

The Peptide Venom Composition of the Fierce Stinging Ant *Tetraponera Aethiops* (Formicidae: Pseudomyrmecinae)

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Table S1. Addressing table of major contigs expressed by *Tetraponera aethiops* venom glands.

	Length (kb)	Hits	Reads Per Million	%	Contig_ORF	Seq ID Name	E-value	Function
CL1015Contig1_1	448	118970	408.07	0.04				
CL1134Contig1_1	1124	122638	420.65	0.04	CL1134Contig1_1_6	sp Q8WRF3 RL32_APIME 60S ribosomal protein L32 OS = <i>Apis mellifera</i> OX = 7460 GN = RpL32 PE = 2 SV = 1	2.45e-82	Translation
CL114Contig1_1	1044	189151	648.79	0.06				
CL114Contig2_1	3807	8616798	29555.53	2.96		U2-PSDTX-Ta1a Genbank Accession Number : MN607169		Venom peptide
CL1185Contig1_1	3361	775505	2659.97	0.27				
CL1193Contig1_1	7145	1682413	5770.66	0.58	CL1193Contig1_1_5	sp Q3ZU95 PA1_VESGE Phospholipase A1 OS = <i>Vespula germanica</i> OX = 30212 PE = 2 SV = 1	7.81e-21	Phospholipase
					CL1193Contig1_1_6	sp Q8K1C7 MOT14_MOUSE Monocarboxylate transporter 14 OS = <i>Mus musculus</i> OX = 10090 GN = Slc16a14 PE = 2 SV = 1	2.00e-37	
					CL1193Contig1_1_6	sp Q3ZU95 PA1_VESGE Phospholipase A1 OS = <i>Vespula germanica</i> OX = 30212 PE = 2 SV = 1	2.42e-43	
CL120Contig1_4	2266	123353	423.1	0.04	CL120Contig1_4_3	sp Q1HPS0 MLR_BOMMO Myosin regulatory light chain 2 OS = <i>Bombyx mori</i> OX = 7091 PE = 1 SV = 1	2.16e-80	Cytoskeleton
CL1275Contig1_1	3598	18623211	63877.43	6.39		U2-PSDTX-Ta1b Genbank Accession Number : MN607170		Venom peptide

CL12Contig1_1	665	23999 4	823.18	0.08	CL12Contig1_1_6	sp Q962Q7 RS23_SPOFR 40S ribosomal protein S23 OS = Spodoptera frugiperda OX = 7108 GN = RpS23 PE = 2 SV = 1	6.30e-90	Translation
CL1321Contig1_1	5444	42983 54	14743.31	1.47				
CL134Contig1_5	2180	10389 5	356.36	0.04	CL134Contig1_5_5	sp P29341 PABP1_MOUSE Polyadenylate-binding protein 1 OS = Mus musculus OX = 10090 GN = Pabpc1 PE = 1 SV = 2	4.23e-145	RNA Maturation
CL134Contig1_6	777	16279 1	558.37	0.06	CL134Contig1_6_4	sp P20965 PABPA_XENLA Polyadenylate-binding protein 1-A OS = Xenopus laevis OX = 8355 GN = pabpc1-a PE = 1 SV = 3	8.47e-97	Transcription
CL1626Contig1_2	3783	36811 9	1262.64	0.13	CL1626Contig1_2_1	sp P31689 DNJA1_HUMAN DnaJ homolog subfamily A member 1 OS = Homo sapiens OX = 9606 GN = DNAJA1 PE = 1 SV = 2	7.89e-160	Protein Maturation
					CL1626Contig1_2_4	sp Q962Q6 RS24_SPOFR 40S ribosomal protein S24 OS = Spodoptera frugiperda OX = 7108 GN = RpS24 PE = 2 SV = 1	1.20e-71	
CL1740Contig1_1	2749	15334 801	52598.21	5.26				
CL1762Contig1_1	394	21365 8	732.84	0.07				
CL1804Contig1_1	3123	43286 324	148471.66	14.8 5		U2-PSDTX-Ta1c Genbank Accession Numbers : MN607168		Venom peptide
CL1844Contig1_1	2272	33442 6	1147.08	0.11	CL1844Contig1_1_1	sp O18640 GBLP_DROME Guanine nucleotide-binding protein subunit beta-like protein OS = Drosophila melanogaster OX = 7227 GN = Rack1 PE = 1 SV = 2	0.0	Cellular Signaling
CL1Contig165_1	4280	38373 0	1316.19	0.13				
CL1Contig387_1	1547	73881 70	25341.35	2.53		U3-PSDTX-Ta1a Genbank Accession Numbers : MN607165		Venom peptide
CL1Contig399_4	1164	10573 5	362.67	0.04	CL1Contig399_4_4	sp P08879 NDKA_DROME Nucleoside diphosphate kinase OS = Drosophila melanogaster OX = 7227 GN = awd PE = 1 SV = 3	8.15e-82	Metabolism

CL2021Contig1_1	2516	11554 9	396.33	0.04	CL2021Contig1_1_6	sp Q9VBV3 TAKT_DROME Protein takeout OS = Drosophila melanogaster OX = 7227 GN = to PE = 2 SV = 1	1.26e-08	Circadian Rythm
CL2229Contig1_1	923	37149 3	1274.22	0.13	CL2229Contig1_1_6	sp Q7KF90 RL31_SPOFR 60S ribosomal protein L31 OS = Spodoptera frugiperda OX = 7108 GN = RpL31 PE = 2 SV = 1	7.20e-62	Translation
CL2248Contig1_1	2074	12327 2	422.82	0.04				
CL235Contig1_1	5969	46548 0	1596.59	0.16	CL235Contig1_1_6	sp B2D0J4 VDPP4_APIME Venom dipeptidyl peptidase 4 OS = Apis mellifera OX = 7460 PE = 1 SV = 1	0.0	Peptide Maturation
CL2441Contig1_1	764	18951 1	650.02	0.07	CL2441Contig1_1_3	sp P68203 RS27A_SPOFR Ubiquitin-40S ribosomal protein S27a OS = Spodoptera frugiperda OX = 7108 PE = 2 SV = 2	1.08e-77	Protein Degradation
CL2597Contig1_2	2581	12108 4	415.32	0.04	CL2597Contig1_2_6	sp Q1HDZ5 EIF3B_BOMMO Eukaryotic translation initiation factor 3 subunit B OS = Bombyx mori OX = 7091 GN = eIF3-S9 PE = 2 SV = 1	0.0	Translation
CL260Contig1_1	15246	34144 8	1171.16	0.12	CL260Contig1_1_2	sp A2T929 RXRAA_DANRE Retinoic acid receptor RXR-alpha-A OS = Danio rerio OX = 7955 GN = rxraa PE = 2 SV = 2	1.05e-142	Transcription / Cytoskeleton
					CL260Contig1_1_6	sp Q75VN3 TCTP_BOMMO Translationally-controlled tumor protein homolog OS = Bombyx mori OX = 7091 GN = Tctp PE = 2 SV = 1	3.88e-91	
CL2682Contig1_1	1709	17304 2	593.53	0.06	CL2682Contig1_1_1	sp Q95ZE8 RL14_DROVI 60S ribosomal protein L14 OS = Drosophila virilis OX = 7244 GN = RpL14 PE = 3 SV = 1	3.28e-44	Translation
CL268Contig1_1	4197	30111 7	1032.83	0.1	CL268Contig1_1_2	sp P62282 RS11_RAT 40S ribosomal protein S11 OS = Rattus norvegicus OX = 10116 GN = Rps11 PE = 1 SV = 3	4.09e-70	Unknown
					CL268Contig1_1_4	sp Q7Z3D4 LYSM3_HUMAN LysM and putative peptidoglycan-binding domain-containing protein 3 OS = Homo sapiens OX = 9606 GN = LYSMD3 PE = 1 SV = 2	2.46e-12	
CL2720Contig1_1	2730	11783 1	404.16	0.04	CL2720Contig1_1_6	sp O17389 TYB_CAEEL Thymosin beta OS = Caenorhabditis elegans OX = 6239 GN = tth-1 PE = 1 SV = 2	3.19e-15	Cytoskeleton

CL2890Contig1_1	2494	105857	363.09	0.04	CL2890Contig1_1_1	sp P55828 RS20_DROME 40S ribosomal protein S20 OS = <i>Drosophila melanogaster</i> OX = 7227 GN = RpS20 PE = 1 SV = 1	8.78e-58	Translation
					CL2890Contig1_1_4	sp P41374 IF2A_DROME Eukaryotic translation initiation factor 2 subunit 1 OS = <i>Drosophila melanogaster</i> OX = 7227 GN = eIF2alpha PE = 2 SV = 1	3.68e-146	
CL3020Contig1_1	1913	279908	960.08	0.1	CL3020Contig1_1_2	sp Q56FG6 RL5_LYSTE 60S ribosomal protein L5 OS = <i>Lysiphlebus testaceipes</i> OX = 77504 GN = RpL5 PE = 2 SV = 1	2.53e-161	Translation
CL3328Contig1_1	4478	141078	483.9	0.05	CL3328Contig1_1_5	sp Q9VFC2 SP88E_DROME Serine protease inhibitor 88Ea OS = <i>Drosophila melanogaster</i> OX = 7227 GN = Spn88Ea PE = 2 SV = 1	6.23e-62	Immunity
CL349Contig1_1	1286	222310	762.52	0.08				
CL3564Contig1_1	8161	1583033	5429.79	0.54	CL3564Contig1_1_3	sp Q3ULZ2 FHDC1_MOUSE FH2 domain-containing protein 1 OS = <i>Mus musculus</i> OX = 10090 GN = Fhdc1 PE = 1 SV = 3	1.18e-88	Cytoskeleton
CL3611Contig1_1	2022	135922	466.21	0.05	CL3611Contig1_1_1	sp P54985 PPIA_BLAGE Peptidyl-prolyl cis-trans isomerase OS = <i>Blattella germanica</i> OX = 6973 GN = CYPA PE = 2 SV = 1	3.85e-92	Protein Maturation
CL3706Contig1_1	2966	323293	1108.89	0.11	CL3706Contig1_1_2	sp Q63159 COQ3_RAT Ubiquinone biosynthesis O-methyltransferase. mitochondrial OS = <i>Rattus norvegicus</i> OX = 10116 GN = Coq3 PE = 2 SV = 2	2.12e-52	Metabolism
					CL3706Contig1_1_5	sp Q03168 ASPP_AEDAE Lysosomal aspartic protease OS = <i>Aedes aegypti</i> OX = 7159 GN = AAEL006169 PE = 1 SV = 2	1.09e-150	
CL3812Contig1_1	7028	214658	736.27	0.07	CL3812Contig1_1_6	sp B1A4F7 VDDP4_VESVU Venom dipeptidyl peptidase 4 OS = <i>Vespula vulgaris</i> OX = 7454 PE = 1 SV = 1	7.39e-125	Peptide Maturation
CL4093Contig1_1	1360	188957	648.12	0.06	CL4093Contig1_1_2	sp O96647 RL10_BOMMA 60S ribosomal protein L10 OS = <i>Bombyx mandarina</i> OX = 7092 GN = RpL10 PE = 2 SV = 1	4.54e-74	Translation

CL4128Contig1_1	2237	102496	351.56	0.04					
CL4129Contig1_1	1117	246219	844.53	0.08	CL4129Contig1_1_6	sp Q10416 HYTA_APIME Hymenoptaecin OS = Apis mellifera OX = 7460 PE = 2 SV = 1	9.76e-18	Immunity	
CL4173Contig1_1	3705	343497	1178.19	0.12	CL4173Contig1_1_4	sp P0CG71 UBIQ1_CAEEL Polyubiquitin-A OS = Caenorhabditis elegans OX = 6239 GN = ubq-1 PE = 3 SV = 1	0.0	Protein Degradation	
CL4485Contig1_1	3472	177527	608.92	0.06	CL4485Contig1_1_4	sp Q962R9 RS10_SPOFR 40S ribosomal protein S10 OS = Spodoptera frugiperda OX = 7108 GN = RpS10 PE = 2 SV = 1	4.44e-70	Translation	
CL4642Contig1_1	1666	709365	2433.11	0.24	CL4642Contig1_1_2	sp Q9W1C9 PEB3_DROME Ejaculatory bulb-specific protein 3 OS = Drosophila melanogaster OX = 7227 GN = EbpIII PE = 2 SV = 2	1.26e-23	Secreted Protein	
CL479Contig1_5	2010	2627473	9012.21	0.9	CL479Contig1_5_5	sp Q9U639 HSP7D_MANSE Heat shock 70 kDa protein cognate 4 OS = Manduca sexta OX = 7130 PE = 2 SV = 1	0.0	Protein Maturation	
CL479Contig1_6	1340	220142	755.08	0.08	CL479Contig1_6_5	sp Q9U639 HSP7D_MANSE Heat shock 70 kDa protein cognate 4 OS = Manduca sexta OX = 7130 PE = 2 SV = 1	2.18e-106	Protein Maturation	
CL4957Contig1_1	3657	172474	591.58	0.06	CL4957Contig1_1_3	sp A8CAG3 RL17_PHLPP 60S ribosomal protein L17 OS = Phlebotomus papatasi OX = 29031 GN = RpL17 PE = 2 SV = 1	6.52e-100	Translation /Secretion	
					CL4957Contig1_1_6	sp Q7L1I2 SV2B_HUMAN Synaptic vesicle glycoprotein 2B OS = Homo sapiens OX = 9606 GN = SV2B PE = 1 SV = 1	4.67e-49		
CL5058Contig1_1	1235	279664	959.24	0.1	CL5058Contig1_1_4	sp Q02878 RL6_HUMAN 60S ribosomal protein L6 OS = Homo sapiens OX = 9606 GN = RPL6 PE = 1 SV = 3	7.07e-58	Translation	
CL521Contig1_1	852	886337	3040.13	0.3	CL521Contig1_1_6	sp P46782 RS5_HUMAN 40S ribosomal protein S5 OS = Homo sapiens OX = 9606 GN = RPS5 PE = 1 SV = 4	7.92e-122	Translation	
CL552Contig1_4	673	209357	718.09	0.07	CL552Contig1_4_6	sp Q962T5 RL24_SPOFR 60S ribosomal protein L24 OS = Spodoptera frugiperda OX = 7108 GN = RpL24 PE = 2 SV = 1	2.07e-72	Translation	
CL573Contig1_1	600	264962	908.82	0.09	CL573Contig1_1_2	sp Q6XIM8 RS15A_DROYA 40S ribosomal protein S15a OS = Drosophila yakuba OX = 7245 GN = RpS15Aa PE = 2 SV = 3	5.18e-84	Translation	

CL575Contig1_1	1770	193468	663.59	0.07				
CL5Contig7_4	1923	147949	507.46	0.05	CL5Contig7_4_2	sp P47830 RL27A_XENLA 60S ribosomal protein L27a OS = Xenopus laevis OX = 8355 GN = rpl27a PE = 2 SV = 2	6.25e-76	RNA Maturation /Translation
					CL5Contig7_4_4	sp Q6AXT8 SF3A2_RAT Splicing factor 3A subunit 2 OS = Rattus norvegicus OX = 10116 GN = Sf3a2 PE = 2 SV = 1	4.48e-112	
CL660Contig1_1	3987	133617	458.3	0.05	CL660Contig1_1_5	sp Q1HRV8 ELVL1_AEDAE Elongation of very long chain fatty acids protein AAEL008004 OS = Aedes aegypti OX = 7159 GN = AAEL008004 PE = 2 SV = 2	2.28e-105	Metabolism
CL669Contig1_1	16668	180230	618.19	0.06	CL669Contig1_1_6	sp B6RSP1 PKHA7_DANRE Pleckstrin homology domain-containing family A member 7 OS = Danio rerio OX = 7955 GN = plekha7 PE = 2 SV = 2	2.99e-37	Secretion
CL955Contig1_1	694	197268	676.63	0.07	CL955Contig1_1_6	sp Q8WRP6 PBGp9_SOLGI Pheromone-binding protein Gp-9 OS = Solenopsis globularia littoralis OX = 176593 GN = Gp-9 PE = 3 SV = 1	3.49e-09	Chemoreception
k25_Locus_10039_Transcript_1_1	2851	152489	523.04	0.05				
k25_Locus_108_Transcript_2_5	3260	209726	719.36	0.07	k25_Locus_108_Transcript_2_5_4	sp P29240 5NTD_DIPOM 5'-nucleotidase OS = Diplobatis ommata OX = 1870830 PE = 2 SV = 1	2.49e-71	Metabolism
					k25_Locus_108_Transcript_2_5_6	sp Q9XZ43 5NTD_LUTLO Protein 5NUC OS = Lutzomyia longipalpis OX = 7200 GN = 5NUC PE = 1 SV = 1	1.09e-34	
k25_Locus_11_Transcript_31_1	6299	5271032	18079.59	1.81	k25_Locus_11_Transcript_31_1_4	sp Q3ZU95 PA1_VESGE Phospholipase A1 OS = Vesputia germanica OX = 30212 PE = 2 SV = 1	1.55e-19	Phospholipase
					k25_Locus_11_Transcript_31_1_6	sp Q68KK0 PA1_SOLIN Phospholipase A1 OS = Solenopsis invicta OX = 13686 PE = 1 SV = 1	2.07e-26	
k25_Locus_1163_Transcript_8_3	710	121774	417.68	0.04	k25_Locus_1163_Transcript_8_3_5	sp Q9NB33 RL44_OCHTR 60S ribosomal protein L44 OS = Ochlerotatus triseriatus OX = 7162 GN = RpL44 PE = 3 SV = 3	4.23e-58	Translation
k25_Locus_1168_Transcript_5_1	5138	102343	351.04	0.04	k25_Locus_1168_Transcript_5_1_1	sp Q9CR60 GOT1B_MOUSE Vesicle transport protein GOT1B OS = Mus musculus OX = 10090 GN = Golt1b PE = 1 SV = 1	7.79e-34	Metabolism

					k25_Locus_1168_Transcript_5_1_6	sp Q7PQV7 ADT2_ANOGA ADP.ATP carrier protein 2 OS = Anopheles gambiae OX = 7165 GN = AGAP002358 PE = 3 SV = 2	3.43e-173	
k25_Locus_1204_Transcript_6_1	2284	252383	865.67	0.09	k25_Locus_1204_Transcript_6_1_5	sp Q4GXXG7 RL18_TIMBA 60S ribosomal protein L18 OS = Timarcha balearica OX = 79517 GN = RpL18 PE = 2 SV = 1	1.45e-105	Translation
k25_Locus_1236_Transcript_1_1	1266	412434	1414.64	0.14	k25_Locus_1236_Transcript_1_1_4	sp P41822 FRI_AEDAE Ferritin subunit OS = Aedes aegypti OX = 7159 GN = FERH PE = 1 SV = 2	1.46e-41	Metabolism
k25_Locus_126_Transcript_5_1	5493	3778623	12960.64	1.3				Metabolism
k25_Locus_1289_Transcript_17_4	1122	145672	499.65	0.05	k25_Locus_1289_Transcript_17_4_1	sp P47830 RL27A_XENLA 60S ribosomal protein L27a OS = Xenopus laevis OX = 8355 GN = rpl27a PE = 2 SV = 2	6.25e-76	Translation
k25_Locus_1373_Transcript_14_1	2718	541864	1858.59	0.19	k25_Locus_1373_Transcript_14_1_2	sp Q9V447 KRH2_DROME Krueppel homolog 2 OS = Drosophila melanogaster OX = 7227 GN = Kr-h2 PE = 1 SV = 1	6.94e-59	Protein Maturation /Translation
					k25_Locus_1373_Transcript_14_1_5	sp Q5R465 RS3_PONAB 40S ribosomal protein S3 OS = Pongo abelii OX = 9601 GN = RPS3 PE = 2 SV = 1	7.22e-52	
k25_Locus_165_Transcript_2_1	833	433100	1485.53	0.15	k25_Locus_165_Transcript_2_1_1	sp P58375 RL30_SPOFR 60S ribosomal protein L30 OS = Spodoptera frugiperda OX = 7108 GN = RpL30 PE = 3 SV = 1	3.37e-59	Translation
k25_Locus_182_Transcript_10_1	4550	136590	468.5	0.05	k25_Locus_182_Transcript_10_1_3	sp Q7KN62 TERA_DROME Transitional endoplasmic reticulum ATPase TER94 OS = Drosophila melanogaster OX = 7227 GN = TER94 PE = 1 SV = 1	0.0	Secretion
k25_Locus_1873_Transcript_1_1	957	110742	379.84	0.04	k25_Locus_1873_Transcript_1_1_3	sp Q8VZ67 Y4919_ARATH Uncharacterized zinc finger CCHC domain-containing protein At4g19190 OS = Arabidopsis thaliana OX = 3702 GN = At4g19190 PE = 2 SV = 1	0.54	Oxidative stress
					k25_Locus_1873_Transcript_1_1_6	sp Q9V3P0 PRDX1_DROME Peroxiredoxin 1 OS = Drosophila melanogaster OX = 7227 GN = Jafrac1 PE = 1 SV = 1	4.60e-105	

k25_Locus_21_Transcript_3_1	3913	58584 8	2009.45	0.2	k25_Locus_21_Transcript_3_1_5	sp P29844 BIP_DROME Endoplasmic reticulum chaperone BiP OS = Drosophila melanogaster OX = 7227 GN = Hsc70-3 PE = 1 SV = 2	0.0	Protein Maturation
k25_Locus_217_Transcript_4_2	1995	34872 4	1196.12	0.12	k25_Locus_217_Transcript_4_2_4	sp Q8TCT9 HM13_HUMAN Minor histocompatibility antigen H13 OS = Homo sapiens OX = 9606 GN = HM13 PE = 1 SV = 1	5.37e-131	Protein Maturation
k25_Locus_2186_Transcript_2_3	3394	14393 4	493.69	0.05				
k25_Locus_2191_Transcript_12_3	3159	13603 4	466.6	0.05	k25_Locus_2191_Transcript_12_3_1	sp Q9V778 ADAS_DROME Alkylldihydroxyacetonephosphate synthase OS = Drosophila melanogaster OX = 7227 GN = ADPS PE = 2 SV = 1	0.0	Metabolism
k25_Locus_254_Transcript_4_4	3407	11817 1	405.33	0.04	k25_Locus_254_Transcript_4_4_1	sp O08623 SQSTM_RAT Sequestosome-1 OS = Rattus norvegicus OX = 10116 GN = Sqstm1 PE = 1 SV = 1	9.72e-30	Protein Degradation
k25_Locus_2739_Transcript_4_1	2745	16403 3	562.63	0.06	k25_Locus_2739_Transcript_4_1_5	sp O96567 DDC_DROSI Aromatic-L-amino-acid decarboxylase OS = Drosophila simulans OX = 7240 GN = Ddc PE = 3 SV = 2	3.23e-170	Metabolism
k25_Locus_317_Transcript_5_2	2304	14700 4	504.22	0.05	k25_Locus_317_Transcript_5_2_5	sp Q9VYY4 C4G15_DROME Cytochrome P450 4g15 OS = Drosophila melanogaster OX = 7227 GN = Cyp4g15 PE = 2 SV = 1	4.21e-175	Metabolism
k25_Locus_3207_Transcript_3_1	3472	13091 4	449.03	0.04	k25_Locus_3207_Transcript_3_1_3	sp Q8MQS8 SP34_APIME Venom serine protease 34 OS = Apis mellifera OX = 7460 PE = 2 SV = 1	1.18e-90	Secreted Protein
k25_Locus_3286_Transcript_1_1	894	23134 1	793.5	0.08	k25_Locus_3286_Transcript_1_1_3	sp Q962U0 RL13A_SPOFR 60S ribosomal protein L13a OS = Spodoptera frugiperda OX = 7108 GN = RpL13A PE = 2 SV = 1	1.91e-105	Translation
k25_Locus_3385_Transcript_1_1	1257	48992 3	1680.43	0.17	k25_Locus_3385_Transcript_1_1_3	sp Q5UAP4 RSSA_BOMMO 40S ribosomal protein SA OS = Bombyx mori OX = 7091 PE = 2 SV = 1	1.39e-124	Translation
k25_Locus_3520_Transcript_10_1	3033	36303 3	1245.2	0.12	k25_Locus_3520_Transcript_10_1_2	sp Q3UST5 CP089_MOUSE UPF0764 protein C16orf89 homolog OS = Mus musculus OX = 10090 PE = 2 SV = 2	1.05e-18	Unknown
k25_Locus_3576_Transcript_3_1	1701	19106 4	655.35	0.07	k25_Locus_3576_Transcript_3_1_5	sp Q5R8Z6 MCFD2_PONAB Multiple coagulation factor deficiency protein 2 homolog OS = Pongo abelii OX = 9601 GN = MCFD2 PE = 2 SV = 1	2.41e-19	Secretion

k25_Locus_402_Transcript_3_1	554	167006	572.83	0.06	k25_Locus_402_Transcript_3_1_4	sp P80455 RS12_DROME 40S ribosomal protein S12 OS = <i>Drosophila melanogaster</i> OX = 7227 GN = RpS12 PE = 1 SV = 2	1.23e-58	Translation
k25_Locus_4241_Transcript_1_1	674	129479	444.11	0.04	k25_Locus_4241_Transcript_1_1_4	sp Q962Q5 RS25_SPOFR 40S ribosomal protein S25 OS = <i>Spodoptera frugiperda</i> OX = 7108 GN = RpS25 PE = 3 SV = 1	2.31e-43	Translation
k25_Locus_433_Transcript_9_1	4376	666502	2286.1	0.23		MKLITLFLVVVLAIFIRPLMPLQMRNTESFAEGSADAF AETNSDSIKI		Venom peptide
k25_Locus_45_Transcript_1_1	5655	1275816	4376.04	0.44	k25_Locus_45_Transcript_1_1_2	sp P07709 NU6M_DROYA NADH-ubiquinone oxidoreductase chain 6 OS = <i>Drosophila yakuba</i> OX = 7245 GN = mt:ND6 PE = 3 SV = 2	6.22e-08	Metabolism
k25_Locus_4540_Transcript_2_1	2437	151912	521.06	0.05	k25_Locus_4540_Transcript_2_1_2	sp Q10714 ACE_DROME Angiotensin-converting enzyme OS = <i>Drosophila melanogaster</i> OX = 7227 GN = Ance PE = 1 SV = 3	0.0	Peptide Maturation
k25_Locus_4724_Transcript_2_1	971	125734	431.27	0.04	k25_Locus_4724_Transcript_2_1_5	sp Q962S0 RS7_SPOFR 40S ribosomal protein S7 OS = <i>Spodoptera frugiperda</i> OX = 7108 GN = RpS7 PE = 2 SV = 1	4.60e-100	Translation
k25_Locus_54_Transcript_3_1	2425	390874	1340.69	0.13	k25_Locus_54_Transcript_3_1_4	sp Q9P735 FAL1_NEUCR ATP-dependent RNA helicase fal-1 OS = <i>Neurospora crassa</i> (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX = 367110 GN = fal-1 PE = 3 SV = 2	1.80e-51	Translation
					k25_Locus_54_Transcript_3_1_6	sp Q02748 IF4A_DROME Eukaryotic initiation factor 4A OS = <i>Drosophila melanogaster</i> OX = 7227 GN = eIF4A PE = 1 SV = 3	8.73e-84	
k25_Locus_547_Transcript_29_1	8082	144921	497.08	0.05	k25_Locus_547_Transcript_29_1_3	sp Q767L8 MDC1_PIG Mediator of DNA damage checkpoint protein 1 OS = <i>Sus scrofa</i> OX = 9823 GN = MDC1 PE = 3 SV = 1	7.17e-42	DNA Repair
k25_Locus_547_Transcript_29_2	4580	136712	468.92	0.05	k25_Locus_547_Transcript_29_2_4	sp P20735 GGT1_PIG Glutathione hydrolase 1 proenzyme OS = <i>Sus scrofa</i> OX = 9823 GN = GGT1 PE = 2 SV = 1	3.37e-97	Metabolism
k25_Locus_575_Transcript_4_1	3876	112409	385.56	0.04	k25_Locus_575_Transcript_4_1_2	sp Q921M4 GOGA2_MOUSE Golgin subfamily A member 2 OS = <i>Mus musculus</i> OX = 10090 GN = Golga2 PE = 1 SV = 3	3.25e-47	Translation

					k25_Locus_575_T ranscript_4_1_5	sp Q69CJ9 RL35_OPHHA 60S ribosomal protein L35 OS = = Ophiophagus hannah OX = 8665 GN = RPL35 PE = 2 SV = 3	4.69e- 45	
k25_Locus_5867 _Transcript_4_1	4342	20252 1	694.64	0.07	k25_Locus_5867_ Transcript_4_1_5	sp P35415 MYSP1_DROME Paramyosin. long form OS = Drosophila melanogaster OX = 7227 GN = Prm PE = 1 SV = 1	0.0	Cytoskeleton
k25_Locus_737_ Transcript_1_1	1004	12314 1	422.37	0.04				
k25_Locus_7606 _Transcript_1_1	919	44160 0	1514.68	0.15	k25_Locus_7606_ Transcript_1_1_6	sp Q945U1 RS15_ELAOL 40S ribosomal protein S15 OS = = Elaeis oleifera OX = 80265 GN = RPS15 PE = 2 SV = 1	4.01e- 77	Translation
k25_Locus_766_ Transcript_35_1	5458	22405 2	768.5	0.08				
k25_Locus_810_ Transcript_1_1	1343	41762 9	1432.46	0.14	k25_Locus_810_T ranscript_1_1_6	sp Q95V39 RL8_SPOFR 60S ribosomal protein L8 OS = Spodoptera frugiperda OX = 7108 GN = RpL8 PE = 2 SV = 1	3.25e- 157	Translation
k25_Locus_97_ Transcript_10_3	1564	13667 40	4687.9	0.47	k25_Locus_97_Tr anscript_10_3_5	sp Q9U639 HSP7D_MANSE Heat shock 70 kDa protein cognate 4 OS = Manduca sexta OX = 7130 PE = 2 SV = 1	0.0	Protein Maturation
k25_Locus_9770 _Transcript_4_1	684	33321 7	1142.93	0.11				
k31_Locus_1107 9_Transcript_6_ 1	2470	10521 6	360.89	0.04	k31_Locus_11079 _Transcript_6_1_ 2	sp Q58ED9 NAA20_DANRE N-alpha-acetyltransferase 20 OS = Danio rerio OX = 7955 GN = naa20 PE = 2 SV = 1	3.15e- 87	Protein Maturation
					k31_Locus_11079 _Transcript_6_1_ 3	sp Q5M8Y1 SPCS2_XENTR Probable signal peptidase complex subunit 2 OS = Xenopus tropicalis OX = 8364 GN = = spcs2 PE = 2 SV = 1	1.72e- 58	
k31_Locus_1149 _Transcript_6_1	4540	25590 7	877.76	0.09	k31_Locus_1149_ Transcript_6_1_2	sp P9WQP7 3BHS_MYCTU 3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase OS = Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX = 83332 GN = Rv1106c PE = 1 SV = 1	4.48e- 04	Translation
					k31_Locus_1149_ Transcript_6_1_6	sp Q4GXG7 RL18_TIMBA 60S ribosomal protein L18 OS = = Timarcha balearica OX = 79517 GN = RpL18 PE = 2 SV = 1	1.45e- 105	

k31_Locus_1256_Transcript_1_2	1926	138848	476.25	0.05	k31_Locus_1256_Transcript_1_2_5	sp P70195 PSB7_MOUSE Proteasome subunit beta type-7 OS = Mus musculus OX = 10090 GN = Psmb7 PE = 1 SV = 1	7.33e-108	Protein Degradation
k31_Locus_1299_Transcript_4_1	2874	1576787	5408.36	0.54				
k31_Locus_142_Transcript_2_1	492	340493	1167.89	0.12	k31_Locus_142_Transcript_2_1_2	sp Q963B7 RL9_SPOFR 60S ribosomal protein L9 OS = Spodoptera frugiperda OX = 7108 GN = RpL9 PE = 2 SV = 1	2.22e-98	Translation
k31_Locus_1543_Transcript_1_1	2987	245729	842.85	0.08	k31_Locus_1543_Transcript_1_1_4	sp Q962R6 RS13_SPOFR 40S ribosomal protein S13 OS = Spodoptera frugiperda OX = 7108 GN = RpS13 PE = 2 SV = 3	1.70e-87	Translation
k31_Locus_1653_Transcript_2_1	1702	487764	1673.03	0.17				
k31_Locus_1695_Transcript_9_1	4325	140309	481.26	0.05	k31_Locus_1695_Transcript_9_1_6	sp P30151 EF1B_XENLA Elongation factor 1-beta OS = Xenopus laevis OX = 8355 GN = eef1b PE = 1 SV = 3	7.13e-75	Translation
k31_Locus_179_Transcript_1_1	5057	174936	600.03	0.06	k31_Locus_179_Transcript_1_1_4	sp P41824 YBOXH_APLCA Y-box factor homolog OS = Aplysia californica OX = 6500 PE = 2 SV = 1	3.61e-42	Transcription
k31_Locus_1890_Transcript_11_1	2810	754103	2586.57	0.26	k31_Locus_1890_Transcript_11_1_2	sp Q5BLY4 ICA_APIIME Icarapin-like OS = Apis mellifera OX = 7460 PE = 2 SV = 1	7.08e-23	Secreted Protein
k31_Locus_1920_Transcript_1_1	866	243884	836.52	0.08	k31_Locus_1920_Transcript_1_1_4	sp P39018 RS19A_DROME 40S ribosomal protein S19a OS = Drosophila melanogaster OX = 7227 GN = RpS19a PE = 1 SV = 3	2.43e-62	Translation
k31_Locus_21_Transcript_1_1	2877	385067	1320.78	0.13	k31_Locus_21_Transcript_1_1_4	sp P29844 BIP_DROME Endoplasmic reticulum chaperone BiP OS = Drosophila melanogaster OX = 7227 GN = Hsc70-3 PE = 1 SV = 2	0.0	Protein Maturation
k31_Locus_2212_Transcript_4_2	1771	299249	1026.42	0.1	k31_Locus_2212_Transcript_4_2_6	sp P30050 RL12_HUMAN 60S ribosomal protein L12 OS = Homo sapiens OX = 9606 GN = RPL12 PE = 1 SV = 1	2.65e-86	Translation
k31_Locus_222_Transcript_2_1	2655	106899	366.66	0.04	k31_Locus_222_Transcript_2_1_5	sp P13008 RS26_DROME 40S ribosomal protein S26 OS = Drosophila melanogaster OX = 7227 GN = RpS26 PE = 1 SV = 1	3.98e-58	Translation
k31_Locus_261_Transcript_21_1	2728	4640291	15916.15	1.59	k31_Locus_261_Transcript_21_1_5	sp P35778 VA3_SOLIN Venom allergen 3 OS = Solenopsis invicta OX = 13686 PE = 1 SV = 2	1.05e-74	Venom allergen

k31_Locus_263_Transcript_6_1	2222	530403	1819.28	0.18	k31_Locus_263_Transcript_6_1_5	sp P09180 RL4_DROME 60S ribosomal protein L4 OS = Drosophila melanogaster OX = 7227 GN = RpL4 PE = 1 SV = 2	4.42e-168	Translation
k31_Locus_3_Transcript_5_1	3218	139260	477.66	0.05	k31_Locus_3_Transcript_5_1_6	sp B4MGF8 TMEDA_DROVI Transmembrane emp24 domain-containing protein bai OS = Drosophila virilis OX = 7244 GN = bai PE = 3 SV = 1	2.19e-83	Secretion
k31_Locus_3122_Transcript_1_1	809	299719	1028.03	0.1	k31_Locus_3122_Transcript_1_1_5	sp Q9W6Y0 RS30_ORYLA 40S ribosomal protein S30 OS = Oryzias latipes OX = 8090 GN = fau PE = 3 SV = 2	3.40e-19	Translation
k31_Locus_3178_Transcript_1_1	3098	116674	400.19	0.04	k31_Locus_3178_Transcript_1_1_4	sp P05300 LAMP1_CHICK Lysosome-associated membrane glycoprotein 1 OS = Gallus gallus OX = 9031 GN = LAMP1 PE = 2 SV = 1	1.54e-23	Protein Degradation
k31_Locus_3301_Transcript_10_1	3031	319224	1094.94	0.11	k31_Locus_3301_Transcript_10_1_5	sp Q3UST5 CP089_MOUSE UPF0764 protein C16orf89 homolog OS = Mus musculus OX = 10090 PE = 2 SV = 2	1.05e-18	Unknown
k31_Locus_3808_Transcript_1_1	1088	124126	425.75	0.04	k31_Locus_3808_Transcript_1_1_4	sp P41973 SODC_DROWI Superoxide dismutase [Cu-Zn] OS = Drosophila willistoni OX = 7260 GN = Sod1 PE = 3 SV = 2	8.40e-63	Oxidative stress
k31_Locus_431_Transcript_14_2	3857	102949	353.11	0.04	k31_Locus_431_Transcript_14_2_6	sp Q9VAF0 S39AD_DROME Zinc transporter ZIP13 homolog OS = Drosophila melanogaster OX = 7227 GN = Zip99C PE = 2 SV = 1	2.00e-52	Metabolism
k31_Locus_49_Transcript_12_1	5983	7923500	27177.53	2.72	U4-PSDTX-Ta1a Genbank Accession Numbers : MN607167			Venom peptide
k31_Locus_5020_Transcript_1_1	970	187814	644.2	0.06	k31_Locus_5020_Transcript_1_1_4	sp P46222 RL11_DROME 60S ribosomal protein L11 OS = Drosophila melanogaster OX = 7227 GN = RpL11 PE = 1 SV = 2	3.13e-106	Translation
k31_Locus_597_Transcript_7_1	3991	1057443	3627.02	0.36	k31_Locus_597_Transcript_7_1_3	sp P29520 EF1A_BOMMO Elongation factor 1-alpha OS = Bombyx mori OX = 7091 PE = 2 SV = 1	0.0	Translation
k31_Locus_647_Transcript_12_3	840	133193	456.85	0.05	k31_Locus_647_Transcript_12_3_3	sp B4PEU8 RS9_DROYA 40S ribosomal protein S9 OS = Drosophila yakuba OX = 7245 GN = RpS9 PE = 2 SV = 1	7.76e-111	Translation
k31_Locus_66_Transcript_1_1	1672	1619399	5554.52	0.56	k31_Locus_66_Transcript_1_1_6	sp Q75VN3 TCTP_BOMMO Translationally-controlled tumor protein homolog OS = Bombyx mori OX = 7091 GN = Tctp PE = 2 SV = 1	1.48e-91	Cytoskeleton

k31_Locus_725_Transcript_46_1	5204	261216	895.97	0.09				
k31_Locus_725_Transcript_46_2	3694	771833	2647.38	0.26				
k31_Locus_82_Transcript_7_2	3549	602425	2066.31	0.21	k31_Locus_82_Transcript_7_2_2	sp Q27294 CAZ_DROME RNA-binding protein cabeza OS = Drosophila melanogaster OX = 7227 GN = caz PE = 2 SV = 2	1.71e-39	Transcription / Apoptosis
					k31_Locus_82_Transcript_7_2_6	sp Q9D2C7 BI1_MOUSE Bax inhibitor 1 OS = Mus musculus OX = 10090 GN = Tmbim6 PE = 1 SV = 1	1.59e-55	
k31_Locus_852_Transcript_8_1	3795	201865	692.39	0.07	k31_Locus_852_Transcript_8_1_1	sp P07602 SAP_HUMAN Prosaposin OS = Homo sapiens OX = 9606 GN = PSAP PE = 1 SV = 2	6.86e-38	Cellular Signaling
k31_Locus_853_Transcript_3_1	2089	643318	2206.57	0.22	k31_Locus_853_Transcript_3_1_3	sp Q8TGP1 YG123_YEAST Putative uncharacterized protein YGL123C-A OS = Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX = 559292 GN = YGL123C-A PE = 5 SV = 1	8.72e-05	Translation
					k31_Locus_853_Transcript_3_1_5	sp P31009 RS2_DROME 40S ribosomal protein S2 OS = Drosophila melanogaster OX = 7227 GN = RpS2 PE = 1 SV = 2	1.43e-131	
k31_Locus_892_Transcript_3_1	1895	337998	1159.33	0.12	k31_Locus_892_Transcript_3_1_6	sp P19889 RLA0_DROME 60S acidic ribosomal protein P0 OS = Drosophila melanogaster OX = 7227 GN = RpLP0 PE = 1 SV = 1	2.17e-155	Translation
k31_Locus_899_Transcript_10_2	2221	112284	385.13	0.04	k31_Locus_899_Transcript_10_2_5	sp Q58FK9 KAT3_RAT Kynurenine--oxoglutarate transaminase 3 OS = Rattus norvegicus OX = 10116 GN = Kyat3 PE = 2 SV = 1	5.44e-128	Protein Maturation
k31_Locus_984_Transcript_1_1	2900	129985	445.85	0.04	k31_Locus_984_Transcript_1_1_2	sp Q8CBY8 DCTN4_MOUSE Dynactin subunit 4 OS = Mus musculus OX = 10090 GN = Dctn4 PE = 1 SV = 1	4.98e-101	Cytoskeleton/ Translation
					k31_Locus_984_Transcript_1_1_4	sp C0HKA1 RS14B_DROME 40S ribosomal protein S14b OS = Drosophila melanogaster OX = 7227 GN = RpS14b PE = 2 SV = 1	7.47e-85	
k37_Locus_1_Transcript_1_2	4050	136602	468.54	0.05	k37_Locus_1_Transcript_1_2_5	sp Q4U3L0 G3P_GLOMM Glyceraldehyde-3-phosphate dehydrogenase OS = Glossina morsitans morsitans OX = 37546 GN = Gapdh PE = 2 SV = 1	0.0	Metabolism

k37_Locus_10_ Transcript_14_1	4476	54127 7	1856.57	0.19	k37_Locus_10_Tr anscript_14_1_6	sp Q68KK0 PA1_SOLIN Phospholipase A1 OS = Solenopsis invicta OX = 13686 PE = 1 SV = 1	1.54e- 51	Phospholipase
k37_Locus_1071_ _Transcript_2_1	2105	10374 6	355.85	0.04	k37_Locus_1071_ Transcript_2_1_5	sp Q4GXG7 RL18_TIMBA 60S ribosomal protein L18 OS = Timarcha balearica OX = 79517 GN = RpL18 PE = 2 SV = 1	8.75e- 70	Translation
k37_Locus_1280_ _Transcript_9_1	9989	13389 1	459.24	0.05	k37_Locus_1280_ Transcript_9_1_6	sp Q24238 APH4_DROME Alkaline phosphatase 4 OS = Drosophila melanogaster OX = 7227 GN = Alp4 PE = 2 SV = 3	1.50e- 66	Metabolism
k37_Locus_1441_ _Transcript_3_4	3432	13890 5	476.44	0.05	k37_Locus_1441_ Transcript_3_4_6	sp Q2PQM7 IDGF4_GLOMM Chitinase-like protein Idgf4 OS = Glossina morsitans morsitans OX = 37546 GN = Idgf4 PE = 2 SV = 1	9.23e- 120	Cellular Signaling
k37_Locus_1903_ _Transcript_4_2	4559	15433 7	529.37	0.05	k37_Locus_1903_ Transcript_4_2_4	sp P28648 CD63_RAT CD63 antigen OS = Rattus norvegicus OX = 10116 GN = Cd63 PE = 1 SV = 2	3.33e- 29	Cellular Signaling
k37_Locus_229_ Transcript_6_1	4838	23686 7	812.45	0.08				
k37_Locus_2459_ _Transcript_1_1	1204	30142 9	1033.9	0.1	k37_Locus_2459_ Transcript_1_1_4	sp Q962U1 RL13_SPOFR 60S ribosomal protein L13 OS = Spodoptera frugiperda OX = 7108 GN = RpL13 PE = 2 SV = 1	6.25e- 94	Translation
k37_Locus_2720_ _Transcript_1_1	517	15861 3	544.04	0.05				
k37_Locus_3057_ _Transcript_4_1	4291	12819 4	439.7	0.04				
k37_Locus_391_ Transcript_6_2	4093	12387 9	424.9	0.04	k37_Locus_391_T ranscript_6_2_6	sp Q1HRV8 ELVL1_AEDAE Elongation of very long chain fatty acids protein AAEL008004 OS = Aedes aegypti OX = 7159 GN = AAEL008004 PE = 2 SV = 2	2.63e- 105	Metabolism
k37_Locus_4169_ _Transcript_1_1	1410	26823 3	920.04	0.09	k37_Locus_4169_ Transcript_1_1_3	sp P15357 RS27A_DROME Ubiquitin-40S ribosomal protein S27a OS = Drosophila melanogaster OX = 7227 GN = RpS27A PE = 1 SV = 2	8.86e- 83	Protein Degradation
k37_Locus_4367_ _Transcript_1_1	1554	13859 3	475.37	0.05	k37_Locus_4367_ Transcript_1_1_5	sp Q4GXU6 RS4_CARGR 40S ribosomal protein S4 OS = Carabus granulatus OX = 118799 GN = RpS4 PE = 2 SV = 1	3.47e- 152	Translation
k37_Locus_45_ Transcript_14_1	5685	26654 401	91424.33	9.14		U1-PSDTX-Ta1a/U4-PSDTX-Ta1a/U5-PSDTX-Ta1a Genbank Accession Numbers : MN607166/ MN607167/ MN607171		Venom peptide

k37_Locus_472_Transcript_5_3	2292	19416 1	665.97	0.07	k37_Locus_472_Transcript_5_3_6	sp Q08169 HUGA_APIME Hyaluronidase OS = Apis mellifera OX = 7460 PE = 1 SV = 1	1.46e-55	Metabolism
k37_Locus_472_Transcript_5_4	2275	26884 2	922.13	0.09	k37_Locus_472_Transcript_5_4_6	sp Q08169 HUGA_APIME Hyaluronidase OS = Apis mellifera OX = 7460 PE = 1 SV = 1	5.72e-59	Metabolism
k37_Locus_49_Transcript_3_1	3765	86335 7	2961.31	0.3	k37_Locus_49_Transcript_3_1_5	sp Q02748 IF4A_DROME Eukaryotic initiation factor 4A OS = Drosophila melanogaster OX = 7227 GN = eIF4A PE = 1 SV = 3	1.23e-138	Translation
k37_Locus_49_Transcript_3_2	512	32744 5	1123.13	0.11				
k37_Locus_540_Transcript_2_1	2408	21402 8	734.11	0.07	k37_Locus_540_Transcript_2_1_4	sp Q9VBV3 TAKT_DROME Protein takeout OS = Drosophila melanogaster OX = 7227 GN = to PE = 2 SV = 1	1.26e-08	Circadian Rythm
k37_Locus_544_Transcript_9_1	2629	18926 3	649.17	0.06				
k37_Locus_594_Transcript_7_2	3499	16843 3	577.72	0.06	k37_Locus_594_Transcript_7_2_5	sp Q9GPH3 ATFC_BOMMO Activating transcription factor of chaperone OS = Bombyx mori OX = 7091 GN = ATFC PE = 2 SV = 1	5.72e-26	Protein Maturation
k37_Locus_6671_Transcript_1_1	2238	40955 2	1404.76	0.14	k37_Locus_6671_Transcript_1_1_1	sp P36241 RL19_DROME 60S ribosomal protein L19 OS = Drosophila melanogaster OX = 7227 GN = RpL19 PE = 1 SV = 2	4.25e-89	Translation
k37_Locus_795_Transcript_8_1	2389	48076 9	1649.03	0.16	k37_Locus_795_Transcript_8_1_2	sp O16797 RL3_DROME 60S ribosomal protein L3 OS = Drosophila melanogaster OX = 7227 GN = RpL3 PE = 1 SV = 3	0.0	Translation
k37_Locus_87_Transcript_5_1	2675	27992 6	960.14	0.1	k37_Locus_87_Transcript_5_1_4	sp P21187 PABP_DROME Polyadenylate-binding protein OS = Drosophila melanogaster OX = 7227 GN = pAbp PE = 1 SV = 3	0.0	RNA Maturation
k37_Locus_921_Transcript_7_2	1145	29579 8	1014.58	0.1	k37_Locus_921_Transcript_7_2_4	sp C0HKA1 RS14B_DROME 40S ribosomal protein S14b OS = Drosophila melanogaster OX = 7227 GN = RpS14b PE = 2 SV = 1	7.47e-85	Translation
k37_Locus_9365_Transcript_5_1	3029	19822 8	679.92	0.07	k37_Locus_9365_Transcript_5_1_3	sp Q5ZIR1 SHLB1_CHICK Endophilin-B1 OS = Gallus gallus OX = 9031 GN = SH3GLB1 PE = 2 SV = 1	3.22e-64	Secretion / Translation

					k37_Locus_9365_Transcript_5_1_6	sp Q962R1 RS18_SPOFR 40S ribosomal protein S18 OS = Spodoptera frugiperda OX = 7108 GN = RpS18 PE = 2 SV = 1	9.35e-85	
k43_Locus_114_Transcript_2_1	2476	214200	734.7	0.07	k43_Locus_114_Transcript_2_1_6	sp Q963B7 RL9_SPOFR 60S ribosomal protein L9 OS = Spodoptera frugiperda OX = 7108 GN = RpL9 PE = 2 SV = 1	3.81e-91	Translation
k43_Locus_133_Transcript_7_1	2837	800213	2744.72	0.27	k43_Locus_133_Transcript_7_1_5	sp Q3ZU95 PA1_VESGE Phospholipase A1 OS = Vespula germanica OX = 30212 PE = 2 SV = 1	4.12e-19	Phospholipase
					k43_Locus_133_Transcript_7_1_5	sp Q68KK0 PA1_SOLIN Phospholipase A1 OS = Solenopsis invicta OX = 13686 PE = 1 SV = 1	4.11e-15	
k43_Locus_1473_Transcript_5_1	3652	407837	1398.88	0.14	k43_Locus_1473_Transcript_5_1_3	sp P14318 MP20_DROME Muscle-specific protein 20 OS = Drosophila melanogaster OX = 7227 GN = Mp20 PE = 2 SV = 2	9.42e-96	Cytoskeleton
k43_Locus_1496_Transcript_10_1	2917	196144	672.77	0.07				
k43_Locus_1586_7_Transcript_1_1	600	449378	1541.36	0.15		U2-PSDTX-Ta1a Genbank Accession Number : MN607169		Venom peptide
k43_Locus_209_Transcript_2_5	3324	118224	405.51	0.04	k43_Locus_209_Transcript_2_5_1	sp O08623 SQSTM_RAT Sequestosome-1 OS = Rattus norvegicus OX = 10116 GN = Sqstm1 PE = 1 SV = 1	9.72e-30	Protein Degradation
k43_Locus_3217_Transcript_3_3	1201	282147	967.76	0.1	k43_Locus_3217_Transcript_3_3_4	sp P30736 RL15_CHITE 60S ribosomal protein L15 OS = Chironomus tentans OX = 7153 GN = RpL15 PE = 3 SV = 3	1.14e-109	Translation
k43_Locus_3840_Transcript_4_2	2659	166658	571.64	0.06	k43_Locus_3840_Transcript_4_2_5	sp Q9NV56 MRGBP_HUMAN MRG/MORF4L-binding protein OS = Homo sapiens OX = 9606 GN = MRGBP PE = 1 SV = 1	7.48e-24	Transcription
k43_Locus_530_Transcript_3_1	1144	168563	578.17	0.06	k43_Locus_530_Transcript_3_1_4	sp Q962R9 RS10_SPOFR 40S ribosomal protein S10 OS = Spodoptera frugiperda OX = 7108 GN = RpS10 PE = 2 SV = 1	4.44e-70	Translation
k43_Locus_588_Transcript_3_1	1555	5439505	18657.45	1.87	k43_Locus_588_Transcript_3_1_3	sp P29183 LIPP_HORSE Pancreatic triacylglycerol lipase (Fragment) OS = Equus caballus OX = 9796 GN = PNLIP PE = 1 SV = 2	8.49e-31	Phospholipase

k43_Locus_684_Transcript_1_1	1148	128005	439.06	0.04					
k43_Locus_713_Transcript_5_1	4230	116545	399.75	0.04	k43_Locus_713_Transcript_5_1_1	sp Q14186 TFDP1_HUMAN Transcription factor Dp-1 OS = Homo sapiens OX = 9606 GN = TFDP1 PE = 1 SV = 1	1.18e-99	Transcription	
k43_Locus_7363_Transcript_5_1	3050	261401	896.6	0.09	k43_Locus_7363_Transcript_5_1_2	sp Q4GXU6 RS4_CARGR 40S ribosomal protein S4 OS = Carabus granulatus OX = 118799 GN = RpS4 PE = 2 SV = 1	2.03e-166	Translation	
					k43_Locus_7363_Transcript_5_1_5	sp A4Q9E4 TTLL2_MOUSE Probable tubulin polyglutamylase TTLL2 OS = Mus musculus OX = 10090 GN = Ttll2 PE = 2 SV = 1	9.34e-79		
k43_Locus_82_Transcript_8_5	2674	760033	2606.91	0.26	k43_Locus_82_Transcript_8_5_4	sp Q9XZ43 5NTD_LUTLO Protein 5NUC OS = Lutzomyia longipalpis OX = 7200 GN = 5NUC PE = 1 SV = 1	9.94e-78	Metabolism	
					k43_Locus_82_Transcript_8_5_5	sp B6EWW8 V5NTD_GLOBR Snake venom 5'-nucleotidase OS = Gloydius brevicaudus OX = 259325 PE = 2 SV = 1	1.27e-39		
k49_Locus_10848_Transcript_1_1	915	150777	517.16	0.05	k49_Locus_10848_Transcript_1_1_4	sp Q02878 RL6_HUMAN 60S ribosomal protein L6 OS = Homo sapiens OX = 9606 GN = RPL6 PE = 1 SV = 3	3.50e-44	Translation	
k49_Locus_11970_Transcript_2_1	2958	108163	371	0.04	k49_Locus_11970_Transcript_2_1_2	sp P84185 ACT5C_ANOGA Actin-5C OS = Anopheles gambiae OX = 7165 GN = Act5C PE = 2 SV = 1	0.0	Cytoskeleton	
k49_Locus_1327_Transcript_9_1	7028	319087	1094.47	0.11					
k49_Locus_1493_Transcript_10_1	3416	101654	348.67	0.03	k49_Locus_1493_Transcript_10_1_2	sp Q2T9X3 SPRY7_BOVIN SPRY domain-containing protein 7 OS = Bos taurus OX = 9913 GN = SPRYD7 PE = 2 SV = 1	1.32e-55	Protein Degradation	
k49_Locus_15244_Transcript_1_1	350	104281	357.68	0.04					
k49_Locus_1637_Transcript_10_1	5305	799829	2743.41	0.27	k49_Locus_1637_Transcript_10_1_6	sp Q24238 APH4_DROME Alkaline phosphatase 4 OS = Drosophila melanogaster OX = 7227 GN = Alp4 PE = 2 SV = 3	3.33e-121	Metabolism	

k49_Locus_2359_Transcript_3_1	4026	116626	400.03	0.04	k49_Locus_2359_Transcript_3_1_3	sp Q9DA39 LFG4_MOUSE Protein lifeguard 4 OS = Mus musculus OX = 10090 GN = Tmbim4 PE = 2 SV = 1	4.06e-56	Anti-apoptosis/ RE morphology/ Translation
					k49_Locus_2359_Transcript_3_1_5	sp Q6PFM4 LNPB_DANRE Endoplasmic reticulum junction formation protein lunapark-B OS = Danio rerio OX = 7955 GN = lnpgb PE = 2 SV = 2	1.41e-64	
					k49_Locus_2359_Transcript_3_1_6	sp Q95WA0 RL26_LITLI 60S ribosomal protein L26 OS = Littorina littorea OX = 31216 GN = RPL26 PE = 2 SV = 1	5.49e-68	
k49_Locus_281_Transcript_3_1	2899	1693164	5807.54	0.58	k49_Locus_281_Transcript_3_1_4	sp Q02942 TRF_BLADI Transferrin OS = Blaberus discoidalis OX = 6981 PE = 1 SV = 1	0.0	Metabolism
k49_Locus_322_Transcript_9_3	1247	404161	1386.27	0.14				
k49_Locus_322_Transcript_9_4	2573	487718	1672.87	0.17	k49_Locus_322_Transcript_9_4_5	sp P17892 LIPR2_MOUSE Pancreatic lipase-related protein 2 OS = Mus musculus OX = 10090 GN = Pnliprp2 PE = 1 SV = 2	1.08e-86	Phospholipase
k49_Locus_397_Transcript_1_1	2724	975919	3347.39	0.33	k49_Locus_397_Transcript_1_1_5	sp P54399 PDI_DROME Protein disulfide-isomerase OS = Drosophila melanogaster OX = 7227 GN = Pdi PE = 2 SV = 1	0.0	Protein Maturation
k49_Locus_4240_Transcript_9_2	2005	220115	754.99	0.08	k49_Locus_4240_Transcript_9_2_2	sp Q963B6 RL10A_SPOFR 60S ribosomal protein L10a OS = Spodoptera frugiperda OX = 7108 GN = RpL10A PE = 2 SV = 1	2.71e-119	Translation
k49_Locus_450_Transcript_3_1	2738	107051	367.18	0.04				
k49_Locus_47_Transcript_1_1	1591	282287	968.24	0.1				
k49_Locus_5739_Transcript_4_1	7855	149510	512.82	0.05	k49_Locus_5739_Transcript_4_1_1	sp Q7M4F3 CUD2_SCHGR Endocuticle structural glycoprotein SgAbd-2 OS = Schistocerca gregaria OX = 7010 PE = 1 SV = 1	4.13e-21	Cuticle
k49_Locus_8888_Transcript_2_1	4025	115905	397.55	0.04	k49_Locus_8888_Transcript_2_1_6	sp P14318 MP20_DROME Muscle-specific protein 20 OS = Drosophila melanogaster OX = 7227 GN = Mp20 PE = 2 SV = 2	8.21e-65	Cytoskeleton
k49_Locus_9979_Transcript_1_1	496	171592	588.56	0.06				

k55_Locus_113_Transcript_10_1	3158	1321901	4534.11	0.45	k55_Locus_113_Transcript_10_1_4	sp Q3T126 CNIH4_BOVIN Protein cornichon homolog 4 OS = Bos taurus OX = 9913 GN = CNIH4 PE = 2 SV = 1	1.60e-39	Secretion / Phospholipase
					k55_Locus_113_Transcript_10_1_6	sp Q68KK0 PA1_SOLIN Phospholipase A1 OS = Solenopsis invicta OX = 13686 PE = 1 SV = 1	1.43e-31	
k55_Locus_12090_Transcript_2_1	2579	103030	353.39	0.04				
k55_Locus_12339_Transcript_1_1	1043	116259	398.77	0.04	k55_Locus_12339_Transcript_1_1_5	sp P41822 FRI_AEDAE Ferritin subunit OS = Aedes aegypti OX = 7159 GN = FERH PE = 1 SV = 2	1.34e-40	Metabolism
k55_Locus_1250_Transcript_14_3	1123	356892	1224.14	0.12	k55_Locus_1250_Transcript_14_3_1	sp Q5G5C4 RS3A_PERAM 40S ribosomal protein S3a OS = Periplaneta americana OX = 6978 GN = Parcxpwex01 PE = 2 SV = 1	2.43e-139	Translation
k55_Locus_1331_Transcript_6_1	4877	235948	809.3	0.08				
k55_Locus_1565_Transcript_7_1	5153	687748	2358.97	0.24	k55_Locus_1565_Transcript_7_1_6	sp Q24238 APH4_DROME Alkaline phosphatase 4 OS = Drosophila melanogaster OX = 7227 GN = Alp4 PE = 2 SV = 3	6.44e-76	Metabolism
k55_Locus_185_Transcript_11_1	1096	462590	1586.68	0.16	k55_Locus_185_Transcript_11_1_5	sp P35778 VA3_SOLIN Venom allergen 3 OS = Solenopsis invicta OX = 13686 PE = 1 SV = 2	1.15e-71	Venom allergen
k55_Locus_2271_Transcript_5_2	1733	273202	937.08	0.09	k55_Locus_2271_Transcript_5_2_2	sp Q9DA39 LFG4_MOUSE Protein lifeguard 4 OS = Mus musculus OX = 10090 GN = Tmbim4 PE = 2 SV = 1	4.66e-50	Translation
					k55_Locus_2271_Transcript_5_2_5	sp Q95WA0 RL26_LITLI 60S ribosomal protein L26 OS = Littorina littorea OX = 31216 GN = RPL26 PE = 2 SV = 1	5.49e-68	
k55_Locus_2505_Transcript_11_2	3085	221164	758.59	0.08	k55_Locus_2505_Transcript_11_2_6	sp B2D0J4 VDPP4_APIME Venom dipeptidyl peptidase 4 OS = Apis mellifera OX = 7460 PE = 1 SV = 1	2.46e-110	Peptide Maturation
k55_Locus_2784_Transcript_7_1	3736	186655	640.22	0.06				
k55_Locus_2784_Transcript_7_2	1355	386247	1324.82	0.13				
k55_Locus_2824_Transcript_2_1	1210	317588	1089.32	0.11	k55_Locus_2824_Transcript_2_1_1	sp Q5UAP4 RSSA_BOMMO 40S ribosomal protein SA OS = Bombyx mori OX = 7091 PE = 2 SV = 1	1.39e-124	Translation

k55_Locus_38_Transcript_120_1	10401	4377671	15015.37	1.5	k55_Locus_38_Transcript_120_1_1	sp Q17750 UFL1_CAEEL E3 UFM1-protein ligase 1 homolog OS = Caenorhabditis elegans OX = 6239 GN = ufl-1 PE = 3 SV = 1	0.17	RNA Maturation
					k55_Locus_38_Transcript_120_1_3	sp Q0JKD0 GLT1_ORYSJ Glutamate synthase 1 [NADH]. chloroplastic OS = Oryza sativa subsp. japonica OX = 39947 GN = Os01g0681900 PE = 2 SV = 1	0.45	
					k55_Locus_38_Transcript_120_1_4	sp Q09575 YRD6_CAEEL Uncharacterized protein K02A2.6 OS = Caenorhabditis elegans OX = 6239 GN = K02A2.6 PE = 4 SV = 1	2.61e-27	
					k55_Locus_38_Transcript_120_1_6	sp Q09575 YRD6_CAEEL Uncharacterized protein K02A2.6 OS = Caenorhabditis elegans OX = 6239 GN = K02A2.6 PE = 4 SV = 1	2.51e-18	
					k55_Locus_38_Transcript_120_1_6	sp Q5F3X4 U5S1_CHICK 116 kDa U5 small nuclear ribonucleoprotein component OS = Gallus gallus OX = 9031 GN = EFTUD2 PE = 2 SV = 1	0.0	
k55_Locus_3981_Transcript_1_1	1058	303870	1042.27	0.1				
k55_Locus_44_Transcript_1_1	1186	336982	1155.84	0.12	k55_Locus_44_Transcript_1_1_1	sp Q75VN3 TCTP_BOMMO Translationally-controlled tumor protein homolog OS = Bombyx mori OX = 7091 GN = Tctp PE = 2 SV = 1	1.06e-85	Cytoskeleton
k55_Locus_485_Transcript_9_1	2206	308425	10578.86	1.06	k55_Locus_485_Transcript_9_1_2	sp Q6XZB0 LIPI_HUMAN Lipase member I OS = Homo sapiens OX = 9606 GN = LIPI PE = 1 SV = 3	5.93e-25	Phospholipase
k55_Locus_485_Transcript_9_2	1849	679023	2329.04	0.23				Chemoreception
k55_Locus_52_Transcript_7_1	2781	101603	348.5	0.03				
k55_Locus_552_Transcript_9_1	3315	267983	919.18	0.09	k55_Locus_552_Transcript_9_1_4	sp P0CG71 UBIQ1_CAEEL Polyubiquitin-A OS = Caenorhabditis elegans OX = 6239 GN = ubq-1 PE = 3 SV = 1	0.0	Protein Degradation
k55_Locus_5854_Transcript_3_1	7511	251601	862.99	0.09	k55_Locus_5854_Transcript_3_1_3	sp Q7M4F3 CUD2_SCHGR Endocuticle structural glycoprotein SgAbd-2 OS = Schistocerca gregaria OX = 7010 PE = 1 SV = 1	4.13e-21	Cuticule

k55_Locus_61_Transcript_6_1	2678	478123	1639.96	0.16	k55_Locus_61_Transcript_6_1_6	sp P29341 PABP1_MOUSE Polyadenylate-binding protein 1 OS = Mus musculus OX = 10090 GN = Pabpc1 PE = 1 SV = 2	0.0	RNA Maturation
k55_Locus_6635_Transcript_3_1	785	191741	657.67	0.07				
k55_Locus_6656_Transcript_3_2	845	113578	389.57	0.04	k55_Locus_6656_Transcript_3_2_4	sp P18101 RL40_DROME Ubiquitin-60S ribosomal protein L40 OS = Drosophila melanogaster OX = 7227 GN = RpL40 PE = 1 SV = 2	2.40e-81	Protein Degradation
k55_Locus_7083_Transcript_1_1	2980	102356	351.08	0.04	k55_Locus_7083_Transcript_1_1_5	sp Q9VFC2 SP88E_DROME Serine protease inhibitor 88Ea OS = Drosophila melanogaster OX = 7227 GN = Spn88Ea PE = 2 SV = 1	2.55e-61	Immunity
k55_Locus_7703_Transcript_1_1	2688	1054862	3618.17	0.36	k55_Locus_7703_Transcript_1_1_1	sp A4IHT0 FIGL1_XENTR Fidgetin-like protein 1 OS = Xenopus tropicalis OX = 8364 GN = fign1 PE = 2 SV = 1	3.88e-134	DNA Repair
k55_Locus_8_Transcript_7_1	4349	15942157	54681.44	5.47	k55_Locus_8_Transcript_7_1_5	sp Q3ZU95 PA1_VESGE Phospholipase A1 OS = Vesputia germanica OX = 30212 PE = 2 SV = 1	2.56e-45	Phospholipase
					k55_Locus_8_Transcript_7_1_6	sp Q3ZU95 PA1_VESGE Phospholipase A1 OS = Vesputia germanica OX = 30212 PE = 2 SV = 1	4.18e-45	
k55_Locus_9803_Transcript_1_1	4289	106632	365.75	0.04	k55_Locus_9803_Transcript_1_1_6	sp Q9UBV2 SE1L1_HUMAN Protein sel-1 homolog 1 OS = Homo sapiens OX = 9606 GN = SEL1L PE = 1 SV = 3	0.0	Protein Maturation
k55_Locus_996_Transcript_10_1	3799	416066	1427.1	0.14				
k61_Locus_10818_Transcript_1_1	1302	298160	1022.69	0.1				
k61_Locus_11296_Transcript_3_1	1613	517779	1775.98	0.18	k61_Locus_11296_Transcript_3_1_5	sp Q94624 RS6_MANSE 40S ribosomal protein S6 OS = Manduca sexta OX = 7130 GN = RpS6 PE = 2 SV = 1	2.98e-125	Translation
k61_Locus_175_Transcript_2_1	2594	357838	1227.38	0.12	k61_Locus_175_Transcript_2_1_2	sp P09180 RL4_DROME 60S ribosomal protein L4 OS = Drosophila melanogaster OX = 7227 GN = RpL4 PE = 1 SV = 2	3.20e-116	Translation
k61_Locus_1787_Transcript_1_1	1871	134466	461.22	0.05	k61_Locus_1787_Transcript_1_1_5	sp Q58FK9 KAT3_RAT Kynurenine--oxoglutarate transaminase 3 OS = Rattus norvegicus OX = 10116 GN = Kyat3 PE = 2 SV = 1	5.73e-91	Protein Maturation

k61_Locus_1873_Transcript_9_2	1132	35973 8	1233.9	0.12	k61_Locus_1873_Transcript_9_2_6	sp Q5G5C4 RS3A_PERAM 40S ribosomal protein S3a OS = Periplaneta americana OX = 6978 GN = Parcxpwex01 PE = 2 SV = 1	2.43e-139	Translation
k61_Locus_2007_Transcript_1_2	904	50234 5	1723.04	0.17	k61_Locus_2007_Transcript_1_2_6	sp Q8WQI7 RL18A_SPOFR 60S ribosomal protein L18a OS = Spodoptera frugiperda OX = 7108 GN = RpL18A PE = 2 SV = 1	6.38e-81	Translation
k61_Locus_2081_Transcript_6_1	3183	11992 3	411.33	0.04	k61_Locus_2081_Transcript_6_1_1	sp P91887 AMPN_PLUXY Aminopeptidase N OS = Plutella xylostella OX = 51655 GN = APN1 PE = 1 SV = 1	2.01e-80	Peptide Maturation
k61_Locus_2381_Transcript_1_1	3338	24358 0	835.48	0.08	k61_Locus_2381_Transcript_1_1_1	sp P12919 PDGFB_FELCA Platelet-derived growth factor subunit B OS = Felis catus OX = 9685 GN = PDGFB PE = 2 SV = 1	1.57e-05	Unknown
k61_Locus_250_Transcript_6_2	2112	20662 0	708.7	0.07	k61_Locus_250_Transcript_6_2_6	sp P29413 CALR_DROME Calreticulin OS = Drosophila melanogaster OX = 7227 GN = Calr PE = 1 SV = 2	0.0	Protein Maturation
k61_Locus_2935_Transcript_2_3	2338	33072 2	1134.37	0.11	k61_Locus_2935_Transcript_2_3_2	sp P06603 TBA1_DROME Tubulin alpha-1 chain OS = Drosophila melanogaster OX = 7227 GN = alphaTub84B PE = 1 SV = 1	0.0	Cytoskeleton
k61_Locus_3810_Transcript_2_1	4984	30465 9	1044.98	0.1	k61_Locus_3810_Transcript_2_1_6	sp Q2TBQ5 RL7A_BOVIN 60S ribosomal protein L7a OS = Bos taurus OX = 9913 GN = RPL7A PE = 2 SV = 3	7.48e-121	Translation
k61_Locus_40_Transcript_1_1	953	53161 2	1823.42	0.18				Cytoskeleton
k61_Locus_438_Transcript_8_1	3543	46369 7	1590.48	0.16	k61_Locus_438_Transcript_8_1_1	sp P0CG71 UBIQ1_CAEEL Polyubiquitin-A OS = Caenorhabditis elegans OX = 6239 GN = ubq-1 PE = 3 SV = 1	0.0	Protein Degradation
k61_Locus_4981_Transcript_2_1	1829	18384 0	630.57	0.06	k61_Locus_4981_Transcript_2_1_1	sp P14318 MP20_DROME Muscle-specific protein 20 OS = Drosophila melanogaster OX = 7227 GN = Mp20 PE = 2 SV = 2	8.73e-89	Cytoskeleton
k61_Locus_500_Transcript_6_4	2349	23908 7	820.07	0.08	k61_Locus_500_Transcript_6_4_6	sp P35502 ESTF_MYZPE Esterase FE4 OS = Myzus persicae OX = 13164 PE = 1 SV = 1	2.35e-81	Unknown
k61_Locus_582_Transcript_6_1	3659	18658 8	639.99	0.06	k61_Locus_582_Transcript_6_1_1	sp P12261 EF1G_ARTSA Elongation factor 1-gamma OS = Artemia salina OX = 85549 PE = 1 SV = 3	9.62e-179	Translation
k65_Locus_104_Transcript_8_1	3715	57846 0	1984.11	0.2	k65_Locus_104_Transcript_8_1_4	sp Q3T126 CNIH4_BOVIN Protein cornichon homolog 4 OS = Bos taurus OX = 9913 GN = CNIH4 PE = 2 SV = 1	1.60e-39	Secretion / Phospholipase

					k65_Locus_104_Transcript_8_1_6	sp Q3ZU95 PA1_VESGE Phospholipase A1 OS = Vespula germanica OX = 30212 PE = 2 SV = 1	1.82e-30	
k65_Locus_1147_Transcript_2_1	3286	1567170	5375.38	0.54	k65_Locus_1147_Transcript_2_1_5	sp P13060 EF2_DROME Elongation factor 2 OS = Drosophila melanogaster OX = 7227 GN = EF2 PE = 1 SV = 4	0.0	Translation
k65_Locus_2088_Transcript_11_1_1	2921	166472	571	0.06	k65_Locus_2088_Transcript_11_1_2	sp Q9V447 KRH2_DROME Krueppel homolog 2 OS = Drosophila melanogaster OX = 7227 GN = Kr-h2 PE = 1 SV = 1	6.94e-59	Protein Maturation / Translation
					k65_Locus_2088_Transcript_11_1_5	sp Q5R465 RS3_PONAB 40S ribosomal protein S3 OS = Pongo abelii OX = 9601 GN = RPS3 PE = 2 SV = 1	7.22e-52	
k65_Locus_26_Transcript_2_1	1745	2180583	7479.38	0.75	MTSDERRSYLPLLLAVIFVLAIVHTPSVESRASADAEAD AFADALAKAIANADPGILGVIARWIWKLILQILAPTAA VEVATRLGLPQK			Venom peptide
k65_Locus_4162_Transcript_4_1	1925	205899	706.23	0.07				
k65_Locus_5275_Transcript_1_1	1660	206711	709.02	0.07	k65_Locus_5275_Transcript_1_1_3	sp P08570 RLA1_DROME 60S acidic ribosomal protein P1 OS = Drosophila melanogaster OX = 7227 GN = RpLP1 PE = 1 SV = 2	3.78e-36	Translation
k65_Locus_596_Transcript_1_1	742	195654	671.09	0.07	k65_Locus_596_Transcript_1_1_5	sp O76756 RS8_APIIME 40S ribosomal protein S8 OS = Apis mellifera OX = 7460 GN = RpS8 PE = 2 SV = 2	2.23e-136	Translation
k65_Locus_7655_Transcript_3_1	2345	333912	1145.31	0.11	k65_Locus_7655_Transcript_3_1_4	sp P32100 RL7_DROME 60S ribosomal protein L7 OS = Drosophila melanogaster OX = 7227 GN = RpL7 PE = 1 SV = 2	1.90e-103	Translation
k65_Locus_83_Transcript_7_1	4005	113652	389.83	0.04				
k65_Locus_8694_Transcript_4_1	2406	2085397	7152.89	0.72	k65_Locus_8694_Transcript_4_1_1	sp P35778 VA3_SOLIN Venom allergen 3 OS = Solenopsis invicta OX = 13686 PE = 1 SV = 2	1.17e-47	Venom allergen
					k65_Locus_8694_Transcript_4_1_1	sp P35778 VA3_SOLIN Venom allergen 3 OS = Solenopsis invicta OX = 13686 PE = 1 SV = 2	9.87e-51	
k65_Locus_9888_Transcript_6_2	1228	168267	577.15	0.06	k65_Locus_9888_Transcript_6_2_6	sp Q6EV04 RS3A_BIPLU 40S ribosomal protein S3a OS = Biphyllus lunatus OX = 197003 PE = 2 SV = 1	1.87e-142	Translation

k69_Locus_1020 2_Transcript_2_2	1480	13427 9	460.58	0.05					
k69_Locus_1049 _Transcript_1_1	548	19660 8	674.36	0.07					
k69_Locus_110_ Transcript_5_1	3341	19212 34	6589.81	0.66	k69_Locus_110_T ranscript_5_1_6	sp Q3ZU95 PA1_VESGE Phospholipase A1 OS = Vespula germanica OX = 30212 PE = 2 SV = 1	8.05e- 45	Phospholipase	
k69_Locus_1158 0_Transcript_1_1	727	19845 2	680.69	0.07	k69_Locus_11580 _Transcript_1_1_6	sp Q75VN3 TCTP_BOMMO Translationally-controlled tumor protein homolog OS = Bombyx mori OX = 7091 GN = Tctp PE = 2 SV = 1	1.20e- 45	Cytoskeleton	
k69_Locus_1227 2_Transcript_1_1	720	24498 3	840.29	0.08	k69_Locus_12272 _Transcript_1_1_4	sp O96647 RL10_BOMMA 60S ribosomal protein L10 OS = Bombyx mandarina OX = 7092 GN = RpL10 PE = 2 SV = 1	3.53e- 112	Translation	
k69_Locus_1235 5_Transcript_5_1	2460	29948 67	10272.36	1.03	k69_Locus_12355 _Transcript_5_1_6	sp P35778 VA3_SOLIN Venom allergen 3 OS = Solenopsis invicta OX = 13686 PE = 1 SV = 2	1.17e- 47	Venom allergen	
					k69_Locus_12355 _Transcript_5_1_6	sp P35778 VA3_SOLIN Venom allergen 3 OS = Solenopsis invicta OX = 13686 PE = 1 SV = 2	1.01e- 71		
k69_Locus_1459 3_Transcript_1_1	598	28645 7	982.54	0.1	k69_Locus_14593 _Transcript_1_1_1	sp P05389 RLA2_DROME 60S acidic ribosomal protein P2 OS = Drosophila melanogaster OX = 7227 GN = RpLP2 PE = 1 SV = 1	2.91e- 24	Translation	
k69_Locus_1496 4_Transcript_1_1	1925	13033 5	447.05	0.04	k69_Locus_14964 _Transcript_1_1_4	sp P35501 ESTE_MYZPE Esterase E4 OS = Myzus persicae OX = 13164 PE = 1 SV = 1	4.99e- 82	Unknown	
k69_Locus_1683 4_Transcript_1_1	739	65913 9	2260.84	0.23		U2-PSDTX-Ta1c Genbank Accession Numbers : MN607168		Venom peptide	
k69_Locus_2100 _Transcript_4_1	7317	13391 4	459.32	0.05	k69_Locus_2100_ Transcript_4_1_1	sp O95602 RPA1_HUMAN DNA-directed RNA polymerase I subunit RPA1 OS = Homo sapiens OX = 9606 GN = POLR1A PE = 1 SV = 2	0.0	Transcription	

k69_Locus_3195_Transcript_5_1	4866	119870	411.15	0.04	k69_Locus_3195_Transcript_5_1_5	sp Q8IZJ3 CPMD8_HUMAN C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8 OS = Homo sapiens OX = 9606 GN = CPAMD8 PE = 1 SV = 2	1.14e-06	Protein Maturation
k69_Locus_4946_Transcript_1_1	2719	246026	843.87	0.08				
k69_Locus_547_Transcript_3_1	2747	23555899	80796.5	8.08				
k69_Locus_64_Transcript_10_4	3190	2483041	8516.81	0.85	k69_Locus_64_Transcript_10_4_6	sp Q9XZ43 5NTD_LUTLO Protein 5NUC OS = Lutzomyia longipalpis OX = 7200 GN = 5NUC PE = 1 SV = 1	4.98e-123	Metabolism
k69_Locus_678_Transcript_6_1	4344	165812	568.73	0.06	k69_Locus_678_Transcript_6_1_1	sp P07602 SAP_HUMAN Prosaposin OS = Homo sapiens OX = 9606 GN = PSAP PE = 1 SV = 2	6.11e-38	Cellular Signaling
k69_Locus_8284_Transcript_2_1	2255	704605	2416.79	0.24				
k69_Locus_87_Transcript_11_1	1120	845555	2900.25	0.29	k69_Locus_87_Transcript_11_1_2	sp Q9BMK4 PA2_APICC Phospholipase A2 OS = Apis cerana cerana OX = 94128 PE = 2 SV = 1	9.55e-26	Phospholipase
k69_Locus_9580_Transcript_1_1	3482	620884	2129.63	0.21	k69_Locus_9580_Transcript_1_1_1	sp B0FWD3 NU5M_AEDAE NADH-ubiquinone oxidoreductase chain 5 OS = Aedes aegypti OX = 7159 GN = mt:ND5 PE = 3 SV = 1	1.83e-60	Metabolism
					k69_Locus_9580_Transcript_1_1_3	sp Q1HR20 NU4M_AEDAE NADH-ubiquinone oxidoreductase chain 4 OS = Aedes aegypti OX = 7159 GN = mt:ND4 PE = 2 SV = 1	3.57e-19	