

# Identification and bioinformatic analysis of neprilysin and neprilysin-like metalloendopeptidases in *Drosophila melanogaster*

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## Abstract

The neprilysin (M13) family of metalloendopeptidases comprises highly conserved ectoenzymes that cleave and thereby inactivate many physiologically relevant peptides in the extracellular space. Impaired neprilysin activity is associated with numerous human diseases. Here, we present a comprehensive list and classification of M13 family members in *Drosophila melanogaster*. Seven *Neprilysin (Nep)* genes encode active peptidases, while 21 *Neprilysin-like (NepI)* genes encode proteins predicted to be catalytically inactive. RNAseq data demonstrate that all 28 genes are expressed during development, often in a tissue-specific pattern. Most *Nep* proteins possess a transmembrane domain, whereas almost all *NepI* proteins are predicted to be secreted.

Symbol	CG #	Genomic location	Expression												Motifs					Refs						
			E	L	PP	P	M	F	Br	Fb	Ht	Ts	Sp	SP	TM	NAY/FY	HExxH	ENIADxGG	CxxW							
Nep1	CG5905	X:5D4-5																	✓	NAFY	HEITH	ENIADNGG	CSVW	1-3		
Nep2	CG9761	3R:82D2																	✓	NAFY	HEITH	ENIADNGG	CEVW	1-6		
Nep3	CG9565	X:19A3																	✓	NAYY	HELTH	ENIADNGG	CEVW	1-3		
Nep4	CG4058	3R:92F4-5																	✓	✓	NAYY	HELTH	ENIADNGG	CEVW	1-3, 7-9	
Nep5	CG6265	3R:97E1																	✓	NAFH	HELTH	ENIADNGG	CRIW	1-3		
Nep6	CG3775	X:11C2																	✓	NAYY	HEMVH	ENIADTEG	CHIW	2		
Nep7	CG5527	3R:98B6																	✓	NAFY	HELTH	ENIADAGG	CRMW	1-2		
frma	CG3239	X:5A1																	✓	-	HELSH	-	-	2, 10		
goe	CG9634	X:15A3-5																		✓	-	-	-	-	1-2, 11	
NepI3	CG31918	2L:25C3																		✓	-	-	-	-	2	
NepI4	CG9505	2L:26C4																		✓	-	HEIMH	-	CPFW	2	
NepI5	CG9507	2L:26C4																		✓	-	HELAH	-	CRIW	2	
NepI6	CG42370	2L:26C4-D1																		✓	-	HELMH	-	CQLW	2	
NepI7	CG15485	2L:33F2																		✓	NAYY	HEMAH	-	CVVW	1	
NepI8	CG4580	2L:36A2																		✓	-	-	-	-	2	
NepI9	CG13283	2L:36B2																		✓	-	-	-	-		
NepI10	CG8550	2R:49A7																		✓	-	HEMNH	-	-	2	
NepI11	CG9780	3R:82A1																		✓	-	-	-	-	2	
NepI12	CG8358	3R:85E3																		✓	-	HELIH	ENIADNSG	CRLW	1	
NepI13	CG4725	3R:94C4																		✓	-	-	-	-	1-2	
NepI14	CG4723	3R:94C4																		✓	-	-	-	-		
NepI15	CG4721	3R:94C4																		✓	-	-	-	-	1-2, 12-13	
NepI16	CG13650	3R:96C1																		✓	-	-	-	-	2	
NepI17	CG14529	3R:98F1																		✓	✓	-	HEMAH	-	-	1-2
NepI18	CG14528	3R:98F1																		✓	-	HEMLH	ENIADSGG	-	1-2	
NepI19	CG14523	3R:98F1																		✓	-	-	ENIADNLA	-	2	
NepI20	CG14527	3R:98F1																		✓	-	HELIH	ENIADNGG	-	1-2	
NepI21	CG14526	3R:98F1																		✓	-	HELIH	ENIADNGG	-	1-2	

**Table 1. Genes encoding *Drosophila melanogaster* neprilysins and neprilysin-like metalloendopeptidases.:** Symbol: symbol of the *Drosophila* gene in FlyBase; CG #: gene model annotation ID; Genomic location: chromosome scaffold and

FlyBase-computed cytological location of the gene; Expression: heat-map representation of expression levels throughout development (yellow/red scale; embryos (E), larvae (L), prepupae (PP), pupae (P), adult males (M) and adult females (F)) and in adult tissues (green scale; brain/CNS (Br), fat body (Fb), heart (Ht), testis (Ts) and spermatheca (Sp)), where white represents undetectable expression; Motifs: presence of a signal peptide (SP) or a single transmembrane domain (TM) is indicated, together with the amino acid sequence (if present) of each of the four conserved sequence motifs required for catalytic activity; Refs: reference(s) identifying/characterizing the *Drosophila* gene/protein: 1) Bland *et al.*, 2008, 2) Sitnik *et al.*, 2014, 3) Meyer *et al.*, 2011, 4) Thomas *et al.*, 2005, 5) Bland *et al.*, 2007, 6) Bland *et al.*, 2009, 7) Meyer *et al.*, 2009, 8) Panz *et al.*, 2012, 9) Hallier *et al.*, 2016, 10) Findlay *et al.*, 2014, 11) Matsuoka *et al.*, 2014, 12) Nfonsam *et al.*, 2012, 13) Banerjee *et al.*, 2021.

## Description

Neprilysins belong to the family of M13 metalloendopeptidases and constitute highly conserved ectoenzymes that cleave and thereby inactivate numerous physiologically relevant peptides in the extracellular space. While the vast majority of these enzymes appear to be membrane-bound, some family members have been identified as soluble secreted proteins (Turner *et al.*, 2001). In humans, seven members of the M13 family are known, namely Neprilysin (NEP), endothelin-converting enzymes (ECE1, ECE2), ECEL1, MMEL1, the KELL blood-group protein and PHEX (Turner and Tanzawa 1997). Among these, NEP is characterized best, with identified substrates including endothelins, angiotensins I and II, enkephalins, bradykinin, atrial natriuretic peptide, substance P and the amyloid-beta peptide (Turner *et al.*, 2001, Nalivaeva *et al.*, 2020). NEP-mediated hydrolysis is critical to maintain the physiological homeostasis of these peptides, and thus represents a prerequisite for proper endocrine signal transmission. Accordingly, impaired neprilysin activity in humans is involved in the pathogenesis of numerous diseases, including hypertension (Molinaro *et al.*, 2002), analgesia (Whitworth 2003), cancer (Turner *et al.*, 2001) and Alzheimer's disease (Iwata *et al.*, 2000, Belyaev *et al.*, 2009). Clinical trials have confirmed the therapeutic potential of modulating neprilysin activity (Jessup 2014).

Previous analyses of the *Drosophila melanogaster* (hereafter, '*Drosophila*') genome have identified up to 24 genes encoding M13 family members (Coates *et al.*, 2000, Isaac *et al.*, 2000, Bland *et al.*, 2008, Sitnik *et al.*, 2014). Five of these (*Nep1–Nep5*) are thought to encode catalytically active neprilysins. However, this has so far been demonstrated only for *Nep2* and *Nep4* (Thomas *et al.*, 2005, Bland *et al.*, 2007, Meyer *et al.*, 2009, Hallier *et al.*, 2016), and *in vivo* substrates are known only for *Nep4* (Hallier *et al.*, 2016). *Nep2* is involved in the regulation of locomotion and geotactic behavior (Bland *et al.*, 2009) and is required for early embryonic development (Sitnik *et al.*, 2014). *Nep4* is implicated in sustaining muscle integrity (Panz *et al.*, 2012) and controls insulin signaling and feeding behavior (Hallier *et al.*, 2016). Neprilysin activity in general appears to be critical to the formation of middle- and long-term memory (Turrel *et al.*, 2016), reproduction (Sitnik *et al.*, 2014) and regulation of pigment dispersing factor signaling within circadian neural circuits (Isaac *et al.*, 2007). Significantly, increased expression of *Nep1* or *Nep2* ameliorates the detrimental effects of amyloid-beta peptide overexpression in *Drosophila* models of Alzheimer's disease (Finelli *et al.*, 2004, Cao *et al.*, 2008, Sofola-Adesakin *et al.*, 2016, Turrel *et al.*, 2017, Turrel *et al.*, 2020). Other *Drosophila* M13 members lack key catalytic residues and are therefore predicted to be inactive or have non-enzymatic functions (Bland *et al.*, 2008, Sitnik *et al.*, 2014). These 'neprilysin-like' proteins include: *Fra mauro* (*Frma*), which is involved in sex peptide responses and is required for female remating receptivity and fertility (Findlay *et al.*, 2014); *Gone early* (*Goe*), which functions in the ovary to limit the number of germline stem cells (Matsuoka *et al.*, 2014); and *CG4721*, which plays a role in eye development and is also involved in lipid and carbohydrate storage (Nfonsam *et al.*, 2012, Banerjee *et al.*, 2021). While these studies have clearly advanced the current understanding of M13 family functionality in *Drosophila*, the overall physiological relevance of individual members is still far from being understood.

We aimed to generate a comprehensive and up-to-date list of *Drosophila* M13 family members and systematically assess evidence for their expression and functional activity. We applied a combination of literature review and bioinformatic analyses (see Methods) to identify a total of 28 *Drosophila* M13 genes, including two (*CG13283* and *CG4723*) that had not been identified in previous studies (Table 1). These were classified into seven neprilysin (*Nep*) and 21 neprilysin-like (*Nep1*) genes and named accordingly. *Nep* classification required the presence of four conserved sequence motifs in the encoded proteins that are critical to catalytic activity in vertebrate neprilysins: HExxH and ENIAD(xGG) represent zinc-binding domains, CxxW is critical to protein folding and maturation, and NAY/FY mediates substrate or inhibitor binding (Turner *et al.*, 2001, Sitnik *et al.*, 2014). The *Nep* genes comprise the previously named *Nep1*, *Nep2*, *Nep3*, *Nep4* and *Nep5* genes, together with *CG3775* (*Nep6*) and *CG5527* (*Nep7*). The 21 *Nep1*-genes encode proteins that exhibit significant similarity to neprilysins in their primary structure, but lack one or more of the motifs required for catalysis. The symbols of *frma* (*CG3239*) and *goe* (*CG9634*) have not been changed, but '*Nep11*' and '*Nep12*' have been added as respective synonyms to recognize the fact they were the first and second *Nep1* genes to be characterized. The remaining *Nep1* genes have been given a numerical suffix,

incremented based on their genomic location. The revised gene nomenclature has been incorporated into FlyBase (<https://flybase.org>, Larkin *et al.*, 2021).

It is evident that *Drosophila* has an expanded set of *Nep* and *Nepl* genes compared to mammals (Coates *et al.*, 2000, Bland *et al.*, 2008). The 28 *Drosophila* genes are distributed throughout the genome and are present on all major chromosome scaffolds except chromosome arm 3L (Table 1). Three distinct clusters of *Nepl* genes are evident. *Nepl4*, *Nepl5* and *Nepl6* are located in a 17.6 kb interval (also containing two other genes) at cytological position 26C4-D1 on 2L; *Nepl13*, *Nepl14* and *Nepl15* are arranged as tandem repeats in head-to-tail orientation in a 7.4 kb interval at 94C4 on 3R; and *Nepl17*, *Nepl18*, *Nepl19*, *Nepl20* and *Nepl21* are arranged as tandem repeats in a 13.1 kb interval at 98F1 on 3R. These *Nepl* clusters are likely to be the result of local duplication events, consistent with previous phylogenetic analyses (Bland *et al.*, 2008, Sitnik *et al.*, 2014).

We analysed genome-wide RNAseq data (Graveley *et al.*, 2011, Leader *et al.*, 2018) to systematically examine evidence for *Nep* and *Nepl* gene expression. As summarized in Table 1, all 28 genes are expressed at some point during development (yellow/red heatmap) and exhibit tissue-specific expression in adults, notably within the brain/CNS, thoracoabdominal ganglion, fat body, heart and reproductive tracts (green heatmap). For the *Nep* genes, *Nep1-4* are expressed throughout development, with *Nep2* being the most highly expressed during the larval-pupal period, whereas *Nep5-7* are only detected at discrete stages. All *Nep* genes, except *Nep3*, are expressed in the male and/or female reproductive tract, with *Nep2* having particularly high expression in spermathecae. Most *Nep* genes are also expressed in the brain/CNS, while around half show expression in the fat body and/or heart. A similar pattern is seen for the *Nepl* genes: most are expressed at all developmental stages, though expression of *Nepl7* and *Nepl8* is undetectable/extremely low throughout development. *Nepl6* and *Nepl21* are notable for their high expression in prepupae, suggesting an important role during metamorphosis. Most *Nepl* genes are expressed in the spermatheca, while only two (*Nepl3* and *Nepl11*) are detectable in the testis. A major share is also expressed in the fat body and heart, and around half of the *Nepl* genes are expressed in the brain/CNS. Amongst the *Nepl* genes, *frma* is expressed at particularly high levels within the fat body and spermathecae. Overall, these expression data are consistent with previous reports (Thomas *et al.*, 2005, Bland *et al.*, 2007, Iijima-Ando *et al.*, 2008, Meyer *et al.*, 2009, Meyer *et al.*, 2011, Findlay *et al.*, 2014, Matsuoka *et al.*, 2014, Sitnik *et al.*, 2014, Banerjee *et al.*, 2021), and further demonstrate that all 28 *Nep* and *Nepl* genes are actively transcribed and therefore potentially functional, likely acting in a stage- and/or tissue-specific manner.

Finally, we examined *Nep/Nepl* protein sequences for evidence of a signal peptide or transmembrane domain that would indicate the proteins are secreted or membrane-localized, respectively (see Methods). Remarkably, two *Nep* and the majority (18) of *Nepl* proteins lack a predicted transmembrane domain and, instead, possess a predicted signal peptide suggesting that they are secreted (Table 1). Although *Nep2* is predicted to possess a transmembrane domain, experimental data indicate that it is secreted, presumably via proteolytic cleavage of a membrane-localized proprotein (Thomas *et al.*, 2005). *Nep4* is unique in encoding either a transmembrane or a secreted isoform as a result of alternative splicing (Meyer *et al.*, 2009), while *Nepl17* encodes a single isoform containing both a signal peptide and a transmembrane domain. One function of the secreted *Nepl* proteins may be to bind and sequester peptide targets of the catalytically active neprilysins. Such a biological role has already been suggested for *Nepl15* (Banerjee *et al.*, 2021) and could establish a novel facet of the neprilysin-mediated regulation of peptide homeostasis.

In summary, we have combined bioinformatic analyses with an evaluation of relevant publications to generate a comprehensive list and classification of genes encoding neprilysin and neprilysin-like proteins in *Drosophila*. The respective dataset has been compiled as a FlyBase gene group report (<https://flybase.org/reports/FBgg0000963.html>). These resources will support further research and understanding of the biological roles of *Nep* and *Nepl* proteins in flies. Identifying the physiological functions and substrates of this set of largely uncharacterized proteins in *Drosophila* may provide clinically relevant insights into neprilysin function in humans.

## Methods

[Request a detailed protocol](#)

Publications identifying/characterizing *Drosophila* neprilysins were identified using PubMed (<https://pubmed.ncbi.nlm.nih.gov>) and FlyBase (<https://flybase.org>, Larkin *et al.*, 2021). Previously published lists of *Drosophila* neprilysins were obtained from Bland *et al.*, 2008, Meyer *et al.*, 2011 and Sitnik *et al.*, 2014. *De novo* identification of *Drosophila* neprilysins was performed using three approaches: (i) searching FlyBase (FB2021\_02) for *Drosophila* proteins containing the InterPro signature “Peptidase M13 family (IPR000718)” (Blum *et al.*, 2021); (ii) identifying orthologs of human M13 peptidases (MME (aka NEP), MMEL1, ECE2, ECE1, KEL, PHEX, ECEL1) using the integrative ortholog prediction tool, DIOPT (v8.0) (Hu *et al.*, 2011) via FlyBase; (iii) querying the MEROPS database (release 12.3; <https://www.ebi.ac.uk/merops/>; Rawlings *et al.*, 2018) for *D. melanogaster* members of the M13 peptidase family. Gene

symbol and genomic location data were obtained from FlyBase (FB2021\_02). Developmental stage expression data are derived from the modENCODE developmental transcriptome RNAseq dataset (Graveley *et al.*, 2011), as implemented as heatmaps within FlyBase; Table 1 shows the mean expression levels for each major developmental stage. Adult tissue expression data and heatmaps are from FlyAtlas2 (<http://flyatlas.gla.ac.uk/FlyAtlas2/index.html>; Leader *et al.*, 2018). Male and female tissue-specific data were quantitatively and qualitatively similar, as were data for the brain/CNS and thoracoabdominal ganglion, and virgin and mated spermathecae; thus, only representative data for female tissues, brain/CNS and mated spermathecae are shown in Table 1. Relatively little *Nep* and *Nep1* expression is seen in the accessory gland or ovary, and so expression in those tissues is not reported in Table 1. Sequence analysis and motif identification was done using TMHMM Server v. 2.0 (<http://www.cbs.dtu.dk/services/TMHMM-2.0/>), SignalP-5.0 Server (<http://www.cbs.dtu.dk/services/SignalP-5.0/>) and Motif Scan ([https://myhits.sib.swiss/cgi-bin/motif\\_scan](https://myhits.sib.swiss/cgi-bin/motif_scan)) with all available motif databases being selected. In addition, all sequences were manually analyzed for the presence of respective motifs, combined with sequence alignments (<http://multalin.toulouse.inra.fr/multalin/>) to ensure proper motif localization.

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## References

- Banerjee S, Woods C, Burnett M, Park SJ, Ja WW, Curtiss J. 2021. The *Drosophila melanogaster* Neprilysin *Nep15* is involved in lipid and carbohydrate storage. *Sci Rep* 11: 2099. PMID: 33483521.
- Belyaev ND, Nalivaeva NN, Makova NZ, Turner AJ. 2009. Neprilysin gene expression requires binding of the amyloid precursor protein intracellular domain to its promoter: implications for Alzheimer disease. *EMBO Rep* 10: 94-100. PMID: 19057576.
- Bland ND, Thomas JE, Audsley N, Shirras AD, Turner AJ, Isaac RE. 2007. Expression of NEP2, a soluble neprilysin-like endopeptidase, during embryogenesis in *Drosophila melanogaster*. *Peptides* 28: 127-35. PMID: 17157960.
- Bland ND, Pinney JW, Thomas JE, Turner AJ, Isaac RE. 2008. Bioinformatic analysis of the neprilysin (M13) family of peptidases reveals complex evolutionary and functional relationships. *BMC Evol Biol* 8: 16. PMID: 18215274.
- Bland ND, Robinson P, Thomas JE, Shirras AD, Turner AJ, Isaac RE. 2009. Locomotor and geotactic behavior of *Drosophila melanogaster* over-expressing neprilysin 2. *Peptides* 30: 571-4. PMID: 19038301.
- Blum M, Chang HY, Chuguransky S, Grego T, Kandasamy S, Mitchell A, Nuka G, Paysan-Lafosse T, Qureshi M, Raj S, Richardson L, Salazar GA, Williams L, Bork P, Bridge A, Gough J, Haft DH, Letunic I, Marchler-Bauer A, Mi H, Natale DA, Necci M, Orengo CA, Pandurangan AP, Rivoire C, Sigrist CJA, Sillitoe I, Thanki N, Thomas PD, Tosatto SCE, Wu CH, Bateman A, Finn RD. 2021. The InterPro protein families and domains database: 20 years on. *Nucleic Acids Res* 49: D344-D354. PMID: 33156333.
- Cao W, Song HJ, Gangi T, Kelkar A, Antani I, Garza D, Konsolaki M. 2008. Identification of novel genes that modify phenotypes induced by Alzheimer's beta-amyloid overexpression in *Drosophila*. *Genetics* 178: 1457-71. PMID: 18245849.
- Coates D, Siviter R, Isaac RE. 2000. Exploring the *Caenorhabditis elegans* and *Drosophila melanogaster* genomes to understand neuropeptide and peptidase function. *Biochem Soc Trans* 28: 464-9. PMID: 10961941.
- Findlay GD, Sitnik JL, Wang W, Aquadro CF, Clark NL, Wolfner MF. 2014. Evolutionary rate covariation identifies new members of a protein network required for *Drosophila melanogaster* female post-mating responses. *PLoS Genet* 10: e1004108. PMID: 24453993.
- Finelli A, Kelkar A, Song HJ, Yang H, Konsolaki M. 2004. A model for studying Alzheimer's Abeta42-induced toxicity in *Drosophila melanogaster*. *Mol Cell Neurosci* 26: 365-75. PMID: 15234342.
- Graveley BR, Brooks AN, Carlson JW, Duff MO, Landolin JM, Yang L, Artieri CG, van Baren MJ, Boley N, Booth BW, Brown JB, Chervas L, Davis CA, Dobin A, Li R, Lin W, Malone JH, Mattiuzzo NR, Miller D, Sturgill D, Tuch BB, Zaleski C, Zhang D, Blanchette M, Dudoit S, Eads B, Green RE, Hammonds A, Jiang L, Kapranov P, Langton L, Perrimon N, Sandler JE, Wan KH, Willingham A, Zhang Y, Zou Y, Andrews J, Bickel PJ, Brenner SE, Brent MR, Chervas P, Gingeras TR, Hoskins RA, Kaufman TC, Oliver B, Celniker SE. 2011. The developmental transcriptome of *Drosophila melanogaster*. *Nature* 471: 473-9. PMID: 21179090.
- Hallier B, Schiemann R, Cordes E, Vitos-Faleato J, Walter S, Heinisch JJ, Malmendal A, Paululat A, Meyer H. 2016. *Drosophila* neprilysins control insulin signaling and food intake via cleavage of regulatory peptides. *Elife* 5: . PMID: 27919317.

- Iijima-Ando K, Hearn SA, Granger L, Shenton C, Gatt A, Chiang HC, Hakker I, Zhong Y, Iijima K. 2008. Overexpression of neprilysin reduces alzheimer amyloid-beta42 (Abeta42)-induced neuron loss and intraneuronal Abeta42 deposits but causes a reduction in cAMP-responsive element-binding protein-mediated transcription, age-dependent axon pathology, and premature death in *Drosophila*. *J Biol Chem* 283: 19066-76. PMID: 18463098.
- Isaac RE, Siviter RJ, Stancombe P, Coates D, Shirras AD. 2000. Conserved roles for peptidases in the processing of invertebrate neuropeptides. *Biochem Soc Trans* 28: 460-4. PMID: 10961940.
- Isaac RE, Johnson EC, Audsley N, Shirras AD. 2007. Metabolic inactivation of the circadian transmitter, pigment dispersing factor (PDF), by neprilysin-like peptidases in *Drosophila*. *J Exp Biol* 210: 4465-70. PMID: 18055635.
- Iwata N, Tsubuki S, Takaki Y, Watanabe K, Sekiguchi M, Hosoki E, Kawashima-Morishima M, Lee HJ, Hama E, Sekine-Aizawa Y, Saido TC. 2000. Identification of the major Abeta1-42-degrading catabolic pathway in brain parenchyma: suppression leads to biochemical and pathological deposition. *Nat Med* 6: 143-50. PMID: 10655101.
- Jessup M. 2014. Neprilysin inhibition--a novel therapy for heart failure. *N Engl J Med* 371: 1062-4. PMID: 25176014.
- Larkin A, Marygold SJ, Antonazzo G, Attrill H, Dos Santos G, Garapati PV, Goodman JL, Gramates LS, Millburn G, Strelets VB, Tabone CJ, Thurmond J, FlyBase Consortium.. 2021. FlyBase: updates to the *Drosophila melanogaster* knowledge base. *Nucleic Acids Res* 49: D899-D907. PMID: 33219682.
- Leader DP, Krause SA, Pandit A, Davies SA, Dow JAT. 2018. FlyAtlas 2: a new version of the *Drosophila melanogaster* expression atlas with RNA-Seq, miRNA-Seq and sex-specific data. *Nucleic Acids Res* 46: D809-D815. PMID: 29069479.
- Matsuoka S, Gupta S, Suzuki E, Hiromi Y, Asaoka M. 2014. gone early, a novel germline factor, ensures the proper size of the stem cell precursor pool in the *Drosophila* ovary. *PLoS One* 9: e113423. PMID: 25420147.
- Meyer H, Panz M, Zmojdzian M, Jagla K, Paululat A. 2009. Neprilysin 4, a novel endopeptidase from *Drosophila melanogaster*, displays distinct substrate specificities and exceptional solubility states. *J Exp Biol* 212: 3673-83. PMID: 19880729.
- Meyer H, Panz M, Albrecht S, Drechsler M, Wang S, Hüsken M, Lehmacher C, Paululat A. 2011. *Drosophila* metalloproteases in development and differentiation: the role of ADAM proteins and their relatives. *Eur J Cell Biol* 90: 770-8. PMID: 21684629.
- Molinaro G, Rouleau JL, Adam A. 2002. Vasopeptidase inhibitors: a new class of dual zinc metallopeptidase inhibitors for cardiorenal therapeutics. *Curr Opin Pharmacol* 2: 131-41. PMID: 11950623.
- Nalivaeva NN, Zhuravin IA, Turner AJ. 2020. Neprilysin expression and functions in development, ageing and disease. *Mech Ageing Dev* 192: 111363. PMID: 32987038.
- Nfonsam LE, Cano C, Mudge J, Schilkey FD, Curtiss J. 2012. Analysis of the transcriptomes downstream of Eyeless and the Hedgehog, Decapentaplegic and Notch signaling pathways in *Drosophila melanogaster*. *PLoS One* 7: e44583. PMID: 22952997.
- Panz M, Vitos-Faleato J, Jendretzki A, Heinisch JJ, Paululat A, Meyer H. 2012. A novel role for the non-catalytic intracellular domain of Neprilysins in muscle physiology. *Biol Cell* 104: 553-68. PMID: 22583317.
- Rawlings ND, Barrett AJ, Thomas PD, Huang X, Bateman A, Finn RD. 2018. The MEROPS database of proteolytic enzymes, their substrates and inhibitors in 2017 and a comparison with peptidases in the PANTHER database. *Nucleic Acids Res* 46: D624-D632. PMID: 29145643.
- Sitnik JL, Francis C, Hens K, Huybrechts R, Wolfner MF, Callaerts P. 2014. Neprilysins: an evolutionarily conserved family of metalloproteases that play important roles in reproduction in *Drosophila*. *Genetics* 196: 781-97. PMID: 24395329.
- Sofola-Adesakin O, Khericha M, Snoeren I, Tsuda L, Partridge L. 2016. pGluA $\beta$  increases accumulation of A $\beta$  in vivo and exacerbates its toxicity. *Acta Neuropathol Commun* 4: 109. PMID: 27717375.
- Thomas JE, Rylett CM, Carhan A, Bland ND, Bingham RJ, Shirras AD, Turner AJ, Isaac RE. 2005. *Drosophila melanogaster* NEP2 is a new soluble member of the neprilysin family of endopeptidases with implications for reproduction and renal function. *Biochem J* 386: 357-66. PMID: 15554877.
- Turner AJ, Tanzawa K. 1997. Mammalian membrane metallopeptidases: NEP, ECE, KELL, and PEX. *FASEB J* 11: 355-64. PMID: 9141502.
- Turner AJ, Isaac RE, Coates D. 2001. The neprilysin (NEP) family of zinc metalloendopeptidases: genomics and function. *Bioessays* 23: 261-9. PMID: 11223883.

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Turrel O, Lampin-Saint-Amaux A, Pr at T, Goguel V. 2016. *Drosophila* Neprilysins Are Involved in Middle-Term and Long-Term Memory. *J Neurosci* 36: 9535-46. PMID: 27629706.

Turrel O, Goguel V, Preat T. 2017. *Drosophila* Neprilysin 1 Rescues Memory Deficits Caused by Amyloid- $\beta$  Peptide. *J Neurosci* 37: 10334-10345. PMID: 28931572.

Turrel O, Rabah Y, Pla ais PY, Goguel V, Preat T. 2020. *Drosophila* Middle-Term Memory: Amnesiac is Required for PKA Activation in the Mushroom Bodies, a Function Modulated by Neprilysin 1. *J Neurosci* 40: 4219-4229. PMID: 32303647.

Whitworth JA. 2003. Emerging drugs in the management of hypertension. *Expert Opin Emerg Drugs* 8: 377-88. PMID: 14661996.

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