

MATRIX

SCIENCE

Mascot Search Results

Protein View

Match to: [gi|157136033](#) Score: 333 Expect: 4e-026
AAEL003393-PA [*Aedes aegypti*]

Nominal mass (M_r): 53940; Calculated pI value: 5.02
NCBI BLAST search of [gi|157136033](#) 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|108881105](#) 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: 40%

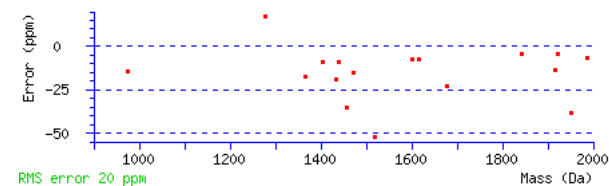
Matched peptides shown in **Bold Red**

1 **MLSSLRNVLS** TGSRVQADLV RNYAAKAAK AAAGAQGKVV AVIGAVVDVQ
51 FDDNLPPILN ALEVQGERGS **LVLEVAQH LG** ENTVRTIAMD GTEGLVRGQR
101 **VLDTGSPIRI** PVGAETLGRI INVIGEPIDE RGP IETNL SA PIHAEAPEFI
151 DMSVEQEILV TGIKVVDLLA PYAKGGK**IGL** FGGAGVGKTV LIMELINNVA
201 **KAHGGYSVFA** VGVERTREGN DLYNEMIEGG VISLKDKTSK VALVYGQMN E
251 **PPGARARVAL** TGLTVAEYFR DQEGQDVLLF IDNIFRFTQA GSEVSALLGR
301 IPSAVGQPT LATDMGSMQE RITTTK KGI TSVAIYVPA DDLTD PAPAT
351 TFAHL DATTV LSR**AIAELGI** YPAVDPLDST SRIMDPNIIG AEHYN IARGV
401 QKILQDYKSL QDIIA ILGMD ELSEEDKLT V ARARKIQ RFL SQPFQVAEVF
451 TGHAGKLVPL EETIKGF TKI L NGELDHLPE VAFY MVGPIE EVVEKAERLA
501 KEAA

Show predicted peptides also

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

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss Sequence
1 - 14	1520.7416	1519.7343	1519.8140	-52	1 -.MLSSLRNVLS TGSR.V (No match)
71 - 85	1677.8896	1676.8823	1676.9210	-23	0 R.LVLEVAQH L GENTVR.T (No match)
86 - 97	1278.6581	1277.6508	1277.6286	17	0 R.TIAMDGTEGLVR. G Oxidation (M) (No match)
101 - 119	1951.0226	1950.0153	1950.0898	-38	1 R.VLDTGSPIRIPVGAETLGR. I (No match)
120 - 131	1367.7294	1366.7221	1366.7456	-17	0 R.IINVIGEPIDER. G (No match)
178 - 188	975.5482	974.5409	974.5549	-14	0 K.IGLFGGAGVGK. T (No match)
189 - 201	1457.7886	1456.7813	1456.8323	-35	0 K.TVLIMELINNVAK. A (No match)
189 - 201	1473.8118	1472.8045	1472.8272	-15	0 K.TVLIMELINNVAK. A Oxidation (M) (No match)
202 - 215	1406.6683	1405.6610	1405.6739	-9	0 K.AHGGYSVFAGVGER. T (No match)
202 - 215	1406.6683	1405.6610	1405.6739	-9	0 K.AHGGYSVFAGVGER. T (Ions score 89)
238 - 255	1917.9587	1916.9514	1916.9778	-14	1 K.TSKVALVYGQMN PPGAR.A (No match)
241 - 255	1601.7986	1600.7913	1600.8031	-7	0 K.VALVYGQMN PPGAR.A (No match)
241 - 255	1617.7932	1616.7859	1616.7981	-8	0 K.VALVYGQMN PPGAR.A Oxidation (M) (No match)
258 - 270	1439.7766	1438.7693	1438.7820	-9	0 R.VALTGLTVAEYFR. D (No match)
258 - 270	1439.7766	1438.7693	1438.7820	-9	0 R.VALTGLTVAEYFR. D (Ions score 75)
271 - 286	1921.9567	1920.9494	1920.9581	-5	0 R.DQEGQDVLLFIDNIFR. F (No match)
287 - 300	1435.7267	1434.7194	1434.7467	-19	0 R.FTQAGSEVSALLGR. I (No match)
364 - 382	1988.0200	1987.0127	1987.0262	-7	0 R.AIAELGIYPVDPLDSTSR. I (No match)
364 - 382	1988.0200	1987.0127	1987.0262	-7	0 R.AIAELGIYPVDPLDSTSR. I (Ions score 59)
383 - 398	1842.9082	1841.9009	1841.9094	-5	0 R.IMDPNIIGAEHYN IAR.G Oxidation (M) (No match)



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