drosophila gene name
ato (atonal)	Arr2 (Arrestin 2)
btv (beethoven)	Bmcp
ck (crinkled)	bw (brown)
plp (pericentrin-like protein), formerly cp309	Cam (Calmodulin)
ct (cut)	tous (testes of unsual size), formerly CG4329
DCX-EMAP (Doublecortin-domain-containing echinoderm-microtubule-associated protein)	Dnai2 (dynein, axonemal, intermediate chain 2), formerly, CG6053
dia (dia phanous)	CG8086
Eb1	CG9313
f (forked)	Dhc1 (Dynein heavy chain 1)
iav (inactive)	Zmynd10 (Zinc finger MYND-type containing 10)
Kap3 (Kinesin associated protein 3)	sosie
Klp64D (Kinesin-like protein at 64D)	CG14921
nan (nanchung)	Dhc36C (Dynein heavy chain at 36C)
nompA (no mechanoreceptor potential A)	Dhc93AB (Dynein heavy chain at 93AB)
nompB (no mechanoreceptor potential B)	gl (glass)
nompC (no mechanoreceptor potential C)	Ir75a (Ionotropic receptor 75a)
rempA (reduced mechanoreceptor potential A)	rdgA (retinal degeneration A)
Rfx	Rh5 (Rhodopsin 5)
tilB (touch insensitive larva B)	Rh6 (Rhodopsin 6)
tko (technical knockout)	sei (seizure)
Tmhs (Tetraspan membrane protein in hair cell stereocilia)	stops (slow termination of phototransduction)
eys (eyes shut)	trp (transient receptor potential)
Ank2 (Ankyrin 2)	trpl (transient receptor potential-like)
scaf (scarface), previously santa-maria	wtrw (water witch)

Genes related to hearing in *D. melanogaster*

	Drosophila gene name	Drosophila gene name					
ato (atonal)		Arr2 (Arrestin 2)					
btv (beethoven)		Втср					
ck (crinkled)		bw (brown)					
plp (pericentrin-like protein), formerly cp309	Cam (Calmodulin)					
ct (cut)		tous (testes of unsual size), formerly CG4329					
DCX-EMAP (Doublecortin-de	omain-containing echinoderm-microtubule-associated protein)	Dnai2 (dynein, axonemal, intermediate chain 2), formerly, CG6053					
dia (diaphanous)		CG8086					
Eb1		CG9313					
f (forked)							
iav (inactive)	We are looking	g at 48 genes					
Kap3 (Kinesin associated pr							
Klp64D (Kinesin-like protein	at 64D)	CG14921					
nan (nanchung)		Dhc36C (Dynein heavy chain at 36C)					
nompA (no mechanorecept	or potential A)	Dhc93AB (Dynein heavy chain at 93AB)					
nompB (no mechanorecept	or potential B)	gl (glass)					
nompC (no mechanorecept	or potential C)	Ir75a (Ionotropic receptor 75a)					
rempA (reduced mechanore	eceptor potential A)	rdgA (retinal degeneration A)					
Rfx		Rh5 (Rhodopsin 5)					
tilB (touch insensitive larva	В)	Rh6 (Rhodopsin 6)					
tko (technical knockout)		sei (seizure)					
Tmhs (Tetraspan membrane	e protein in hair cell stereocilia)	stops (slow termination of phototransduction)					
eys (eyes shut)		trp (transient receptor potential)					
Ank2 (Ankyrin 2)		trpl (transient receptor potential-like)					
scaf (scarface), previously sa	anta-maria	wtrw (water witch)					

Problems with online BLAST

D. simulans D. mauritania D. melanogaster D. teissieri D.yakuba D. erecta D. ananassae

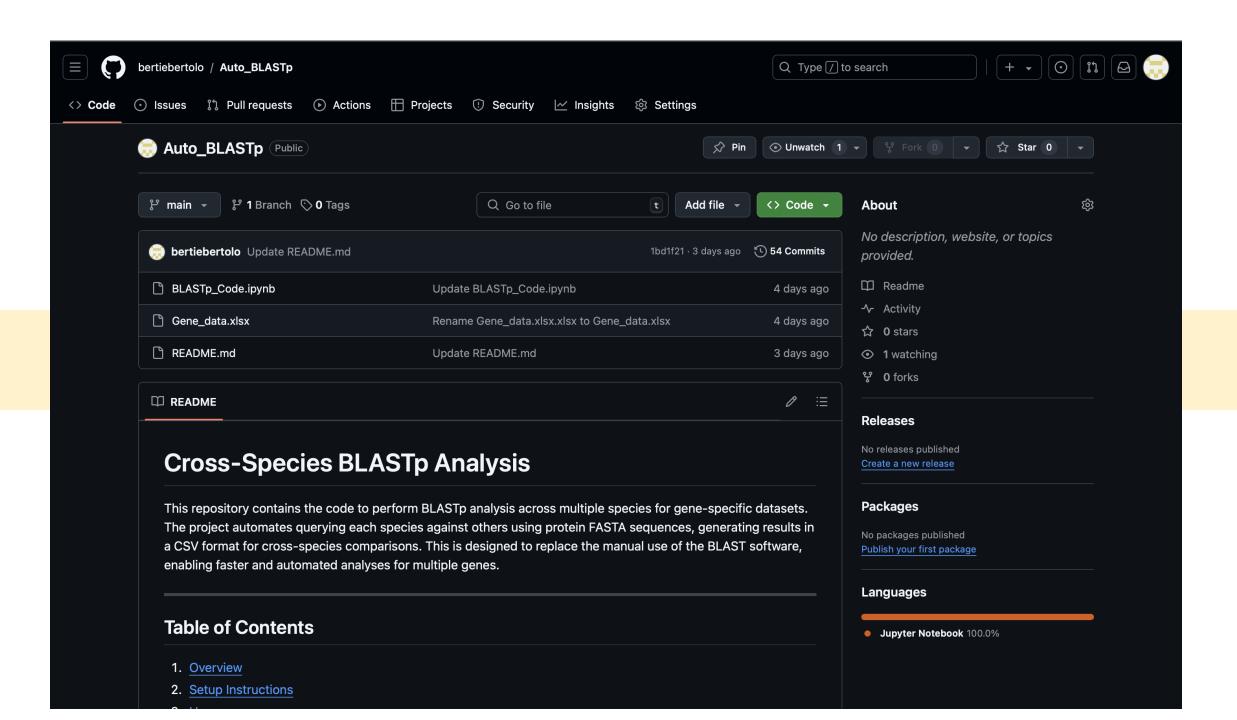


We are looking to use BLAST on 48 proteins comparing *D. melanogaster* to 6 species, and often a species has multiple isoforms of one protein



Using usual software would just take too long, would have to repeat over 288 times

Introducing AutoBLASTp



Cross-Species BLASTp Analysis

This repository contains the code to perform BLASTp analysis across multiple species for gene-specific datasets. The project automates querying each species against others using protein FASTA sequences, generating results in a CSV format for cross-species comparisons. This is designed to replace the manual use of the BLAST software, enabling faster and automated analyses for multiple genes.

Normal BLASTp vs AutoBLAST

Normal BLASTp

Search the amino acid sequence for the query and subject on the NCBI website



Input protein sequences manually



Performs cross-species BLAST between these two species for this protein

Repeat for all species and genes

Normal BLASTp vs AutoBLAST

Repeat

Normal BLASTp

Search the amino acid sequence for the query and subject on the NCBI website



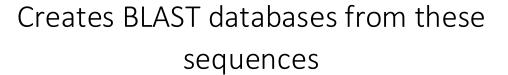
Input protein sequences manually



Performs cross-species BLAST between these two species for this protein

AutoBLASTp

Searches for and downloads protein sequences in FASTA format from the NCBI database





Performs cross-species BLAST from an inputted species against all other species in the data for all proteins

Gene name	Gene ID	Species
ato (atonal)	LOC6501111	Drosophila ananassae
ato (atonal)	LOC6552921	Drosophila erecta
ato (atonal)	LOC117143303	Drosophila mauritiana
ato (atonal)	ato (atonal)	Drosophila melanogaster
ato (atonal)	LOC6728957	Drosophila simulans
ato (atonal)	LOC122621719	Drosophila teissieri
ato (atonal)	LOC6536187	Drosophila yakuba
btv (beethoven)		6497899 Drosophila ananassae
btv (beethoven)		6549278 Drosophila erecta
btv (beethoven)		117138104 Drosophila mauritiana
btv (beethoven)	btv	Drosophila melanogaster
btv (beethoven)		6732637 Drosophila simulans
btv (beethoven)		122613759 Drosophila teissieri
btv (beethoven)		6529435 Drosophila yakuba
ck (crinkled)	LOC6497810	Drosophila ananassae
ck (crinkled)	LOC6543016	Drosophila erecta
ck (crinkled)	LOC117147720	Drosophila mauritiana
ck (crinkled)	ck (crinkled)	Drosophila melanogaster
ck (crinkled)	LOC6732390	Drosophila simulans
ck (crinkled)	LOC122615024	Drosophila teissieri
ck (crinkled)	LOC6529039	Drosophila yakuba

Gene name	Gene ID	Species
ato (atonal)	LOC6501111	Drosophila ananassae
ato (atonal)	LOC6552921	Drosophila erecta
ato (atonal)	LOC117143303	Drosophila mauritiana
ato (atonal)	ato (atonal)	Drosophila melanogaster
ato (atonal)	LOC6728957	Drosophila simulans
ato (atonal)	LOC122621719	Drosophila teissieri

Gene ID is best to use! Gene name can work but for most species, but gene ID is best for finding the protein data from the NCBI dataset

ck (crinkled)	LOC6497810	Drosophila ananassae
ck (crinkled)	LOC6543016	Drosophila erecta
ck (crinkled)	LOC117147720	Drosophila mauritiana
ck (crinkled)	ck (crinkled)	Drosophila melanogaster
ck (crinkled)	LOC6732390	Drosophila simulans
ck (crinkled)	LOC122615024	Drosophila teissieri
ck (crinkled)	LOC6529039	Drosophila yakuba

nompB no mechanoreceptor potential B [Drosophila melanogaster (fruit fly)] nompB intraflagellar transport protein 88-like protein nompB [Drosophila yakuba]

Gene ID: 35414, updated on 2-Nov-2024

Summary

Official Symbol nompB provided by FlyBase

Official Full Name no mechanoreceptor potential B provided by FlyBase

Primary source FLYBASE:FBgn0016919

Locus tag Dmel CG12548

See related AllianceGenome:FB:FBgn0016919

Gene type protein coding
RefSeg status REVIEWED

Organism Drosophila melanogaster

Lineage Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera;

Ephydroidea; Drosophilidae; Drosophila; Sophophora

Also known as 146590_s_at; CG12548; CG14465; CG15190; CG4137; Dmel\CG12548; IFT88; nomp;

Summary Predicted to enable kinesin binding activity. Involved in intraciliary transport; non-motile

in non-motile cilium. Orthologous to human IFT88 (intraflagellar transport 88). [provided

Orthologs all

Try the new Gene table

Try the new Transcript table

Summary

Gene symbol nompB

Gene ID: 6529209, updated on 15-May-2024

Gene description intraflagellar transport protein 88-like protein nompB

Locus tag Dyak GE12986

See related EnsemblRapid:LOC6529209

Gene type protein coding

RefSeq status MODEL

NEW

Organism Drosophila yakuba

Lineage Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopte

Ephydroidea; Drosophila; Sophophora

Also known as GE12986; GE12986-PB; GE12986-PC

Orthologs fruit fly all

Try the new Gene table

Try the new <u>Transcript table</u>

nompB no mechanoreceptor potential B [Drosophila melanogaster (fruit fly)] nompB intraflagellar transport protein 88-like protein nompB [Drosophila yakuba]

Summary

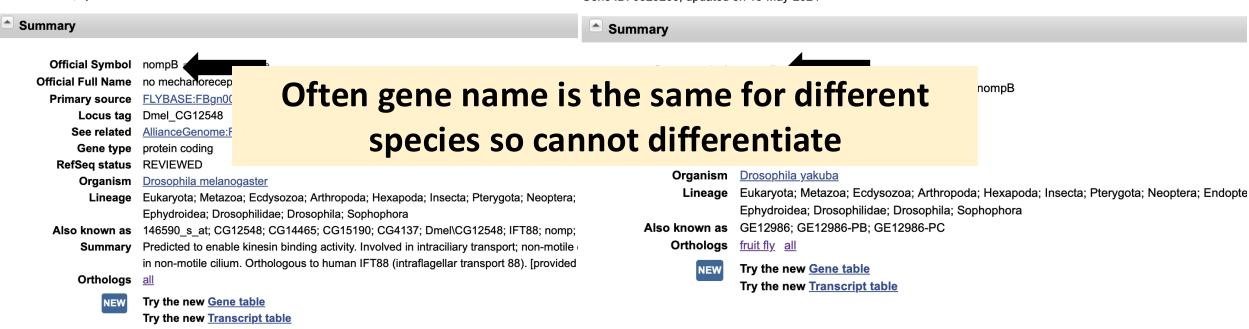
Gene ID: 35414, updated on 2-Nov-2024

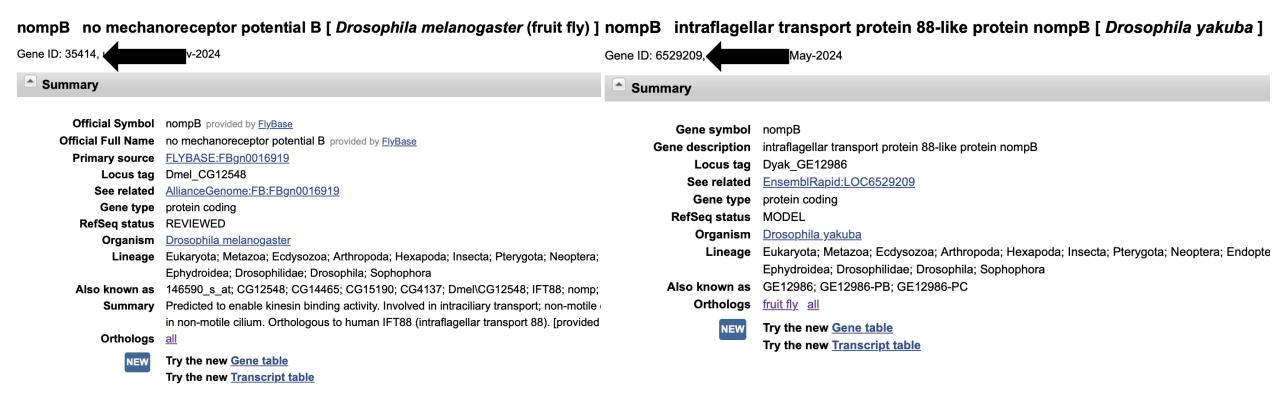


Gene symbol nompB Gene description intraflagellar transport protein 88-like protein nompB Locus tag Dyak GE12986 See related EnsemblRapid:LOC6529209 Gene type protein coding RefSeg status MODEL Organism Drosophila yakuba Lineage Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopte Ephydroidea; Drosophila; Sophophora Also known as GE12986; GE12986-PB; GE12986-PC Orthologs fruit fly all NEW Try the new Gene table Try the new Transcript table

nompB no mechanoreceptor potential B [Drosophila melanogaster (fruit fly)] nompB intraflagellar transport protein 88-like protein nompB [Drosophila yakuba]

Gene ID: 35414, updated on 2-Nov-2024 Gene ID: 6529209, updated on 15-May-2024





nompB no mechanoreceptor potential B [Drosophila melanogaster (fruit fly)] nompB intraflagellar transport protein 88-like protein nompB [Drosophila yakuba] Gene ID: 35414, v-2024 Gene ID: 6529209, May-2024 Summary Summary Official Symbol nompB provided by FlyRasa Official Full Name no mechanorecep Gene ID is always unique to each species and nompB Primary source FLYBASE:FBgn00 Locus tag Dmel CG12548 See related AllianceGenome:F gene, so best to use gene ID Gene type protein coding RefSeq status REVIEWED Organism Drosophila yakuba Organism Drosophila melanogaster Lineage Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopte Lineage Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Ephydroidea; Drosophila; Sophophora Ephydroidea; Drosophilidae; Drosophila; Sophophora Also known as GE12986; GE12986-PB; GE12986-PC **Also known as** 146590 s at; CG12548; CG14465; CG15190; CG4137; Dmel\CG12548; IFT88; nomp; Orthologs fruit fly all **Summary** Predicted to enable kinesin binding activity. Involved in intraciliary transport; non-motile in non-motile cilium. Orthologous to human IFT88 (intraflagellar transport 88). [provided NEW Try the new Gene table Orthologs all

Try the new <u>Gene table</u>
Try the new <u>Transcript table</u>

Try the new Transcript table

Output example

Query ID	Subject ID	% Identity	Alignment Length	Mismatche s	Gap Opens	Query Start	Query End	Subject Start	Subject End	E-value	Bit Score	Target Species
sp P48987.2 ATO_DROM E	XP_043655611. 1	96.497	314	9	2	1	312	1	314	0.0	623	Drosophila_teissieri
NP_731223.1	XP_043655611. 1	96.497	314	9	2	1	312	1	314	0.0	623	Drosophila_teissieri
AAF54209.1	XP_043655611. 1	96.497	314	9	2	1	312	1	314	0.0	623	Drosophila_teissieri
sp P48987.2 ATO_DROM E	XP_002096778. 1	95.527	313	13	1	1	312	1	313	0.0	598	Drosophila_yakuba
NP_731223.1	XP_002096778. 1	95.527	313	13	1	1	312	1	313	0.0	598	Drosophila_yakuba
AAF54209.1	XP_002096778. 1	95.527	313	13	1	1	312	1	313	0.0	598	Drosophila_yakuba
sp P48987.2 ATO_DROM E	XP_032312302. 1	77.301	326	44	6	1	312	1	310	4.9E- 170	462	Drosophila_ananassa e
NP_731223.1	XP_032312302. 1	77.301	326	44	6	1	312	1	310	4.9E- 170	462	Drosophila_ananassa e
AAF54209.1	XP_032312302. 1	77.301	326	44	6	1	312	1	310	4.9E- 170	462	Drosophila_ananassa e
sp P48987.2 ATO_DROM E	XP_001980994. 1	95.556	315	11	1	1	312	1	315	0.0	619	Drosophila_erecta
NP_731223.1	XP_001980994. 1	95.556	315	11	1	1	312	1	315	0.0	619	Drosophila_erecta
AAF54209.1	XP_001980994. 1	95.556	315	11	1	1	312	1	315	0.0	619	Drosophila_erecta
sp P48987.2 ATO_DROM E	XP_016035637. 1	97.115	312	8	1	1	312	1	311	0.0	626	Drosophila_simulans
NP_731223.1	XP_016035637. 1	97.115	312	8	1	1	312	1	311	0.0	626	Drosophila_simulans

Thresholds used

In some cases, multiple sections of the same subject sequence were analysed

Query ID	_	% Identity	Alignment Length	Mismatches	Gap Opens	Query Start	Query End	Subject Start	Subject End	E-value	Bit Score	Target Species
NP_001401034 .1	XP_043648147 .1	96.566	2417	72	2	153	2567	3	2410	0.0	4820. 0	Drosophila_teissieri
NP_001401034 .1	XP_043648147 .1	95.438	1666	65	5	2721	4382	11705	13363	0.0	2953. 0	Drosophila_teissieri
NP_001401033 .1	XP_043648147 .1	95.536	2442	67	3	16	2455	9	2410	0.0	4814. 0	Drosophila_teissieri
NP_001401033 .1	XP_043648147 .1	94.121	1939	86	7	2444	4361	11432	13363	0.0	3348. 0	Drosophila_teissieri

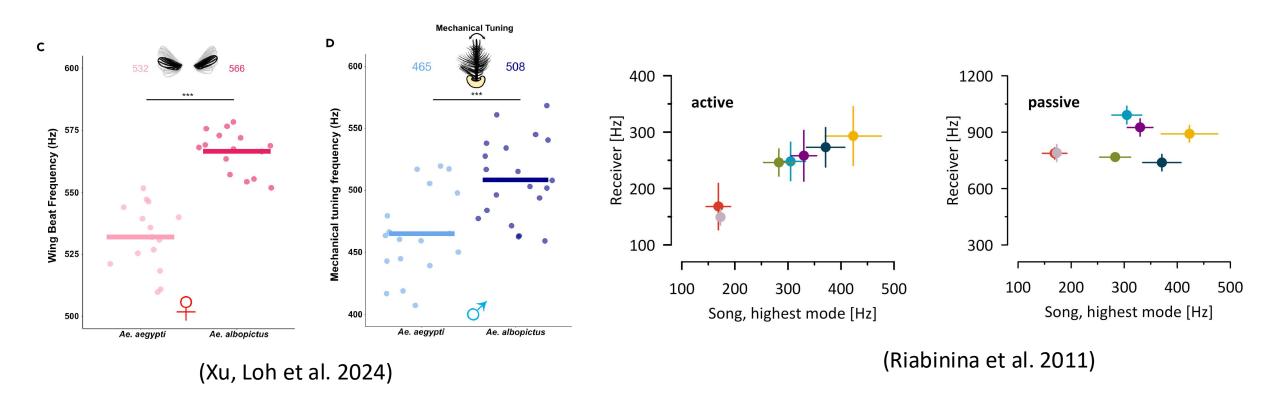
Thresholds used

In some cases, multiple sections of the same subject sequence were analysed

Query ID	Subject ID	% Identity	Alignment Length	Mismatches	Gap Opens	Query Start	Query End	Subject Start	Subject End	E-value	Bit Score	Target Species
NP_001401034 .1	1.1 anginitette, a timesitata of 7070 was implemented											
NP_001401034 .1	and for the e-value a threshold of 0.001 This was implemented since some of these sections											Drosophila_teissieri
NP_001401033 .1	xP_0436 were irrelevant.											Drosophila_teissieri
NP_001401033 .1	XP_043648147 .1	94.121	1939	86	7	2444	4361	11432	13363	0.0	3348. 0	Drosophila_teissieri

Conclusion - How can this be used in the future

Species-Specific Hearing: *Drosophila* and mosquito species exhibit unique hearing functions and frequency sensitivities.



Interspecific differences in WBFs and tuning

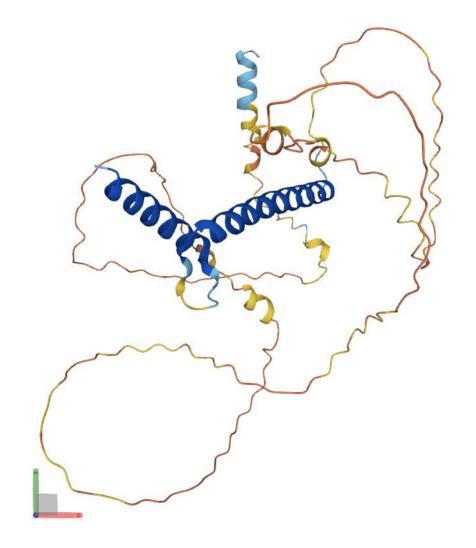
Protein Variations: Differences in proteins related to hearing may account for these differences.

AutoBLASTp Analysis: Comparing amino acid sequences using AutoBLASTp can reveal key differences in auditory proteins.

Query ID	Subject ID	% Identity		Mismatch es	Gap Opens	Query Start		Subject Start	Subject End	E- value	Bit Score	Target Species
sp P48987.2 ATO_DRO ME	XP_04365561 1.1	96.497	314	9	2	1	312	1	314	0.0	623	Drosophila_teissieri
NP_731223.1	XP_04365561 1.1	96.497	314	9	2	1	312	1	314	0.0	623	Drosophila_teissieri
AAF54209.1	XP_04365561 1.1	96.497	314	9	2	1	312	1	314	0.0	623	Drosophila_teissieri
sp P48987.2 ATO_DRO ME	XP_00209677 8.1	95.527	313	13	1	1	312	1	313	0.0	598	Drosophila_yakuba

Interspecific differences in WBFs and tuning

Structural Implications: Variations in amino acid sequences could result in distinct 3D protein structures. Tools like AlphaFold can help visualize these differences.



Full protocol and code (Work in Progress)

