

Supplementary Information

Table S1. Reviewed entries of transcriptome data based on salivary and venom gland samples available for venomous arthropod species. Public database of NCBI (SRA archive, TSA archive, dbEST and GenBank) were screened for venom gland derived EST or NGS data transcripts. Operated search-terms were “salivary gland”, “venom gland”, “poison gland”, “venom”, “poison sack”.

Species name	Systematic status	Database source	Experiment Title	Study Title	Instrument	Submitter	Study Accession	Sample Accession	Total Size, Mb
Crustacea									
<i>Xibalbanus</i> (former <i>Speleonectes</i>) <i>tulumensis</i>	Remipedia, Speleonectidae	SRX282054	454 Venom gland Transcriptome Speleonectes	The First Venomous Crustacean Revealed by Transcriptomics and Functional Morphology: Remipede Venom Glands Express a Unique Toxin Cocktail Dominated by Enzymes and a Neurotoxin, MBE 2014, 31 (1)	454 GS FLX Titanium	vReumont, NHM London	SRP026153	SRR857228	639
Hexapoda									
Diptera									
<i>Aedes aegypti</i>	Culicidae	dbEST	Total RNA isolated from Aedes aegypti salivary gland Normalized cDNA library	Verjovski-Almeida,S., Eiglmeier,K., El-Dorry,H. etal, unpublished , 2005	Sanger dideoxy	Instituto de Quimica - Universidade de Sao Paulo	dbEST: 21107 Sequences		
<i>Anopheles albimanus</i>	Culicidae	dbEST	Adult female Anopheles albimanus salivary gland cDNA library	EST survey of the Anopheles albimanus transcriptome, 2007, unpublished	Sanger dideoxy	Centro de Investigacion Sobre Enfermedades Infecciosas, Mexico	dbEST: 801 Sequences		
<i>Anopheles darlingii</i>	Culicidae	dbEST	The salivary gland transcriptome of the neotropical malaria vector Anopheles darlingi reveals accelerated evolution o genes relevant to hematophagyf	BMC Genomics 10 (1): 57 2009	Sanger dideoxy	National Institute of Allergy and Infectious Diseases	dbEST: 2576 Sequences		
<i>Anopheles dirus</i>	Culicidae	SRX309996	Adult female Anopheles dirus salivary glands	An insight into the sialomes of Psorophora albipes, Anopheles dirus and An. freeborni	Illumina HiSeq 2000	NIAID	SRP026153	SRS448457	9453.44
<i>Anopheles freeborni</i>	# Culicidae	SRX309997	Adult female Anopheles freeborni salivary glands	An insight into the sialomes of Psorophora albipes, Anopheles dirus and An. freeborni	Illumina HiSeq 2000	NIAID	SRP026153	SRS448458	9727.64
<i>Anopheles freeborni</i>	Culicidae	dbEST	LIBEST_024537 Adult female Anopheles freeborni salivary glands	An insight into the sialotranscriptome of Anopheles freeborni, 2009, unpublished	Sanger dideoxy	National Institute of Allergy and Infectious Diseases	dbEST: 456 Sequences		
<i>Anopheles funestus</i>	Culicidae	dbEST	LIBEST_020312 Adult female Anopheles funestus salivary glands	An insight into the sialotranscriptome of Anopheles funestus, 2006, unpublished	Sanger dideoxy	National Institute of Allergy and Infectious Diseases	dbEST: 959 Sequences		
<i>Anopheles gambiae</i>	# Culiciade	SRX383889	Diversity of the Anopheles gambiae mosquito microbiota and interactions with Plasmodium falciparum in the mosquito midgut	Anopheles gambiae mosquitoes were sampled in aquantic habitats at the L4 and pupae stages in five localities (Ahala, Nkolbisson, Nkolomdom, Mvan, Odza) Metagenome	454 GS FLX Titanium	IRD-MIVEGEC	SRP033327	SRS507861	1414.95
<i>Anopheles stephensi</i>	Culicidae	dbEST	LIBEST_023855 Anopheles stephensi salivary gland library	Exploring the salivary gland transcriptome and proteome of the Anopheles stephensi mosquito, Insect Biochem. Mol. Biol. 33 (7): 717-732 2003	Sanger dideoxy	National Institute of Allergy and Infectious Diseases	dbEST: 1407 Sequences		
<i>Corethrella appendiculata</i>	Corethrellidae	SRX334950	Corethrella apendiculata salivary transcriptome	An insight into the sialomes of Corethrella apendiculata and Lutzomyia umbratilis	Illumina HiSeq 2000	NIAID	SRP028800	SRS464921	6051.57
<i>Corethrella appendiculata</i>	Corethrellidae	SRX328781	Corethrella appendiculata salivary gland transcriptome from adult female flies	Corethrella appendiculata salivary glands transcriptome	Illumina HiSeq 2000	NIAID	SRP028303	SRS464921	6051.57
<i>Culex quinquefasciatus</i>	Culicidae	dbEST	LIBEST_024959 Adult female salivary gland cDNA library	An insight into the salivary transcriptome and proteome of the adult female mosquito Culex pipiens quinquefasciatus, Insect Biochem. Mol. Biol. 34 (6): 543-563 2004	Sanger dideoxy	National Institute of Allergy and Infectious Diseases	dbEST: 531 Sequences		
<i>Culex tarsalis</i>	Culicidae	dbEST	An insight into the sialotranscriptome of Culex tarsalis mosquitoes	unidirectional library was constructed using long distance PCR (Smart cDNA kit) and Lambda Triplex2 vector	Sanger dideoxy	NIAID	dbEST: 1690 Sequences		
<i>Culicoides sonorensis</i>	Culicidae	dbEST	LIBEST_015690 Culicoides sonorensis female salivary gland	Expressed sequence tags from Culicoides sonorensis adult female salivary glands, 2004, unpublished	Sanger dideoxy	College of Agriculture, WY, USA	dbEST: 1258 Sequences		
<i>Glossina morsitans morsitans</i>	# Calyptratae, Glossinidae	SRX342351	Insights into the trypanosome transmission process revealed through transcriptomic analysis of parasitized tsetse salivary glands	Glossina morsitans morsitans strain:Yale Strain Transcriptome or Gene expression	Illumina HiSeq 1000	Yale University	SRP029394	SRS475187	3778.27
<i>Glossina morsitans morsitans</i>	Calyptratae, Glossinidae	SRX342350	Insights into the trypanosome transmission process revealed through transcriptomic analysis of parasitized tsetse salivary glands	Glossina morsitans morsitans strain:Yale Strain Transcriptome or Gene expression	Illumina HiSeq 1000	Yale University	SRP029394	SRS475186	5368.78
<i>Lucilia sericata</i> *	Calliphoridae	SRX099046	salivary glands 2	Developmental Profile of the Lucilia sericata Transcriptome	454 GS FLX Titanium	Texas A&M University	SRP007609	SRS254720	0.54
<i>Lucilia sericata</i> *	Calliphoridae	SRX087352	salivary glands	Developmental Profile of the Lucilia sericata Transcriptome	454 GS FLX Titanium	Texas A&M University	SRP007609	SRS254720	0.47
<i>Lutzomyia umbratilis</i>	# Psychodidae	SRX334951	Lutzomyia umbratilis salivary transcriptome collected from Municipality of Rio Preto da Eva, Amazonas State, Brazil	An insight into the sialomes of Corethrella apendiculata and Lutzomyia umbratilis	Illumina HiSeq 2000	NIAID	SRP028800	SRS470186	6622.79
<i>Lutzomyia intermedia</i>	Psychodidae	dbEST	LIBEST_027862 Lutzomyia intermedia adult female salivary gland, unpublished 2012	Functional transcriptomics of wild caught Lutzomyia intermedia salivary glands: Identification of a protective salivary protein against Leishmania braziliensis infection	Sanger dideoxy	National Institute of Allergy and Infectious Diseases	dbEST: 1473 Sequences		
<i>Mayetola ddestructor</i>	Cecydomyiidae	dbEST	Transcript abundance of genes encoding secreted salivary effector proteins in different geographic collections of acecidomyiid gall midge (Diptera: Cecidomyiidae)	Johnson,A.J., Shukle,R.H., Chen,M.S., Srivastava,S., 2013 unpublished	Sanger dideoxy	USDA Hessian fly Research lab, 2013	dbEST: 1859 Sequences		

<i>Orseolia oryzae</i>	Cecydomyiidae	dbEST	LIBEST_021761 Asian rice gall midge salivary gland cDNA	Comparative salivary gland transcriptomics of three gall midges, 2007, unpublished	Sanger dideoxy	USDA-ARS/Purdue University	dbEST: 1259 Sequences		
<i>Phlebotomus arabicus</i>	Psychodidae	dbEST	LIBEST_024076 Adult female Phlebotomus arabicus salivary gland	Analysis of salivary transcripts and antigens of the sand fly Phlebotomus arabicus, BMC Genomics 10 (1): 282 2009	Sanger dideoxy	National Institute of Allergy and Infectious Diseases	dbEST: 1069 Sequences		
<i>Phlebotomus orientalis</i>	Psychodidae	dbEST	Comparative analysis of salivary gland transcriptomes of Phlebotomus orientalis sand flies from endemic and non-endemic foci of visceral leishmaniasis	PLoS Negl Trop Dis 8 (2): E2709, 2014	Sanger dideoxy	National Institute of Allergy and Infectious Diseases	dbEST: 1648 Sequences		
<i>Phlebotomus papatasi</i>	Psychodidae	dbEST	Analysis of salivary gland transcripts of the Tunisian strain of Phlebotomus papatasi: on the search for vector-based vaccine candidates and markers of exposure	Abdeladhim,M., Jochim,R.C., Ben Ahmed,M., Zhioua,E., unpublished	Sanger dideoxy	National Institute of Allergy and Infectious Diseases, 2012	dbEST: 1345 Sequences		
<i>Phlebotomus sergenti</i>	Psychodidae	dbEST	LIBEST_026197 PSSG, PLoS Negl Trop Dis 6 (5): e1660 2012	Salivary Gland Transcriptomes and Proteomes of Phlebotomus tobbi and Phlebotomus sergenti, Vectors of Leishmaniasis	Sanger dideoxy	National Institute of Allergy and Infectious Diseases	dbEST: 1090 Sequences		
<i>Phlebotomus tobbi</i>	Psychodidae	dbEST	LIBEST_026201 PTbSG, PLoS Negl Trop Dis 6 (5): e1660 2012	Salivary Gland Transcriptomes and Proteomes of Phlebotomus tobbi and Phlebotomus sergenti, Vectors of Leishmaniasis	Sanger dideoxy	National Institute of Allergy and Infectious Diseases	dbEST: 1142 Sequences		
<i>Psorophora albipes</i>	Culicidae	SRX309995	Adult female Psorophora albipes salivary gland library	An insight into the sialomes of Psorophora albipes, Anopheles dirus and An. freeborni	Illumina HiSeq 2000	NIAID	SRP026153	SRS448456	8803.71
<i>Rhynchoscara americana</i>	Sciaridae	dbEST	Analysis of expressed sequence tags from Rhynchosciara, americana salivary glands	Insect Mol. Biol. 15 (2): 109-118, 2006	Sanger dideoxy	Instituto de Ciencias Biomedicas, Sao Paulo	dbEST: 8574 Sequences		
<i>Simulium guianense</i>	Simuliidae	dbEST	An insight into the sialome of Simulium guianense (DIPTERA:SIMULIIDAE), the main vector of River Blindness in Brazil	BMC Genomics 12: 612 2011	Sanger dideoxy	NIAID	dbEST: 1788 Sequences		
<i>Simulium nigrimanum</i>	Simuliidae	dbEST	An insight into the sialotranscriptome of the black fly Simulium nigrimanum	Ribeiro,J.M.C., Valenzuela,J.G., Pham,V.M., unpublished 2009	Sanger dideoxy	NIAID	dbEST:2147 Sequences		
<i>Simulium vittatum</i>	Simuliidae	dbEST	An insight into the sialome of the adult black fly, Simulium vittatum	Andersen,J.F., Champagne,D., Pham,V.M. et al. , unpublishedv 2008	Sanger dideoxy	NIAID	dbEST: 1748 Sequences		
<i>Sitodiplosis mosellana</i>	Cecydomyiidae	dbEST	LIBEST_021762 Orange wheat blossom midge salivary gland cDNA	Comparative salivary gland transcriptomics of three gall midges, unpublished	Sanger dideoxy	USDA-ARS/Purdue University	dbEST: 1217 Sequences		
<i>Stomoxys calcitrans</i>	Muscidae	dbEST	LIBEST_017328 Adult salivary gland cDNA library XWJRABMK	The salivary gland transcriptome of the the stable fly, Stomoxys calcitrans	Sanger dideoxy	National Institute of Allergy and Infectious Diseases	dbEST: 837 Sequences		
<i>Toxorhynchites amboinensis</i>	Culicidae	dbEST	LIBEST_020384 Toxorhynchites amboinensis adult salivary gland, 2006	An insight into the sialotranscriptome of adult Toxorhynchites amboinensis mosquitoes, unpublished	Sanger dideoxy	National Institute of Allergy and Infectious Diseases	dbEST: 871 Sequences		
<i>Drosophila melanogaster</i> *	# Drosophilidae	SRX494065	Illumina Transcriptome Sequencing of third instar larvae, wandering stage, salivary glands	modENCODE D. melanogaster Total RNA-Seq	Illumina HiSeq 2000	BDGP	SRP001696	SRS118282	9255.94
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX494036	Illumina Transcriptome Sequencing of third instar larvae, wandering stage, salivary glands	modENCODE D. melanogaster Total RNA-Seq	Illumina HiSeq 2000	BDGP	SRP001696	SRS118282	5933.14
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX493985	Illumina Transcriptome Sequencing of WPP, salivary glands	modENCODE D. melanogaster Total RNA-Seq	Illumina HiSeq 2000	BDGP	SRP001696	SRS118286	5435.88
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX493955	Illumina Transcriptome Sequencing of WPP, salivary glands	modENCODE D. melanogaster Total RNA-Seq	Illumina HiSeq 2000	BDGP	SRP001696	SRS118286	8171.06
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450804	GSM1315402: JIL-1_null _mutant_Z2_2 Sample 4; Drosophila melanogaster; RNA-Seq	GSE54440: Genome wide analysis of transcriptome wild type and JIL-1 mutant [RNA-seq: 4 samples]	Illumina HiSeq 2000	GEO	SRP035882	SRS544195	1632.95
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450803	GSM1315401: JIL-1_null _mutant_Z2_1 Sample 3; Drosophila melanogaster; RNA-Seq	GSE54440: Genome wide analysis of transcriptome wild type and JIL-1 mutant [RNA-seq: 4 samples]	Illumina HiSeq 2000	GEO	SRP035882	SRS544192	1186.71
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450802	GSM1315400: WT_Z2 Sample 2; Drosophila melanogaster; RNA-Seq	GSE54440: Genome wide analysis of transcriptome wild type and JIL-1 mutant [RNA-seq: 4 samples]	Illumina HiSeq 2000	GEO	SRP035882	SRS544191	1247.88
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450801	GSM1315399: WT_1 Sample 1; Drosophila melanogaster; RNA-Seq	GSE54440: Genome wide analysis of transcriptome wild type and JIL-1 mutant [RNA-seq: 4 samples]	Illumina HiSeq 2000	GEO	SRP035882	SRS544190	906.52
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450800	GSM1315392: H3K9me2_Z2_2 Sample 13; Drosophila melanogaster; ChIP-Seq	GSE54438: Genome-wide analysis of H3K9me2 and JIL-1 kinase mediated histone H3S10 phosphorylation in drosophila [ChIP-seq: 13 samples]	Illumina HiSeq 2000	GEO	SRP035881	SRS544189	836.61
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450799	GSM1315391: Z2_input_2 Sample 12; Drosophila melanogaster; ChIP-Seq	GSE54438: Genome-wide analysis of H3K9me2 and JIL-1 kinase mediated histone H3S10 phosphorylation in drosophila [ChIP-seq: 13 samples]	Illumina HiSeq 2000	GEO	SRP035881	SRS544187	1176.57
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450798	GSM1315390: H3K9me2_WT_2 Sample 11; Drosophila melanogaster; ChIP-Seq	GSE54438: Genome-wide analysis of H3K9me2 and JIL-1 kinase mediated histone H3S10 phosphorylation in drosophila [ChIP-seq: 13 samples]	Illumina HiSeq 2000	GEO	SRP035881	SRS544188	1630.75
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450797	GSM1315389: Input3 Sample 10; Drosophila melanogaster; ChIP-Seq	GSE54438: Genome-wide analysis of H3K9me2 and JIL-1 kinase mediated histone H3S10 phosphorylation in drosophila [ChIP-seq: 13 samples]	Illumina HiSeq 2000	GEO	SRP035881	SRS544186	1408.88
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450796	GSM1315388: Input2 Sample 9; Drosophila melanogaster; ChIP-Seq	GSE54438: Genome-wide analysis of H3K9me2 and JIL-1 kinase mediated histone H3S10 phosphorylation in drosophila [ChIP-seq: 13 samples]	Illumina Genome Analyzer II	GEO	SRP035881	SRS544185	802.44
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450795	GSM1315387: Input1 Sample 8; Drosophila melanogaster; ChIP-Seq	GSE54438: Genome-wide analysis of H3K9me2 and JIL-1 kinase mediated histone H3S10 phosphorylation in drosophila [ChIP-seq: 13 samples]	Illumina Genome Analyzer II	GEO	SRP035881	SRS544184	312.55
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450794	GSM1315386: Z2_input Sample 7; Drosophila melanogaster; ChIP-Seq	GSE54438: Genome-wide analysis of H3K9me2 and JIL-1 kinase mediated histone H3S10 phosphorylation in drosophila [ChIP-seq: 13 samples]	Illumina Genome Analyzer II	GEO	SRP035881	SRS544183	1027.71
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450793	GSM1315385: H3K9me2_Z2 Sample 6; Drosophila melanogaster; ChIP-Seq	GSE54438: Genome-wide analysis of H3K9me2 and JIL-1 kinase mediated histone H3S10 phosphorylation in drosophila [ChIP-seq: 13 samples]	Illumina Genome Analyzer II	GEO	SRP035881	SRS544182	870.38

<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450792	GSM1315384: H3K9me2_WT Sample 5; Drosophila melanogaster; ChIP-Seq	GSE54438: Genome-wide analysis of H3K9me2 and JIL-1 kinase mediated histone H3S10 phosphorylation in drosophila [ChIP-seq: 13 samples]	Illumina Genome Analyzer II	GEO	SRP035881	SRS544181	813.05
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450791	GSM1315383: H3S10ph_AM Sample 4; Drosophila melanogaster; ChIP-Seq	GSE54438: Genome-wide analysis of H3K9me2 and JIL-1 kinase mediated histone H3S10 phosphorylation in drosophila [ChIP-seq: 13 samples]	Illumina Genome Analyzer II	GEO	SRP035881	SRS544180	787.31
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450790	GSM1315382: H3S10ph_CS Sample 3; Drosophila melanogaster; ChIP-Seq	GSE54438: Genome-wide analysis of H3K9me2 and JIL-1 kinase mediated histone H3S10 phosphorylation in drosophila [ChIP-seq: 13 samples]	Illumina Genome Analyzer II	GEO	SRP035881	SRS544179	539.34
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450789	GSM1315381: 5C9_2 Sample 2; Drosophila melanogaster; ChIP-Seq	GSE54438: Genome-wide analysis of H3K9me2 and JIL-1 kinase mediated histone H3S10 phosphorylation in drosophila [ChIP-seq: 13 samples]	Illumina Genome Analyzer II	GEO	SRP035881	SRS544178	617.76
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX450788	GSM1315380: 5C9_1 Sample 1; Drosophila melanogaster; ChIP-Seq	GSE54438: Genome-wide analysis of H3K9me2 and JIL-1 kinase mediated histone H3S10 phosphorylation in drosophila [ChIP-seq: 13 samples]	Illumina Genome Analyzer II	GEO	SRP035881	SRS544177	366.7
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX244146	GSM1084205: Salivary gland subjected to RNAi against H1; Drosophila melanogaster; RNA-Seq	GSE44399: Analysis of Drosophila salivary glands and Kc cells with depleted levels of linker histone H1 (Illumina smRNA-Seq)	Illumina Genome Analyzer II	GEO	SRP018798	SRS397406	139.23
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX244145	GSM1084204: Salivary gland subjected to RNAi against Nautilus; Drosophila melanogaster; RNA-Seq	GSE44399: Analysis of Drosophila salivary glands and Kc cells with depleted levels of linker histone H1 (Illumina smRNA-Seq)	Illumina Genome Analyzer II	GEO	SRP018798	SRS397405	133.96
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX109302	GSM838794: PolyA Spanning Reads from Drosophila melanogaster, RNA ID=581; Drosophila melanogaster; RNA-Seq	GSE33905: Identification of polyA sites in Drosophila melanogaster	Illumina HiSeq 2000	GEO	SRP009459	SRS281019	522.46
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX109301	GSM838793: PolyA Spanning Reads from Drosophila melanogaster, RNA ID=580; Drosophila melanogaster; RNA-Seq	GSE33905: Identification of polyA sites in Drosophila melanogaster	Illumina HiSeq 2000	GEO	SRP009459	SRS281018	464.61
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX109296	GSM838788: PolyA Spanning Reads from Drosophila melanogaster, RNA ID=569; Drosophila melanogaster; RNA-Seq	GSE33905: Identification of polyA sites in Drosophila melanogaster	Illumina HiSeq 2000	GEO	SRP009459	SRS281013	868.49
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX109295	GSM838787: PolyA Spanning Reads from Drosophila melanogaster, RNA ID=568; Drosophila melanogaster; RNA-Seq	GSE33905: Identification of polyA sites in Drosophila melanogaster	Illumina HiSeq 2000	GEO	SRP009459	SRS281012	837.17
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX101449	GSM818470: SuUR-/- larval salivary gland rep 2	Expression profile of third instar larval salivary gland tissue	Illumina Genome Analyzer II	GEO	SRP008977	SRS267268	471.86
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX101448	GSM818469: larval salivary gland rep 2	Expression profile of third instar larval salivary gland tissue	Illumina Genome Analyzer II	GEO	SRP008977	SRS267267	469.2
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX101447	GSM818468: SuUR-/- larval salivary gland rep1	Expression profile of third instar larval salivary gland tissue	Illumina Genome Analyzer II	GEO	SRP008977	SRS267266	305.48
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX101446	GSM818467: larval salivary gland rep 1	Expression profile of third instar larval salivary gland tissue	Illumina Genome Analyzer II	GEO	SRP008977	SRS267265	234.03
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX097296	GSM790737: SuUR_3SG_orc2_ChIP	ChIP-Seq of ORC2 bound to third instar salivary gland DNA in WT and mutant Drosophila, analyzed by Illumina sequencing	Illumina Genome Analyzer II	GEO	SRP008233	SRS261341	439.68
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX097295	GSM790736: OrR_3SG_orc2_ChIP	ChIP-Seq of ORC2 bound to third instar salivary gland DNA in WT and mutant Drosophila, analyzed by Illumina sequencing	Illumina Genome Analyzer II	GEO	SRP008233	SRS261340	418.75
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX050609	GSM694135: SG Orc ChIP-Seq extraction2_seq1 aliquote 2	GSE28069: SG ORC ChIP-Seq experiment	Illumina Genome Analyzer	GEO	SRP006149	SRS183190	399.71
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX050608	GSM694134: SG Orc ChIP-Seq extraction2_seq1 aliquote 1	GSE28069: SG ORC ChIP-Seq experiment	Illumina Genome Analyzer	GEO	SRP006149	SRS183189	415.97
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX050607	GSM694133: SG Orc ChIP-Seq extraction1_seq1 aliquote 2	GSE28069: SG ORC ChIP-Seq experiment	Illumina Genome Analyzer	GEO	SRP006149	SRS183188	372.83
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX050606	GSM694132: SG Orc ChIP-Seq extraction1_seq1 aliquote 1	GSE28069: SG ORC ChIP-Seq experiment	Illumina Genome Analyzer	GEO	SRP006149	SRS183187	397.4
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX102377	PolII Rpb3 ChIP-seq data from D. melanogaster	PolII Rpb3 ChIP-seq data from D. melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001439	ERS139353	1317.41
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX102380	PolII Rpb3 ChIP-seq data from D. melanogaster	PolII Rpb3 ChIP-seq data from D. melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001439	ERS139356	1887.17
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX102379	PolII Rpb3 ChIP-seq data from D. melanogaster	PolII Rpb3 ChIP-seq data from D. melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001439	ERS139355	1280.34
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX102378	PolII Rpb3 ChIP-seq data from D. melanogaster	PolII Rpb3 ChIP-seq data from D. melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001439	ERS139354	1342.57
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX102376	PolII Rpb3 ChIP-seq data from D. melanogaster	PolII Rpb3 ChIP-seq data from D. melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001439	ERS139352	1496.78
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX102375	PolII Rpb3 ChIP-seq data from D. melanogaster	PolII Rpb3 ChIP-seq data from D. melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001439	ERS139351	1927.03
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX102374	PolII Rpb3 ChIP-seq data from D. melanogaster	PolII Rpb3 ChIP-seq data from D. melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001439	ERS139350	1340.55
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX102373	PolII Rpb3 ChIP-seq data from D. melanogaster	PolII Rpb3 ChIP-seq data from D. melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001439	ERS139349	1302.27
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX102372	PolII Rpb3 ChIP-seq data from D. melanogaster	PolII Rpb3 ChIP-seq data from D. melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001439	ERS139348	1852.84
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX102371	PolII Rpb3 ChIP-seq data from D. melanogaster	PolII Rpb3 ChIP-seq data from D. melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001439	ERS139347	1368.48
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX102370	PolII Rpb3 ChIP-seq data from D. melanogaster	PolII Rpb3 ChIP-seq data from D. melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001439	ERS139346	1212.71

<i>Drosophila melanogaster</i> *	Drosophilidae	ERX102368	PolII Rpb3 ChIP-seq data from D. melanogaster	PolII Rpb3 ChIP-seq data from D. melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001439	ERS139344	1224.68
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX101811	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001422	ERS138513	489.15
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX101810	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001422	ERS138512	462.98
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX101809	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001422	ERS138511	234.79
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX101808	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001422	ERS138510	376.95
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX101807	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001422	ERS138509	454.51
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX101806	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001422	ERS138508	365.23
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX101805	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001422	ERS138507	585.93
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX101804	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	MOF, H4 and H4K16ac ChIP-seq experiments in D.melanogaster	Illumina Genome Analyzer II	EMBL Heidelberg	ERP001422	ERS138506	341.15
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX004312	ChIP-seq profiling of Drosophila melanogaster salivary glands to identify targets for NSL1 and MCRS2.	ChIP-seq profiling of Drosophila melanogaster salivary glands to identify targets for NSL1 and MCRS2.	Illumina Genome Analyzer	EMBL_Heidelberg	ERP000176	ERS008771	216.9
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX004311	ChIP-seq profiling of Drosophila melanogaster salivary glands to identify targets for NSL1 and MCRS2.	ChIP-seq profiling of Drosophila melanogaster salivary glands to identify targets for NSL1 and MCRS2.	Illumina Genome Analyzer	EMBL_Heidelberg	ERP000176	ERS008770	155.41
<i>Drosophila melanogaster</i> *	Drosophilidae	ERX004310	ChIP-seq profiling of Drosophila melanogaster salivary glands to identify targets for NSL1 and MCRS2.	ChIP-seq profiling of Drosophila melanogaster salivary glands to identify targets for NSL1 and MCRS2.	Illumina Genome Analyzer	EMBL_Heidelberg	ERP000176	ERS008769	255.17
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX042031	Illumina Transcriptome Sequencing of D. melanogaster Dissected Tissue: White Prepupae Salivary Glands	D. melanogaster Dissected Tissue RNASeq	Illumina Genome Analyzer II	BDGP	SRP003905	SRS118286	1077.73
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX029409	Illumina Transcriptome Sequencing of D. melanogaster Dissected Tissue: White Prepupae Salivary Glands	D. melanogaster Dissected Tissue RNASeq	Illumina Genome Analyzer II	BDGP	SRP003905	SRS118286	3098.94
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX029403	Illumina Transcriptome Sequencing of D. melanogaster Dissected Tissue: L3 Salivary Glands	D. melanogaster Dissected Tissue RNASeq	Illumina Genome Analyzer II	BDGP	SRP003905	SRS118282	2099.28
<i>Drosophila melanogaster</i> *	Drosophilidae	SRX029402	Illumina Transcriptome Sequencing of D. melanogaster Dissected Tissue: L3 Salivary Glands	D. melanogaster Dissected Tissue RNASeq	Illumina Genome Analyzer II	BDGP	SRP003905	SRS118282	1202.66
Hemiptera									
<i>Acyrtosiphon pisum</i>	"Homoptera", Aphididae	dbEST	LIBEST_026773 Pea Aphid Salivary Gland, J. Proteome Res. 10 (4): 1505-1518 2011	Predicted effector molecules in the salivary secretome of the pea aphid (Acyrtosiphon pisum): a dual transcriptomic/proteomic approach	Sanger dideoxy	Kansas State University	dbEST: 9420 Sequences		
<i>Bemisia tabaci</i> *	Stenomorrhyncha, Aleyrodidae	SRX085155	Transcriptional Analysis of the Salivary Gland of an Invasive Whitefly	De novo characterization and comparison of the whitefly transcriptome	Illumina HiSeq 2000	Zhejiang University	SRP002099	SRS212048	726.3
<i>Cimex lectularius</i>	Cimicomorpha, Cimicidae	dbEST	LIBEST_024964 Bed bug salivary gland cDNA library	An insight into the sialotranscriptome of the bed bug Cimex lectularius, unpublished, 2009	Sanger dideoxy	National Institute of Allergy and Infectious Diseases	dbEST: 1969 Sequences		
<i>Dipetalogaster maximus</i>	Heteroptera, Reduviidae	dbEST	LIBEST_026797 Adult and Vth instar salivary gland cDNA	Insight into the Salivary Transcriptome and Proteome of Dipetalogaster maxima, J. Proteome Res. 2010	Sanger dideoxy	National Institute of Allergy and Infectious Diseases	dbEST: 2671 Sequences		
<i>Empoasca fabae</i> *	Auchenorrhyncha, Cicadellidae	SRX075974	Transcriptome analysis of the salivary glands of potato leafhopper, Empoasca fabae	Transcriptome analysis of the salivary glands of potato leafhopper, Empoasca fabae	454 GS FLX	Ohio Agriculture Research Development Center	SRP007107	SRS211856	302.27
<i>Homalodisca vitripennis</i>	Auchenorrhyncha, Cicadellidae	dbEST	LIBEST_020516 Homalodisca vitripennis salivary gland	Salivary gland gene expression in glassy-winged sharpshooter Homalodisca vitripennis (syn. H. coagulata) (Hemiptera: Cicadellidae), J. Insect Sci. 2006 submitted	Sanger dideoxy	US Horticultural Research Laboratory	dbEST: 3934 Sequences		
<i>Lygus lineolaris</i> *	Heteroptera, Miridae	SRX046115	Lygus lineolaris adult salivary gland	Sialotranscriptome of Lygus lineolaris	Illumina Genome Analyzer II	USDA-ARS	SRP005942	SRS173774	711.29
<i>Macrosiphum euphorbiae</i> *	"Homoptera", Aphididae	SRX181231	Macrosiphum euphorbiae salivary gland library	Macrosiphum euphorbiae strain:Tomato Transcriptome or Gene expression identification, and microarray design	Illumina Genome Analyzer II	University of California, Riverside	SRP015258	SRS359862	7122.26
<i>Myzus persicae</i>	"Homoptera", Aphididae	dbEST	LIBEST_020087 Myzus persicae, tobacco lineage, aphid salivary gland library, BMC Genomics 8 (1): 423 2007	Genomic resources for Myzus persicae: EST sequencing, SNP	Sanger dideoxy	Boyce Thompson Institute for Plant Research, USA	dbEST: 3233 Sequences		
<i>Nilaparvata lugens</i>	"Homoptera", Delphacidae	SRX277326	Salivary glands of M population	Salivary glands of TN1 and M populations of Nilaparvata lugens Transcriptome or Gene expression	Illumina HiSeq 2000	Institute of Insect Science, Zhejiang University	SRP022256	SRS420379	2549.88
<i>Nilaparvata lugens</i>	"Homoptera", Delphacidae	SRX276866	Salivary glands of M populations of Nilaparvata lugens	Salivary glands of TN1 and M populations of Nilaparvata lugens Transcriptome or Gene expression	Illumina HiSeq 2000	Institute of Insect Science, Zhejiang University	SRP022256	SRS419991	2549.88
<i>Nilaparvata lugens</i>	"Homoptera" Delphacidae	SRX276865	Salivary glands of TN1 populations of Nilaparvata lugens Transcriptome	Salivary glands of TN1 and M populations of Nilaparvata lugens Transcriptome or Gene expression	Illumina HiSeq 2000	Institute of Insect Science, Zhejiang University	SRP022256	SRS419990	2359.6
<i>Oncopeltus fasciatus</i>	Heteroptera, Lygaeidae	dbEST	LIBEST_020788 Adult Oncopeltus fasciatus salivary gland library AOFSG-1	An insight into the sialotranscriptome of the seed-feeding bug, Oncopeltus fasciatus, 2007, unpublished	Sanger dideoxy	NIAID	dbEST: 1115 Sequences		
<i>Orius laevigatus</i>	Heteroptera, Anthoridae	dbEST	LIBEST_028432 Orius laevigatus salivary gland-specific EST library, 2014, unpublished	Differential gene expression profiles in the salivary gland of Orius laevigatus	Sanger dideoxy	NIAID	dbEST: 501 Sequences		
<i>Panstrongylus megistus</i>	# Heteroptera, Reduviidae	SRX556590	Panstrongylus megistus sialotranscriptome from fifth instar nymphs	Panstrongylus megistus sialotranscriptome	Illumina HiSeq 2000	NIAID	SRP042602	SRS623586	4420.32
<i>Panstrongylus megistus</i>	Heteroptera, Reduviidae	dbEST	LIBEST_023287 Panstrongylus megistus salivary gland cDNA, 2008, unpublished	EST and proteome from Panstrongylus megistus	Sanger dideoxy	Faculdade de Medicina, Brazil	dbEST: 45 Sequences		

<i>Rhodnius brethesi</i>	Heteroptera, Reduviidae	dbEST	LIBEST_023095 Rhodnius brethesi salivary gland cDNA library, 2008 unpublished	Transcriptome and proteome of salivary glands of two species of Rhodnius	Sanger dideoxy	Faculdade de Medicina, Brazil	dbEST: 45 Sequences		
<i>Rhodnius prolixus</i>	Heteroptera, Reduviidae	dbEST	LIBEST_020692 Fifth instar salivary gland cDNA library	Exploring the sialome of the blood-sucking bug Rhodnius prolixus, Insect Biochem. Mol. Biol. 34 (1): 61-79 2004	Sanger dideoxy	NIAID	dbEST: 1439 Sequences		
<i>Rhodnius robustus</i>	Heteroptera, Reduviidae	dbEST	LIBEST_023096 Rhodnius robustus salivary gland cDNA library, , 2008 unpublished	Transcriptome and proteome of salivary glands of two species of Rhodnius	Sanger dideoxy	Faculdade de Medicina, Brazil	dbEST: 121 Sequences		
<i>Triatoma brasiliensis</i>	Heteroptera, Reduviidae	dbEST	LIBEST_020002 Adult Triatoma brasiliensis salivary gland, 2006, unpublished	The sialome of the blood-sucking bug Triatoma brasiliensis	Sanger dideoxy	NIAID	dbEST: 2115 Sequences		
<i>Triatoma infestans</i>	# Heteroptera, Reduviidae	SRX470503	Transcriptome from nymphal salivary glands of the Argentinian strain of Triatoma infestans	Variation in Triatoma infestans salivary proteins between developmental stages and geographic regions	Illumina MiSeq	NIAID	SRP037779	SRS557645	6465.92
<i>Triatoma infestans</i>	Heteroptera, Reduviidae	dbEST	LIBEST_021264 Triatoma infestans salivary gland cDNA library, 2007, unpublished	An insight into the sialome of the blood sucking bug Triatoma infestans	Sanger dideoxy	NIAID	dbEST: 1738 Sequences		
<i>Triatoma infestans</i>	Heteroptera, Reduviidae	SRX470459	Transcriptome from adult salivary glands of the Argentinian strain of Triatoma infestans	Variation in Triatoma infestans salivary proteins between developmental stages and geographic regions	Illumina MiSeq	NIAID	SRP037779	SRS557602	4752.2
<i>Triatoma infestans</i>	Heteroptera, Reduviidae	SRX470458	Transcriptome from nymphal salivary glands of thecolonized Bolivian strain of Triatoma infestans	Variation in Triatoma infestans salivary proteins between developmental stages and geographic regions	Illumina MiSeq	NIAID	SRP037779	SRS557601	5395.19
<i>Triatoma infestans</i>	Heteroptera, Reduviidae	SRX470457	Transcriptome from adult salivary glands of the colonized Bolivian strain of Triatoma infestans	Variation in Triatoma infestans salivary proteins between developmental stages and geographic regions	Illumina MiSeq	NIAID	SRP037779	SRS557600	5141.65
<i>Triatoma infestans</i>	Heteroptera, Reduviidae	SRX470456	Transcriptome from nymphal salivary glands of the F1 Bolivian strain of Triatoma infestans	Variation in Triatoma infestans salivary proteins between developmental stages and geographic regions	Illumina MiSeq	NIAID	SRP037779	SRS557599	8203.77
<i>Triatoma infestans</i>	Heteroptera, Reduviidae	SRX470455	Transcriptome from adult salivary glands of the F1 Bolivian strain of Triatoma infestans	Variation in Triatoma infestans salivary proteins between developmental stages and geographic regions	Illumina MiSeq	NIAID	SRP037779	SRS557598	4584.25
<i>Triatoma infestans</i>	Heteroptera, Reduviidae	SRX470454	Transcriptome from nymphal salivary glands of the Peruvian strain of Triatoma infestans	Variation in Triatoma infestans salivary proteins between developmental stages and geographic regions	Illumina MiSeq	NIAID	SRP037779	SRS557597	5963.7
<i>Triatoma infestans</i>	Heteroptera, Reduviidae	SRX470453	Transcriptome from adult salivary glands of the Chile strain of Triatoma infestans	Variation in Triatoma infestans salivary proteins between developmental stages and geographic regions	Illumina MiSeq	NIAID	SRP037779	SRS557596	4374.88
<i>Triatoma infestans</i>	Heteroptera, Reduviidae	SRX470450	Transcriptome from nymphal salivary glands of the Chile strain of Triatoma infestans	Variation in Triatoma infestans salivary proteins between developmental stages and geographic regions	Illumina MiSeq	NIAID	SRP037779	SRS557593	6191.22
<i>Triatoma infestans</i>	Heteroptera, Reduviidae	SRX470446	Transcriptome from adult salivary glands of the Chile strain of Triatoma infestans	Variation in Triatoma infestans salivary proteins between developmental stages and geographic regions	Illumina MiSeq	NIAID	SRP037779	SRS557588	4148.11
<i>Triatoma matogrossensis</i>	Heteroptera, Reduviidae	dbEST	LIBEST_026620 Salivary gland cDNA library T_mat_sg1, 2010, unpublished	An insight into the sialotranscriptome of the blood sucking bug, Triatoma matogrossensis	Sanger dideoxy	NIAID	dbEST: 2230 Sequences		
<i>Triatoma rubida</i>	Heteroptera, Reduviidae	dbEST	LIBEST_027558 Triatoma rubida salivary gland library TrubSG1, J. Med. Entomol. 49 (3): 563-572 2012	An insight into the sialotranscriptome of Triatoma rubida (Hemiptera: Heteroptera)	Sanger dideoxy	NIAID	dbEST: 2230 Sequences		
Hymenoptera									
<i>Aphidius ervi</i>	Ichneumonoidea, Brachonidae	TSA	Aphidius ervi venom apparatus transcriptome	PRJNA235942 ID: 235942; 2 Biosamples SAMN02592763, SAMN02592762	Sanger dideoxy	Registration date: 20-Jan-2014, INRA-UNS-CNRS	TSA: 21 Nucleotide Sequences		
<i>Apis</i>	Apidae	GenBank	Only few single nucleotide and protein sequences available in GenBank. Some derived from Genom-Sequencing. No larger gland library data available						
<i>Dinoponera quadriceps</i>	Vespoidea, Formicidae	TSA	Transcriptome analysis of the venom gland of giant ant D. quadriceps: study of hymenopterans venomic	PRJNA217939 ID: 21793; 1 Biosample SAMN02343703	Ion Torrent	Registration date: 5-Sep-2013, Federal University of Ceara	TSA: 6510 Nucleotide Sequences		
<i>Leptopilina heteroma</i>	Cinipoidea, Figitidae	dbEST	Parasitoid wasp long gland-reservoir-ovipositor complex expression profile	Partial venom gland transcriptome of a Drosophila parasitoid wasp, Leptopilina heterotoma, reveals novel and shared bioactive profiles with stinging Hymenoptera, Gene 526 (2): 195-204 2013	cDNA, Sanger Clones	Biology Department at the City College of NY	dbEST: 558 Nucleotide Sequences		
<i>Meteorus pulchricornis</i>	Ichneumonoidea, Brachonidae	dbEST	Major constituents of Meteorus pluchricornis venom gland	full-length enriched parasitoid wasp cDNA library Meteorus pulchricornis cDNA clone	cDNA, Sanger Clones	Nagoya University	dbEST: 435 Nucleotide Sequences		
<i>Microctonus aethiopoides</i>	Ichneumonoidea, Brachonidae	SRX000111		Partial identification of the constituents of Microctonus sp. parasitoid venoms.	454 GS 20	Federal University of Ceara	SRP000093	SRS000282	67.53
<i>Microctonus hyperodae</i>	Ichneumonoidea, Brachonidae	dbEST	LIBEST_022104 Microctonus hyperodae venom cDNAs	The constituents of Microctonus sp. parasitoid venoms, Insect Mol. Biol. 17 (3): 313-324 2008	cDNA, Sanger Clones	AgResearch Ltd, New Zealand	dbEST: 1104 Nucleotide Sequences		
<i>Microplitis demolitor</i>	Ichneumonoidea, Brachonidae	SRX337940	Microplitis demolitor venom gland transcriptome	Microplitis demolitor Parasitism Transcriptome	Illumina HiSeq 2000	University of Georgia	SRP028964	SRS472314	7853.89
<i>Sirex noctilio</i>	Symphyta, Siricidae	SRX286030	Wood wasp Sirex noctilio venom gland transcriptome	Sirex noctilio Transcriptome or Gene expression	Illumina HiSeq 2000	University of Georgia	SRP022976	SRS428957	15759.54
<i>Tetramorium bicarinatum</i>	Vespoidea, Formicidae	dbEST	Profiling the venom gland transcriptome of Tetramorium bicarinatum (Hymenoptera: Formicidae): the first transcriptome analysis of an ant species	Toxicon 70: 70-81 2013,	cDNA, Sanger Clones	Equipe Venins et Activites Biologiques VACBIO EA 4357	dbEST: 308 Nucleotide Sequences		
Lepidoptera									
<i>Maruca vitrata</i> *	Lepidoptera, Cambridae	SRX032895	Maruca midgut and salivary gland expressed sequence tags	Rapid development and application of single nucleotide polymorphism (SNP) markers from transcriptome sequence to detect variation in the legume pod borer Maruca vitrata (Lepidoptera: Crambidae) population of West Africa.	454 GS FLX	Purdue University	SRP002836	SRS140290	97.4
Thysanoptera									

<i>Frankliniella occidentalis</i>	Thysanoptera, Thripidae	SRX457729	F. occidentalis salivary gland transcriptome replicate 3 UF	Frankliniella occidentalis Transcriptome or Gene expression	Illumina HiSeq 2500	UC Davis	SRP036079	SRS549985	1119.77
<i>Frankliniella occidentalis</i>	Thysanoptera, Thripidae	SRX457727	F. occidentalis salivary gland transcriptome replicate 3 UM	Frankliniella occidentalis Transcriptome or Gene expression	Illumina HiSeq 2500	UC Davis	SRP036079	SRS549984	2121.91
<i>Frankliniella occidentalis</i>	Thysanoptera, Thripidae	SRX457726	F. occidentalis salivary gland transcriptome replicate 3 IF	Frankliniella occidentalis Transcriptome or Gene expression	Illumina HiSeq 2500	UC Davis	SRP036079	SRS549983	2762.55
<i>Frankliniella occidentalis</i>	Thysanoptera, Thripidae	SRX457725	F. occidentalis salivary gland transcriptome replicate 3 IM	Frankliniella occidentalis Transcriptome or Gene expression	Illumina HiSeq 2500	UC Davis	SRP036079	SRS549982	2578.14
<i>Frankliniella occidentalis</i>	Thysanoptera, Thripidae	SRX457723	F. occidentalis salivary gland transcriptome replicate 2 UF	Frankliniella occidentalis Transcriptome or Gene expression	Illumina HiSeq 2500	UC Davis	SRP036079	SRS549981	2526.27
<i>Frankliniella occidentalis</i>	Thysanoptera, Thripidae	SRX457722	F. occidentalis salivary gland transcriptome replicate 2 UM	Frankliniella occidentalis Transcriptome or Gene expression	Illumina HiSeq 2500	UC Davis	SRP036079	SRS549980	2051.34
<i>Frankliniella occidentalis</i>	Thysanoptera, Thripidae	SRX457721	F. occidentalis salivary gland transcriptome replicate 2 IF	Frankliniella occidentalis Transcriptome or Gene expression	Illumina HiSeq 2500	UC Davis	SRP036079	SRS549979	2255.69
<i>Frankliniella occidentalis</i>	Thysanoptera, Thripidae	SRX457719	F. occidentalis salivary gland transcriptome replicate 2 IM	Frankliniella occidentalis Transcriptome or Gene expression	Illumina HiSeq 2500	UC Davis	SRP036079	SRS549978	2731.38
<i>Frankliniella occidentalis</i>	Thysanoptera, Thripidae	SRX457718	F. occidentalis salivary gland transcriptome replicate 1 UF	Frankliniella occidentalis Transcriptome or Gene expression	Illumina HiSeq 2500	UC Davis	SRP036079	SRS549977	2706.6
<i>Frankliniella occidentalis</i>	Thysanoptera, Thripidae	SRX457717	F. occidentalis salivary gland transcriptome replicate 1 UM	Frankliniella occidentalis Transcriptome or Gene expression	Illumina HiSeq 2500	UC Davis	SRP036079	SRS549976	2849.82
<i>Frankliniella occidentalis</i>	Thysanoptera, Thripidae	SRX457716	F. occidentalis salivary gland transcriptome replicate 1 IF	Frankliniella occidentalis Transcriptome or Gene expression	Illumina HiSeq 2500	UC Davis	SRP036079	SRS549975	2658.3
<i>Frankliniella occidentalis</i>	Thysanoptera, Thripidae	SRX456543	F. occidentalis salivary gland transcriptome replicate 1 IM	Frankliniella occidentalis Transcriptome or Gene expression	Illumina HiSeq 2500	UC Davis	SRP036079	SRS549275	1992.86

Myriapoda

Chilopoda

<i>Cormocephalus westwoodi</i>	#	Scolopendromorpha, Scolopendridae	SRX273033	C westwoodi venom gland transcriptome	Cormocephalus westwoodi venom gland transcriptome	454 GS FLX+	University of Queensland	SRS417525	57.24
<i>Cormocephalus westwoodi</i>		Scolopendromorpha, Scolopendridae	TSA	Clawing through evolution: toxin diversification and convergence in the ancient lineage Chilopoda (Centipedes), Mol. Biol. Evol. (2014)	Bioproject: PRJNA200641, Biosample SAMN02086962	454 GS FLX+	University of Queensland	TSA: 50 Nucleotide Sequences	
<i>Ethmostigmus rubripes</i>	#	Scolopendromorpha, Scolopendridae	SRX275340	Ethmostigmus rubripes (Sydney) venom gland transcriptome	Ethmostigmus rubripes venom gland transcriptome	454 GS FLX+	University of Queensland	SRS418654	52.29
<i>Ethmostigmus rubripes</i>		Scolopendromorpha, Scolopendridae	TSA	Clawing through evolution: toxin diversification and convergence in the ancient lineage Chilopoda (Centipedes), Mol. Biol. Evol. (2014)	BioProject: PRJNA200639, BioSample: SAMN02086961	454 GS FLX+	University of Queensland	TSA: 204 Nucleotide Sequences	
<i>Ethmostigmus rubripes</i>	#	Scolopendromorpha, Scolopendridae	SRX275322	Ethmostigmus rubripes venom gland transcriptome	Ethmostigmus rubripes venom gland transcriptome	454 GS FLX+	University of Queensland	SRS418648	29.52
<i>Ethmostigmus rubripes</i>	#	Scolopendromorpha, Scolopendridae	SRX272980	E rubripes venom gland transcriptome	Ethmostigmus rubripes venom gland transcriptome	454 GS FLX+	University of Queensland	SRS417478	117.47
<i>Scolopendra alternans</i>	#	Scolopendromorpha, Scolopendridae	SRX275341	Scolopendra alternans (Haiti) venom gland transcriptome	Scolopendra alternans venom gland transcriptome	454 GS FLX+	University of Queensland	SRS418655	92.42
<i>Scolopendra alternans</i>		Scolopendromorpha, Scolopendridae	TSA	Clawing through evolution: toxin diversification and convergence in the ancient lineage Chilopoda (Centipedes), Mol. Biol. Evol. (2014)	BioProject: PRJNA200753, BioSample: SAMN02116184	454 GS FLX+	University of Queensland	TSA: 52 Nucleotide Sequences	
<i>Scolopendra morsitans</i>	#	Scolopendromorpha, Scolopendridae	SRX273031	S morsitans venom gland transcriptome	Scolopendra morsitans venom gland transcriptome	454 GS FLX+	University of Queensland	SRS417523	151.65
<i>Scolopendra morsitans</i>		Scolopendromorpha, Scolopendridae	TSA	Clawing through evolution: toxin diversification and convergence in the ancient lineage Chilopoda (Centipedes), Mol. Biol. Evol. (2014)	BioProject: PRJNA200640, BioSample: SAMN02086963	454 GS FLX+	University of Queensland	TSA: 186 Nucleotide Sequences	
<i>Scolopendra subspinies</i>		Scolopendromorpha, Scolopendridae	dbEST	Venomic and Transcriptomic Analysis of Centipede Scolopendra subspinies dehaani	J. Proteome Res. 11 (12), 6197-6212 (2012) - Unverified Sequences	cDNA, Sanger Clones	Chinese Acadademy of Sciences	dbEST: 1110 Nucleotide Sequences	
<i>Scolopendra subspinies dehaani</i>		Scolopendromorpha, Scolopendridae	dbEST	Venomic and Transcriptomic Analysis of Centipede Scolopendra subspinies dehaani	J. Proteome Res. 11 (12), 6197-6212 (2012) - Unverified Sequences	cDNA, Sanger Clones	Chinese Acadademy of Sciences	dbEST: 1114 Nucleotide Sequences	
<i>Thereuopoda longicornis</i>	#	Notostigmomporpha, Scutigerae	SRX450808 is not public	Thereuopoda longicornis Venom gland transcriptome	PRJNA213032 ID: 213032; 1 Biosample SAMN02261726	454 GS FLX+	7/23/2013, University of Queensland	TSA: 117 Nucleotide Sequences	
<i>Thereuopoda longicornis</i>		Notostigmomporpha, Scutigerae	TSA	Clawing through evolution: toxin diversification and convergence in the ancient lineage Chilopoda (Centipedes), Mol. Biol. Evol. (2014)	BioProject: PRJNA213032, BioSample: SAMN02261726	454 GS FLX+	University of Queensland	TSA: 117 Nucleotide Sequences	

Chelicerata

Araneae

<i>Agelena orientalis</i>	Aranaeomorphae, Agelenidae	dbEST	LIBEST_022253 Agelena orientalis venom gland	Selection strategy and the design of hybrid oligonucleotid primers for RACE-PCR: cloning a family of toxin-like sequences from Agelena orientalis, BMC Mol. Biol. 8: 32 2007	cDNA, Sanger Clones	School of Biological Sciences, Royal Holloway, London	dbEST: 79 Nucleotide Sequences	
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<i>Araneus ventricosus</i>	Aranaeomorphae, Araneidae	dbEST	LIBEST_027937 Araneus ventricosus venom gland library	A combined de novo sequencing and cDNA library approach to venom analysis of the venom from spider Araneus ventricosus, unpublished, 2012	cDNA, Sanger Clones	College of Life Sciences of Hunan Normal University, China	dbEST: 200 Nucleotide Sequences
<i>Chilobrachys guangxiensis</i>	Mygalomorphae, Theraphosidae	dbEST	LIBEST_022795 Spider venom gland Library	Transcriptome analysis revealed novel possible venom components and cellular processes of the tarantula Chilobrachys jingzhao venom gland	cDNA, Sanger Clones	Hunan Normal University, China	dbEST: 247 Nucleotide Sequences
<i>Haplopelma hainanum</i>	Mygalomorphae, Theraphosidae	dbEST	LIBEST_025501 Ornithoconus hainana venom gland	Cellular transcripts analysis of the tarantula Ornithoconus hainana venom gland, 2009, unpublished	cDNA, Sanger Clones	Hunan Normal University, China	dbEST: 189 Nucleotide Sequences
<i>Haplopelma schmidt</i>	Mygalomorphae, Theraphosidae	SRX482727	venom gland transcriptome of the spider Ornithoconus huwena	Ornithoconus huwena Transcriptome	454 GS FLX	Hunan Normal University	SRP039535 SRS567179 144.95
<i>Haplopelma schmidt</i>	Mygalomorphae, Theraphosidae	SRX482727	venom gland transcriptome of the spider Ornithoconus huwena	Ornithoconus huwena Transcriptome	454 GS FLX	Hunan Normal University	SRP039535 SRS567179 144.95
<i>Lasiodora parahybana</i>	Mygalomorphae, Theraphosidae	ERX323957	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353669 0.32
<i>Lasiodora parahybana</i>	Mygalomorphae, Theraphosidae	ERX323950	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353662 11.25
<i>Lasiodora parahybana</i>	Mygalomorphae, Theraphosidae	ERX323989	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353701 0.21
<i>Lasiodora parahybana</i>	Mygalomorphae, Theraphosidae	ERX323988	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353700 4.14
<i>Lasiodora parahybana</i>	Mygalomorphae, Theraphosidae	ERX323974	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353686 6.35
<i>Lasiodora parahybana</i>	Mygalomorphae, Theraphosidae	ERX323973	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353685 0.74
<i>Lasiodora parahybana</i>	Mygalomorphae, Theraphosidae	ERX323967	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353679 5.18
<i>Lasiodora parahybana</i>	Mygalomorphae, Theraphosidae	ERX323965	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353677 4.51
<i>Lasiodora parahybana</i>	Mygalomorphae, Theraphosidae	ERX323964	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353676 9.97
<i>Lasiodora parahybana</i>	Mygalomorphae, Theraphosidae	ERX323963	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353675 0.04
<i>Lasiodora parahybana</i>	Mygalomorphae, Theraphosidae	ERX323962	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353674 0.3
<i>Latrodectus hesperus</i>	# Aranaeomorphae, Araneidae	SRX512000	Total Transcriptome Sequencing of Latrodectus hesperus Venome Gland	Latrodectus hesperus Transcriptome or Gene expression	Illumina Genome Analyzer Iix	Washington and Lee	SRP040992 SRS589437 5528.23
<i>Latrodectus tredecimguttatus</i>	Aranaeomorphae, Araneidae	SRX337503	Latrodectus tredecimguttatus	Latrodectus tredecimguttatus transcriptome sequencing (Liang Songping)	Illumina HiSeq 2000	Fudan university	SRP028953 SRS471950 2661.32
<i>Loxosceles laeta</i>	Aranaeomorphae, Sycariidae	dbEST	LIBEST_022106 Spider Loxosceles laeta cDNA library	Transcriptome analysis of Loxosceles laeta (Araneae, Sicariidae) spider venomous gland using expressed sequence tags, BMC Genomics 9 (1): 279 2008	cDNA, Sanger Clones	Instituto Butantan, Brazil	dbEST: 1358 Nucleotide Sequences
<i>Poecilotheria regalis</i>	Mygalomorphae, Theraphosidae	ERX323951	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353663 8.6
<i>Poecilotheria regalis</i>	Mygalomorphae, Theraphosidae	ERX323949	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353661 87.16
<i>Poecilotheria regalis</i>	Mygalomorphae, Theraphosidae	ERX323948	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353660 6.57
<i>Poecilotheria regalis</i>	Mygalomorphae, Theraphosidae	ERX323947	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353659 0.42
<i>Poecilotheria regalis</i>	Mygalomorphae, Theraphosidae	ERX323946	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353658 3.66
<i>Poecilotheria regalis</i>	Mygalomorphae, Theraphosidae	ERX323945	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353657 2.07
<i>Poecilotheria regalis</i>	Mygalomorphae, Theraphosidae	ERX323971	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353683 0.36
<i>Poecilotheria regalis</i>	Mygalomorphae, Theraphosidae	ERX323970	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353682 6.23
<i>Poecilotheria regalis</i>	Mygalomorphae, Theraphosidae	ERX323969	--	Microbial life in snake and spider venoms	Ion Torrent PGM	UWEST	ERP004004 ERS353681 4.42
Araneae with less than 10 sequences in dbEST							
<i>Hadronyche modesta</i>	Aranaeomorphae, Hexathelidae	dbEST					dbEST: 8 Nucleotide Sequences
<i>Latrodectus hesperus</i>	Aranaeomorphae, Araneidae	dbEST					dbEST: 2 Nucleotide Sequences
<i>Loxosceles gaucho</i>	Aranaeomorphae, Sycariidae	dbEST					dbEST: 1 Nucleotide Sequences
<i>Parawixia bistriata</i>	Aranaeomorphae, Araneidae	dbEST					dbEST: 1 Nucleotide Sequences

Scorpiones								
<i>Australobuthus xerolimniorum</i>		SRX288424	Scorpion's sting: Molecular evolution and diversification of scorpion peptide toxins	Australobuthus xerolimniorum Transcriptome or Gene expression	454 GS FLX Titanium	University of Queensland	SRP023476	SRS431074
<i>Centruroides tecomanus</i> (77)		dbEST	LIBEST_027996 Centruroides tecomanus adult venom gland cDNA, PLoS ONE 8 (6): e66486 2013	Mass Fingerprinting of the Venom and Transcriptome of Venom Gland of Scorpion Centruroides tecomanus	cDNA, Sanger Clones	Instituto de Biotecnologia UNAM, Mexico	dbEST: 77	Nucleotide Sequences
<i>Cercophonius squama</i>		SRX288425	Scorpion's sting: Molecular evolution and diversification of scorpion peptide toxins	Cercophonius squama Transcriptome or Gene expression	454 GS FLX Titanium	University of Queensland	SRP023477	SRS431075
<i>Hadrurus gertschi</i> (68)		dbEST	LIBEST_020910 Scorpion venom gland library 1	Transcriptome analysis of the venom gland of the Mexicanscorpion Hadrurus gertschi (Arachnida: Scorpiones)	cDNA, Sanger Clones	Instituto de Biotecnologia UNAM, Mexico	dbEST: 68	Nucleotide Sequences
<i>Heterometrus petersii</i> (262)		dbEST	LIBEST_022599 Heterometrus petersii venom gland Library, Proteomics 10 (13): 2471-2485 2010	Molecular diversity of toxic components from the scorpionHeterometrus petersii venom revealed by proteomic and transcriptome analysis	cDNA, Sanger Clones	Wuhan University, China	dbEST: 262	Nucleotide Sequences
<i>Hottentotta judaicus</i> (174)		dbEST/ GenBank	Toxicon 2011,	The tale of a resting gland: Transcriptome of a replete venom glandfrom the scorpion Hottentotta judaicus	cDNA, Sanger Clones	University of Queensland	dbEST/GenBank: 174	Sequences (mRNA)
<i>Isometrus maculatus</i> (328)		dbEST	LIBEST_022574 Isometrus maculatus venom gland Library, J Proteomics 75 (5): 1563-1576 2012	Extreme diversity of scorpion venom peptides and proteinsrevealed by transcriptomic analysis; Implication for proteome evolution of scorpion venom arsenal	cDNA, Sanger Clones	Wuhan University, China	dbEST: 328	Nucleotide Sequences
<i>Isometroides vescus</i>		SRX288426	Scorpion's sting: Molecular evolution and diversification of scorpion peptide toxins	Isometroides vescus Transcriptome or Gene expression	454 GS FLX Titanium	University of Queensland	SRP023478	SRS431076 104.66
<i>Lychas buchari</i>		SRX288427	Scorpion's sting: Molecular evolution and diversification of scorpion peptide toxins	Lychas buchari Transcriptome or Gene expression	454 GS FLX Titanium	University of Queensland	SRP023479	SRS431077 123.79
<i>Lychas mucronatus</i> (1068)		dbEST	LIBEST_025068 Yun Nan scorpion Lychas mucronatus venom gland, BMC Genomics 11 (1): 452 2010	Comparative venom gland transcriptome analysis of the scorpion Lychas mucronatus reveals intraspecific toxic genediversity and new venomous components	cDNA, Sanger Clones	Wuhan University, China	dbEST: 1068	Nucleotide Sequences
<i>Parabuthus stridulus</i> (17)		dbEST	LIBEST_028270 Parabuthus stridulus telsons cDNA Library	Partial transcriptomic profiling of toxins from the venom gland of the scorpion Parabuthus stridulus	cDNA, Sanger Clones	University of Leuven, Belgium	dbEST: 17	Nucleotide Sequences
<i>Scorpio maurus palmatus</i> (102)		dbEST	LIBEST_028230 cDNA library of Scorpio maurus palmatus venom gland, Toxicon 74: 193-207 2013	Venom proteomic and venomous glands transcriptomic analysis of the Egyptian scorpion Scorpio maurus palmatus (Arachnida: Scorpionidae)	cDNA, Sanger Clones	Instituto de Biotecnologia UNAM, Mexico	dbEST: 102	Nucleotide Sequences
<i>Scorpiops jendeki</i> (871)		dbEST	LIBEST_024185 Scorpiops jendeki venom gland Library, BMC Genomics 10 (1): 290 2009	Transcriptome analysis of the venom gland of the scorpion Scorpiops jendeki: implication for the evolution of the scorpion venom arsenal	cDNA, Sanger Clones	Wuhan University, China	dbEST: 871	Nucleotide Sequences
<i>Scorpiops margerisonae</i> (360)		dbEST	LIBEST_026383 Scorpiops margerisonae venom gland Library, J Proteomics 75 (5): 1563-1576 2012	Extreme diversity of scorpion venom peptides and proteins revealed by transcriptomic analysis; Implication for proteome evolution of scorpion venom arsenal	cDNA, Sanger Clones	Wuhan University, China	dbEST: 360	Nucleotide Sequences
<i>Tityus serrulatus</i> (1354)		dbEST	LIBEST_027645 Venom gland of Tityus serrulatus library, unpublished 2012	Transcriptome analysis of the Tityus serrulatus scorpion venomous gland in the context of Chelicerates transcriptomes	cDNA, Sanger Clones	Instituto de Ciencias Biologicas, Brazil	dbEST: 1354	Nucleotide Sequences
<i>Tityus stigmurus</i> (153)		dbEST	LIBEST_027444 Scorpion Tityus stigmurus cDNA library, BMC Genomics 13: 362 2012	Profiling the resting venom gland of the scorpion Tityus stigmurus through a transcriptomic survey	cDNA, Sanger Clones	Universidade Federal do Rio Grande do Norte, Brazil	dbEST: 153	Nucleotide Sequences
<i>Urodacus manicatus</i>		SRX288428	Scorpion's sting: Molecular evolution and diversification of scorpion peptide toxins	Urodacus manicatus Transcriptome or Gene expression venomous gland in the context of Chelicerates transcriptomes	454 GS FLX Titanium	University of Queensland	SRP023480	SRS431078 121.09
Parasitiformes								
<i>Amblyomma cajennense</i>	Acari, Ixodidae	SRX498136	Amblyomma cajennense salivary gland transcriptome with or without Rickettsia amblyommii at different days of feeding	Amblyomma cajennense salivary gland transcriptome	454 GS FLX	National Institute of Allergy and Infectious Disease	SRP040462	SRS580020 196.72
<i>Amblyomma maculatum</i>	Acari, Ixodidae	SRX341007	Amblyomma maculatum salivary glands treated with LacZ or SEF RNAi	Amblyomma maculatum strain:Mississippi Sandhill Crane National Wildlife Refuge (Gautier, MS) Transcriptome or Gene expression	Illumina HiSeq 2000	National Institute of Allergy and Infectious Disease	SRP029293	SRS474275 3193.14
<i>Amblyomma maculatum</i>	Acari, Ixodidae	SRX062231	First run	Pyrosequence results from a cDNA library from the salivary glands of adult female Amblyomma maculatum ticks	454 GS FLX Titanium	National Institute of Allergy and Infectious Disease	SRP006754	SRS192897 1885.3
<i>Amblyomma triste</i>	Acari, Ixodidae	SRX504079	Salivary gland transcriptome of Amblyomma triste adults and nymphs fed on dogs and guinea pigs	Amblyomma triste salivary gland transcriptome	454 GS FLX	NIAID	SRP040463	SRS584144 46.93
<i>Amblyomma triste</i>	Acari, Ixodidae	SRX504078	Salivary gland transcriptome of Amblyomma triste adults and nymphs fed on dogs and guinea pigs	Amblyomma triste salivary gland transcriptome	454 GS FLX	NIAID	SRP040463	SRS584143 54.95
<i>Amblyomma triste</i>	Acari, Ixodidae	SRX504077	Salivary gland transcriptome of Amblyomma triste adults and nymphs fed on dogs and guinea pigs	Amblyomma triste salivary gland transcriptome	454 GS FLX	NIAID	SRP040463	SRS584142 73.41
<i>Amblyomma triste</i>	Acari, Ixodidae	SRX504076	Salivary gland transcriptome of Amblyomma triste adults and nymphs fed on dogs and guinea pigs	Amblyomma triste salivary gland transcriptome	454 GS FLX	NIAID	SRP040463	SRS584141 63.96
<i>Amblyomma triste</i>	Acari, Ixodidae	SRX504075	Salivary gland transcriptome of Amblyomma triste adults and nymphs fed on dogs and guinea pigs	Amblyomma triste salivary gland transcriptome	454 GS FLX	NIAID	SRP040463	SRS584140 56.92
<i>Ixodes ricinus</i>	# Acari, Ixodidae	SRX213145	Ixodes ricinus nymph and adult salivary gland Illumina data	Ixodes ricinus Transcriptome or Gene expression	Illumina Genome Analyzer II	NIAID	SRP017700	SRS381885 16351.9
<i>Ixodes ricinus</i>	Acari, Ixodidae	SRX213144	Ixodes ricinus nymph and adult salivary gland Illumina data	Ixodes ricinus Transcriptome or Gene expression	Illumina Genome Analyzer Iix	NIAID	SRP017700	SRS381884 6895.63
Parasitiformes in dbEST								
<i>Amblyomma americanum</i>	Acari, Ixodidae	dbEST					dbEST: 4067	Nucleotide Sequences
<i>Amblyomma rotundatum</i>	Acari, Ixodidae	dbEST					dbEST: 1230	Nucleotide Sequences
<i>Amblyomma tuberculatum</i>	Acari, Ixodidae	dbEST					dbEST: 387	Nucleotide Sequences
<i>Antricola delacruzi</i>	Acari, Argasidae	dbEST					dbEST: 1120	Nucleotide Sequences
<i>Argas monolakensis</i>	Acari, Argasidae	dbEST					dbEST: 2914	Nucleotide Sequences

<i>Dermacentor andersoni</i>	Acari, Ixodidae	dbEST	dbEST: 88 Nucleotide Sequences
<i>Hyalomma marginatum rufipes</i>	Acari, Ixodidae	dbEST	dbEST: 2110 Nucleotide Sequences
<i>Ixodes ricinus</i>	Acari, Ixodidae	dbEST	dbEST: 1969 Nucleotide Sequences
<i>Ixodes scapularis</i>	Acari, Ixodidae	dbEST	dbEST: 8050 Nucleotide Sequences
<i>Ornithodoros coriaceus</i>	Acari, Argasidae	dbEST	dbEST: 923 Nucleotide Sequences
<i>Ornithodoros moubata</i>	Acari, Argasidae	dbEST	dbEST: 122 Nucleotide Sequences
<i>Ornithodoros parkeri</i>	Acari, Argasidae	dbEST	dbEST: 1563 Nucleotide Sequences
<i>Rhipicephalus annulatus</i>	Acari, Ixodidae	dbEST	dbEST: 1 Nucleotide Sequences
<i>Rhipicephalus microplus</i>	Acari, Ixodidae	dbEST	dbEST: 97 Nucleotide Sequences
<i>Rhipicephalus sanguineus</i>	Acari, Ixodidae	dbEST	dbEST: 2281 Nucleotide Sequences