"The *Drosophila melanogaster* PeptideAtlas facilitates the use of peptide data for improved fly proteomics and genome annotation."

Additional File 2

Explanatory screenshots of a PeptideAtlas session using the HTML interface

This figure shows an exemplary PeptideAtlas user session at www.drosophila-peptideatlas.org and is to be read clockwise. The user wants to know a proteotypic peptide for the Heterogeneous Nuclear Ribonucloprotein Hrb87F (CG12749), more specifically its splice form CG12749-PA. **Upper left:** Result of a Protein Query for CG12749-PA: a condensed representation of the protein and its aligned PAps. **Upper right:** In the Peptide Query, one can narrow down the search by allowing only PAps specific for this gene and, even further, the splice variant CG12749-PA. In addition, the constraint is applied, that a peptide has to be observed at least twice. This way, PeptideAtlas pinpoints to 2 of the 44 peptides one of which (PAp00011594) has been observed 62 times. Both PAps would typically be chosen as PTPs for the design of an SRM assay. **Lower right:** Clicking on a PAp accession provides detailed information about this peptide. The 64 observations divide into 16 in the charge state 2+ and 46 in 3+. **Lower left:** In particular, one can view and download consensus spectra for either of those charge states.

CG12749-PA

Protein Name	CG12749-PA
Gene Name	CG12749
Description	pep:known chromosome:BDGP4.3:3R:9483045:9486241:-1 gene:CG12749 transcript:CG12749-RA
Total peptides	411

Sequence Motifs

Sequence Position

Observed Peptides

Sequence Coverage

Unlikely (theoretical)

Sequence Position

■ Observed peptide with single genome mapping
□ Observed peptide with ambiguous genome mapping
▨ Protein coverage by observed peptides
▨ Peptides unlikely to be observed

Sequence

MAEQNDSNGN YDDGEEITEP EQLRKLFIGG LDYRTTDDGL KAHFEKWGNI VDVVVMKDPK TKRSRGFGFI
TYSQSYMIDN AQNARPHKID GRTVEPKRAV PRQEIDSPNA GATVKKLFVG GLRDDHDEEC LREYFKDFGQ
IVSVNIVSDK DTGKKRGFAF IEFDDYDPVD KIILQKTHSI KNKTLDVKKA IAKQDMDRQG GGGGRGGPRA
GGRGGGGDRG QGGGGWGGQN RQNGGNWGG AGGGGGFGNS GGNFGGGQGG SGGGWNQQGG SGGGPWNNQG
GGNGGWNGGG GGGYGGGNSN GSWGGNGGGG GGGGGFGNEY QQSYGGGPQR NSNFGNNRPA PYSQGGGGGG
FNKGNQGGGQ GFAGNNYNTG GGGQGGNMGG GNRRY

Atlas Build: DrosophilaMelanogaster_0.2

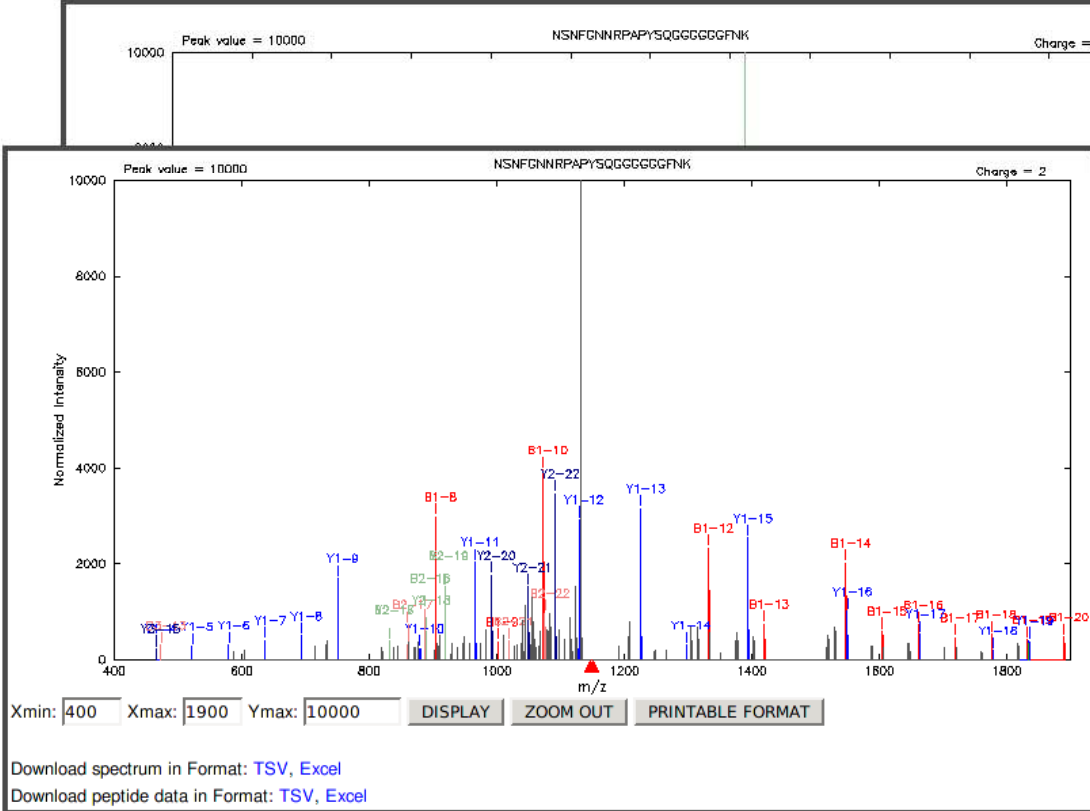|	?	
Protein Name Constraint:	?	CG12749-PA
Upload File Of Proteins:	?	[ ] Browse...
Gene Name Constraint:	?	
Description Constraint:	?	
Peptide Name Constraint:	?	
Peptide Sequence Constraint:	?	
Best Probability Constraint:	?	
Number of Observations Constraint:	?	>1
Number of Different Samples Constraint:	?	
Empirical Proteotypic Score Constraint:	?	
Number of Proteins Mapped Constraint:	?	=1
Number of Genome Locations Mapped Constraint:	?	=1
Is Exon Spanning?:	?	[ ]
Samples:	?	Embryos 0-24h AEL / Embryos up to the blastoderm stage (2hours after egg laying) / Fatbodies from 20%sucrose-treated and untreated larvae / Fatbodies from rapamycin-treated and untreated larvae
Display Options:	?	Show Chromosomal Mappings / DASFormat / Show SQL Query

QUERY REFRESH Reset

Peptide Accession ▲▼	N Obs ▲▼	Peptide Sequence ▲▼	Chrom ▲▼	Start Position ▲▼	End Position ▲▼	Strand ▲▼	N Protein Mappings ▲▼	Best Prob ▲▼	N Unique Locations on Genome ▲▼
PAp00011594	Nobs=62	NSNFGNNRPAPYSQGGGGGGFNK	3R	9484360	9484428	-	1	1.000	1
PAp00022812	Nobs=3	FAGNNYNTGGGGQGGNMGGGNR	3R	9484198	9484263	-	1	1.000	1

PAp00011594

Peptide Accession	PAp00011594
Peptide Sequence	NSNFGNNRPAPYSQGGGGGGFNK
Best Probability	1
Times Observed:	62

Genome Mappings: 1

Chr	Protein	Residues on Exon	Exon Range	Strand
3R	CG12749-PA	NSNFGNNRPAPYSQGGGGGGFNK	9484360 - 9484428	-

Modified Peptides

Modified Sequence	Charge	Mono Parent m/z	Best Prob	# Obs	# Siblings	Sample IDs	Consensus Spectrum
NSNFGNNRPAPYSQGGGGGGFNK	2	1149.0263	1	16	95.8	80,88,68,88 [6 more]	
NSNFGNNRPAPYSQGGGGGGFNK	3	766.3535	1	46	96.0	91,87,80,88 [10 more]	

Observed in Samples:

49	S2 cells, nuclear fraction
50	Kc cells membrane fraction
51	S2 cells; membrane fraction
52	Heads from adult flies, membrane fraction
61	Kc cells, Chromatin fraction
68	Cytoplasmic fractions (soluble proteins) from Adult Drosophila heads
76	Dm_S2_nuc_FFE
78	Embryos 0-24h AEL
86	Gelfiltration of exponentially growing Kc-cell total lysate
88	S2cells cytoplasmic fraction
90	Dm_Pupae_Membranes
91	Heads from adult flies, nuclear fraction

NSNFGNNRPAPYSQGGGGGGFNK   Charge = 3
Peak value = 10000

NSNFGNNRPAPYSQGGGGGGFNK   Charge = 2
Peak value = 10000

Xmin: 400 Xmax: 1900 Ymax: 10000 DISPLAY ZOOM OUT PRINTABLE FORMAT

Download spectrum in Format: TSV, Excel
Download peptide data in Format: TSV, Excel