

Mascot Search Results

Protein View

Match to: [gi|157119815](#) Score: 225 Expect: 2.5e-015  
AAEL008787-PA [*Aedes aegypti*]

Nominal mass ( $M_r$ ): 68528; Calculated pI value: 5.26  
NCBI BLAST search of [gi|157119815](#) against nr  
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Aedes aegypti](#)  
Links to retrieve other entries containing this sequence from NCBI Entrez:  
[gi|122002537](#) from [Aedes albopictus](#)  
[gi|145559538](#) from [Aedes aegypti](#)  
[gi|61971317](#) from [Aedes albopictus](#)  
[gi|108875173](#) from [Aedes aegypti](#)

Fixed modifications: Carbamidomethyl (C)  
Variable modifications: Oxidation (M)  
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P  
Sequence Coverage: 29%

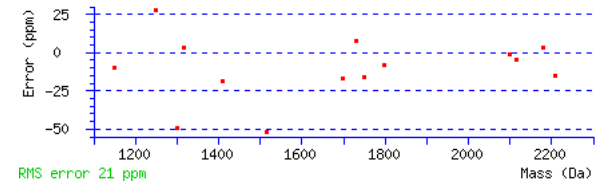
Matched peptides shown in **Bold Red**

1 MSTLKKISDE DRESK**FGYVF AVSGPVVTAE** RMSGSAMYEL VR**VGYVELVG**  
51 **EIIR**LEGDMA TIQVYEETSG VTVGDPVLRT GKPLSVELGP GIMGSIFDGI  
101 QRPLKDINEL TSSIYIPKGV NIPCLSRQTS WGFNPLNVKV **GSHITGGDLY**  
151 **GLVHENTLVK** HKLLVPPRAK GTVRYIAPP NYTVDDIILE TEFDGEINKW  
201 **SMLQVWPVRQ** PRPVTEKLPA NHPLLTGQRV LDSLFPCVQG GTTAIPGAFG  
251 CGKTVISQAL SKY**NSDVII YVCG**ERGNE MSEVLR**DFPE** L**SV**EIDGVTE  
301 **SIMKR**TALVA **NTSNMP**VAAR **EAS**IYTGITL SEYFRDMGYN VSMMDSTSR  
351 WAELREISG **RLAEMP**ADSG **YPAYL**GARLA SFYERAGRVK CLGNPEREGS  
401 VSIVGAVSPP GGD**FSD**PVTS ATLGIVQVFW GLDKKLAQRK HFP**SIN**WLIS  
451 YSKY**MRALDD** **FYDKNF**QEFV **PLR**TKVKEIL QEEEDLSEIV QLVGKASLAE  
501 TDKITLEVAK LLKDDFLQON SYSAYDRFCP FYKTVGMLRN **MIGFYDMARH**  
551 AVETTAQSEN KITWNVIRDS MGNILYQLSS MKFKDPVKDG EAK**IKADFDQ**  
601 **LYEDLQQA**FR NLED

Show predicted peptides also

Sort Peptides By ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start	End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence
16	31	1698.8561	1697.8488	1697.8777	-17	0	K.FGYVFAVSGPVVTAER.M (No match)
16	31	1698.8561	1697.8488	1697.8777	-17	0	K.FGYVFAVSGPVVTAER.M (Ions score 65)
43	54	1410.7363	1409.7290	1409.7554	-19	0	R.VGYVELVGEIIR.L (No match)
43	54	1410.7363	1409.7290	1409.7554	-19	0	R.VGYVELVGEIIR.L (Ions score 36)
140	160	2209.1272	2208.1199	2208.1539	-15	0	K.VGSHITGGDLYGLVHENTLVK.H (No match)
200	209	1301.6184	1300.6111	1300.6750	-49	0	K.WSMLQVWPVR.Q (No match)
200	209	1317.6819	1316.6746	1316.6700	4	0	K.WSMLQVWPVR.Q Oxidation (M) (No match)
263	277	1731.8138	1730.8065	1730.7934	8	0	K.YSNSDVIIYVCGGER.G (No match)
287	305	2181.0813	2180.0740	2180.0671	3	1	R.DFPELSVEIDGVTESIMKR.T Oxidation (M) (No match)
306	320	1515.7159	1514.7086	1514.7875	-52	0	R.TALVANTSNMPVAAR.E (No match)
321	335	1749.8416	1748.8343	1748.8621	-16	0	R.EASITYTGITLSEYFR.D (No match)
321	335	1749.8416	1748.8343	1748.8621	-16	0	R.EASITYTGITLSEYFR.D (Ions score 46)
362	378	1797.8328	1796.8255	1796.8403	-8	0	R.LAEMPADSGYPAYLGAR.L Oxidation (M) (No match)
457	473	2117.0234	2116.0161	2116.0266	-5	1	R.ALDDFYDKNFQEFVPLR.T (No match)
465	473	1149.5933	1148.5860	1148.5978	-10	0	K.NFQEFVPLR.T (No match)
540	549	1249.5691	1248.5618	1248.5267	28	0	R.NMIGFYDMAR.H 2 Oxidation (M) (No match)
594	610	2100.0376	2099.0303	2099.0323	-1	1	K.IKADFDQLYEDLQQA <b>FR</b> .N (No match)



Mascot: <http://www.matrixscience.com/>