

Scale chr4: | 307,500 | 308,000 | 308,500 | 309,000 | 309,500 | 310,000 | 310,500 | 311,000 | 311,500 |

Functional Residues

2 kb | dm6

APPRIS - Principal Isoforms  
Couldn't open [https://apprisws.bioinfo.cnio.es/pub/trackHub/dm6/appris\\_method.appris.bb](https://apprisws.bioinfo.cnio.es/pub/trackHub/dm6/appris_method.appris.bb)

APPRIS - protein domains  
Couldn't open [https://apprisws.bioinfo.cnio.es/pub/trackHub/dm6/appris\\_method.spade.bb](https://apprisws.bioinfo.cnio.es/pub/trackHub/dm6/appris_method.spade.bb)

APPRIS - functional residues  
Couldn't open [https://apprisws.bioinfo.cnio.es/pub/trackHub/dm6/appris\\_method.firestar.bb](https://apprisws.bioinfo.cnio.es/pub/trackHub/dm6/appris_method.firestar.bb)

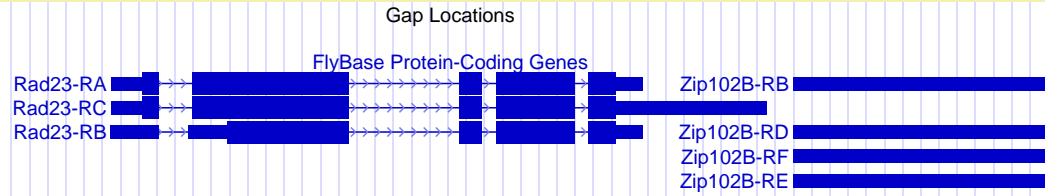
APPRIS - protein structural information  
Couldn't open [https://apprisws.bioinfo.cnio.es/pub/trackHub/dm6/appris\\_method.matador3d.bb](https://apprisws.bioinfo.cnio.es/pub/trackHub/dm6/appris_method.matador3d.bb)

APPRIS - species conservation  
Couldn't open [https://apprisws.bioinfo.cnio.es/pub/trackHub/dm6/appris\\_method.corsair.bb](https://apprisws.bioinfo.cnio.es/pub/trackHub/dm6/appris_method.corsair.bb)

APPRIS - predictions of trans-membrane helices  
Couldn't open [https://apprisws.bioinfo.cnio.es/pub/trackHub/dm6/appris\\_method.thump.bb](https://apprisws.bioinfo.cnio.es/pub/trackHub/dm6/appris_method.thump.bb)

APPRIS - presence and location of signal peptides  
Couldn't open [https://apprisws.bioinfo.cnio.es/pub/trackHub/dm6/appris\\_method.crash.bb](https://apprisws.bioinfo.cnio.es/pub/trackHub/dm6/appris_method.crash.bb)

Gap



FlyBase Pseudogenes  
FlyBase Non-protein Coding Genes

miRNA  
ncRNA  
tRNA  
miscRNA

Repeating Elements by RepeatMasker

RepeatMasker

