

**Table S2 List of all *Osiris* genes identified from the 13 complete insect genomes.**

**ID:** All IDs are for the first transcript/peptide (-RA/-PA) unless noted otherwise

**Direct:** 1/-1 show the direction relative to Osi2 (1 as the same direction).

**Start/End:** Start and end positions for the coding sequences. For *A. pisum*, transcript start/end positions are shown. When genes are not on the same chromosome or supercontig, only the strand information (+/-) is shown.

**Color codes:**  annotation changed by us in this report

**(*Osiris* group assignment)**

no color based on both synteny and similarity

based on synteny but similarity not conclusive

**Table S2 List of all *Osiris* genes identified from the 13 complete insect genomes.**

Osiris 1								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG15585	308	3R	1	1999367	2000555	3	
<i>D. pseudoobscura</i>	GA13829	304	2	1	15819977	15818610	3	GA13829-PB (FBpp0298266)
<i>D. virilis</i>	GJ14243	323	scaffold_12822	1	1897146	1895783	3	
<i>D. grimshawi</i>	GD14014a	307	scaffold_14624	1	2876740	2875141	3	based on the last 2 exons of GH14014 GeneWise+Augustus model 2875141..2875544,2875805..2875927,2876344..2876740
<i>An. gambiae</i>	AGAP004121	284	2R	1	50327269	50328282	3	
<i>Ae. aegypti</i>	AAEL015156	282	supercont1.1530	1	22088	5471	3	
<i>Cu. quinquefasciatus</i>	CPIJ006985	293	Supercontig3.144	1	369648	358007	3	
<i>B. mori</i>	None							
<i>Ap. mellifera</i>	au8.g4218a	276	Group15.14	1	546442	548486	4	Based on au8.g4218 ex1-ex4: (546442..546663, 547241..547508,547660..547920, 548407..548486) Similarity is weak, no signature domains; but cluster on
<i>Ca. floridanus</i>	None							
<i>T. castaneum</i>	None							
<i>Ac. pisum</i>	None							
<i>P. humanus</i>	None							

NPFR1								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG1147	485	3R	1	2014920	2019871	4	4 isoforms, all identical aa seqs
<i>D. pseudoobscura</i>	GA11019	498	2	1	15808917	15807000	3	
<i>D. virilis</i>	GJ14245	516	scaffold_12822	1	1885599	1883380	3	
<i>D. grimshawi</i>	GH14016	511	scaffold_14624	1	2866563	2864216	3	
<i>An. gambiae</i>	AGAP004123	425	2R	1	50350559	50354332	3	
<i>Ae. aegypti</i>	AAEL010626	351	supercont1.491	1	826221	794272	3	
<i>Cu. quinquefasciatus</i>	CPIJ006984	400	supercont3.144	1	326156	314299	3	
<i>B. mori</i>	BGIBMGA00001	383	nscaf1071	-1	456503	450075	4	Located after Osi24
<i>Ap. mellifera</i>	None							
<i>Ca. floridanus</i>	None							
<i>T. castaneum</i>	TC011655	619	ChLG9	1	20609466	20598308	6	TCOGS2:GLEAN_11655 (XP_967689 contains NPFR1+Osi24)
<i>Ac. pisum</i>	ACYPI007664	391	GL349633	+	115595	205777	6	
<i>P. humanus</i>	PHUM025830	364	DS235004.1	1	376037	377170	2	

Osiris 24								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG15589	533	3R	1	2030167	2032903	5	
<i>D. pseudoobscura</i>	GA13830	537	2	1	15796968	15795081	5	
<i>D. virilis</i>	GJ14246	472	scaffold_12822	1	1850145	1847962	6	
<i>D. grimshawi</i>	GH14017	497	scaffold_14624	1	2854383	2852256	5	
<i>An. gambiae</i>	AGAP004124	409	2R	1	50384354	50387218	5	
<i>Ae. aegypti</i>	AAEL010627	445	supercont1.491	1	449215	396633	5	
<i>Cu. quinquefasciatus</i>	CPIJ006981	427	supercont3.144	1	144904	128341	5	
<i>B. mori</i>	BGIBMGA000025	479	nscaf1071	-1	273107	262711	7	Located before NPFR1
<i>Ap. mellifera</i>	GB18863	473	Group15.14	1	552773	555471	4	AmeI_2.0_OGSv1_gmap (XP_001121409 LG15:4223598..4226296, no longer in NCBI)
<i>Ca. floridanus</i>	CFLO15236	471	scaffold309	1	116909	101296	6	OGSv1.0 (EFN64650/GL441542.1)
<i>T. castaneum</i>	GLEAN_11656	418	ChLG9	1	20593022	20590333	4	Glean_5_19_06 (XP_967689 contains NPFR1+Osi24)
<i>Ac. pisum</i>	ACYPI52893	501	GL349761	1	61451	21695	7	
<i>P. humanus</i>	PHUM026040	295	DS235004.1	1	403565	405857	5	5'-end missing

Osiris 2								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG1148-PA	390	3R	1	2037184	2039100	4	isoform
	CG1148-PB	390	3R	1	2037184	2039100	4	isoform
<i>D. pseudoobscura</i>	GA13830	404	2	1	15789619	15788078	4	
<i>D. virilis</i>	GJ14247	397	scaffold_12822	1	1842804	1841325	4	
<i>D. grimshawi</i>	GH14018	406	scaffold_14624	1	2847740	2845905	4	
<i>An. gambiae</i>	AGAP004125	369	2R	1	50398489	50399671	2	
<i>Ae. aegypti</i>	AAEL010623	365	supercont1.491	1	232553	231401	2	missing the 3' end
<i>Cu. quinquefasciatus</i>	CPIJ008149	362	Supercontig 3.179	1	692137	690987	2	
<i>B. mori</i>	BGIBMGA000040	142	nscaf1071	1	584271	584699	1	missing 3' half, weak similarity
<i>Ap. mellifera</i>	GB15845	325	Group15.14	1	558576	559878	4	Amel_2.0_OGSv1_gmap (XP_001121449.1, LG15:4536711..4539563)
<i>Ca. floridanus</i>	CFLO15237	317	scaffold309	1	97058	94081	4	OGSv1.0 (EFN64649/GL441542.1)
<i>T. castaneum</i>	TC011657	319	ChLG9	1	20588465	20587053	5	TCOGS2, XP_967536.1
<i>Ac. pisum</i>	ACYPI007856	377	GL349761	1	7604	120	3	
<i>P. humanus</i>	PHUM026050	369	DS235004.1	1	413407	415968	3	

Osiris 3								
Genome	Acc#	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG1150	288	3R	1	2041786	2043639	3	
<i>D. pseudoobscura</i>	GA11035	289	2	1	15785557	15784397	3	
<i>D. virilis</i>	GJ14248	282	scaffold_12822	1	1837891	1836711	3	
<i>D. grimshawi</i>	GH14019	284	scaffold_14624	1	2842701	2841453	3	
<i>An. gambiae</i>	AGAP004126	295	2R	1	50423391	50425056	3	
<i>Ae. aegypti</i>	AAEL010624	287	supercont1.491	1	153272	137568	3	
<i>Cu. quinquefasciatus</i>	CPIJ008148	269	supercont3.179	1	677815	663250	3	
<i>B. mori</i>	BGIBMGA000042	212	nscaf1071	1	620089	626738	4	missing regions at both ends
<i>Ap. mellifera</i>	GB19141	294	Group15.14	1	565917	567581	2	Amel_2.0_OGSv1_gmap (XP_001121482.1 LG15:4544707..4547498)
<i>Ca. floridanus</i>	CFLO15238	278	scaffold309	1	85571	84078	2	OGSv1.0 (EFN64648/GL441542.1)
<i>T. castaneum</i>	TC011658	276	ChLG9	1	20584063	20582557	4	TCOGS2, XP_967452.1
<i>Ac. pisum</i>	ACYPI001904	303	GL349870	+	639943	646593	3	
<i>P. humanus</i>	PHUM026160	300	DS235004.1	1	431224	433412	5	

Osiris 4								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG10303	393	3R	-1	2047384	2044255	4	
<i>D. pseudoobscura</i>	GA10232	405	2	-1	15780992	15783643	4	
<i>D. virilis</i>	GJ14490	399	scaffold_12822	-1	1832406	1835997	4	
<i>D. grimshawi</i>	GH14283	403	scaffold_14624	-1	2837162	2840675	4	
<i>An. gambiae</i>	AGAP004127	306	2R	-1	50430646	50429581	3	
<i>Ae. aegypti</i>	AAEL010625	312	supercont1.491	-1	88165	101794	3	
<i>Cu. quinquefasciatus</i>	CPIJ008147	317	supercont3.179	-1	651118	653972	3	
<i>B. mori</i>	None							
<i>Ap. mellifera</i>	None							
<i>Ca. floridanus</i>	None							
<i>T. castaneum</i>								
<i>Ac. pisum</i>	None							
<i>P. humanus</i>	None							

Osiris 5								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG15590-PA	202	3R	1	2053428	2054461	2	isoform
	CG15590-PB	201	3R	1	2053428	2054458	2	isoform
<i>D. pseudoobscura</i>	GA13832	212	2	1	15775460	15774575	2	
<i>D. virilis</i>	GJ14249	210	scaffold_12822	1	1823924	1822411	2	
<i>D. grimshawi</i>	GH14020	219	scaffold_14624	1	2830195	2828423	2	
<i>An. gambiae</i>	AGAP012556	228	UNKN	-	15940121	15939378	2	
<i>Ae. aegypti</i>	AAEL010628	257	supercont1.491	-1	36946	50288	2	
	AAEL010631	249	supercont1.491	1	12724	1865	2	
<i>Cu. quinquefasciatus</i>	CPIJ008146	251	supercont3.179	1	634575	623303	2	
<i>B. mori</i>	BGIBMGA00004	163	nscaf1071	1	688056	693867	3	Weak similarity
<i>Ap. mellifera</i>	au8.g4221a	293	Group15.14	1	572124	573215	3	Based on au8.g4221.t1 ex1-ex3, (572124..572628,572715..572822,572947..573215) (XP_001121508 LG15:4551244..4552330, no
<i>Ca. floridanus</i>	CFLO15239	152	scaffold309	1	78191	77108	3	OGSv1.0 (EFN64647/GL441542.1) missing 5' region
<i>T. castaneum</i>	TC011659	229	ChLG9	1	20578022	20576613	2	5a, TCOGS2, XP_976093.1
	TC012811	232	ChLG9	-1	20581262	20582060	5	5b, TCOGS2, Osi5-like?
<i>Ac. pisum</i>	None							
<i>P. humanus</i>	None							



Osiris 6								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG1151	312	3R	1	2060458	2062024	2	
<i>D. pseudoobscura</i>	GA26494	288	2	1	15768074	15766825	2	
<i>D. virilis</i>	GJ14250	294	scaffold_12822	1	1813629	1812417	2	
<i>D. grimshawi</i>	GH14022	297	scaffold_14624	1	2820796	2819537	2	
<i>An. gambiae</i>	AGAP004129	237	2R	1	50491387	50492715	2	
<i>Ae. aegypti</i>	AAELO14433	240	supercont1.1116	+	181441	189732	2	
<i>Cu. quinquefasciatus</i>	CPIJ008144	240	supercont3.179	1	530566	525882	2	
<i>B. mori</i>	None							
<i>Ap. mellifera</i>	GB19629	257	Group15.14	1	580714	581723	3	Amel_2.0_OGSv1_gmap (XP_001121541.1 LG15:4559825..4560843)
<i>Ca. floridanus</i>	CFLO15240	273	scaffold309	1	70694	69570	3	OGSv1.0 (EFN64646/GL441542.1)
<i>T. castaneum</i>	None							
<i>Ac. pisum</i>	ACYPI000840	287	GL349857	-	605198	602013	4	
<i>P. humanus</i>	None							

Osiris 7								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG1153	288	3R	1	2074929	2075795	1	
<i>D. pseudoobscura</i>	GA11054	287	2	1	15754289	15753426	1	
<i>D. virilis</i>	GJ14251	288	scaffold_12822	1	1797298	1796432	1	
<i>D. grimshawi</i>	GH14023	291	scaffold_14624	1	2805530	2804655	1	
<i>An. gambiae</i>	AGAP004130	297	2R	1	50520138	50521031	1	
<i>Ae. aegypti</i>	None							
<i>Cu. quinquefasciatus</i>	CPIJ008141	288	supercont3.179	1	431192	430326	1	
<i>B. mori</i>	BGIBMGA000044	261	nscaf1071	1	709297	710082	1	
<i>Ap. mellifera</i>	GB13419	277	Group15.14	1	587513	589282	3	Amel_2.0_OGSv1_gmap (XP_624937.1 LG15:4566421..4568940)
<i>Ca. floridanus</i>	CFLO15241a	275	scaffold309	1	63969	61248	3	CFLO15241:ex1-ex3 AUGUSTUS model 61248..61630,63407..63582,63701..63969 (EFN64645=Osi7+Osi8)
<i>T. castaneum</i>	TC011660	278	ChLG9	1	20571810	20570974	1	TCOGS2, XP_967197.1
<i>Ac. pisum</i>	ACYPI002725	298	GL349857	-	577533	574085	3	
<i>P. humanus</i>	PHUM026170	272	DS235004.1	1	443236	446107	3	

Osiris 8								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG15591	274	3R	1	2080997	2082114	2	
<i>D. pseudoobscura</i>	GA13833	287	2	1	15747924	15746989	2	
<i>D. virilis</i>	GJ14253a	276	scaffold_12822	1	1786185	1785242	3	GJ14253+GJ14254 AUGUSTUS: 1785242..1785634,1785675..1785839,1785913..1786185
<i>D. grimshawi</i>	GH14024	281	scaffold_14624	1	2798067	2797160	2	
<i>An. gambiae</i>	AGAP004128	282	2R	1	50448638	50449565	2	extra 3 aa's before M
<i>Ae. aegypti</i>	AAEL004275	247	supercont1.113	-	492815	491930	2	
<i>Cu. quinquefasciatus</i>	CPIJ008140	280	supercont3.179	1	388401	387495	2	
<i>B. mori</i>	BGIBMGA000009	236	nscaf1071	-1	828580	820371	3	
<i>Ap. mellifera</i>	GB10057	264	Group15.14	1	592556	593593	2	Amel_2.0_OGSv1_gmap (XP_003249793.1 LG15:4571385..4573071)
<i>Ca. floridanus</i>	CFLO15241b	259	scaffold309	1	56944	55895	2	CFLO15241:ex4-ex5 AUGUSTUS model 55895..56178,56447..56944 (starts with 'atatt') (EFN64645=Osi7+Osi8)
<i>T. castaneum</i>	TC011661	254	ChLG9	1	20567569	20566676	2	TCOGS2, XP_967101.1
<i>Ac. pisum</i>	ACYPI005238	254	GL349857	-	550960	544609	3	
<i>P. humanus</i>	None							

Osiris 9								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG15592	233	3R	1	2086135	2087371	3	
<i>D. pseudoobscura</i>	GA13834	232	2	1	15742961	15741569	3	
<i>D. virilis</i>	GJ14255	231	scaffold_12822	1	1780683	1779314	3	
<i>D. grimshawi</i>	GH14025	231	scaffold_14624	1	2792525	2791171	3	
<i>An. gambiae</i>	AGAP004131	238	2R	1	50568998	50570643	3	
<i>Ae. aegypti</i>	AAEL004280	237	supercont1.113	-	282815	276138	3	
<i>Cu. quinquefasciatus</i>	CPIJ008139	235	supercont3.179	1	291863	289386	3	
<i>B. moriyama</i>	BGIBMGA000013	239	nscaf1071	-1	731188	722003	3	9f
	BGIBMGA000045	241	nscaf1071	1	756455	761654	3	9e
	BGIBMGA000012b	243	nscaf1071	-1	776934	775097	3	9d 000012 contains two Osi9 Augustus model nscaf1071:775097..775440,776272..776524,776800..776934
	BGIBMGA000012a	341	nscaf1071	-1	780388	777716	5	9c 000012 contains two Osi9 Augustus model nscaf1071:777716..778070,779043..779240,779318..779351,779496..779742,780197..780388
	BGIBMGA000011	235	nscaf1071	-1	795081	788764	3	9b
	BGIBMGA000010	240	nscaf1071	-1	813664	807853	3	9a
<i>Ap. mellifera</i>	GB19626	255	Group15.14	1	599571	600600	3	Amel_2.0_OGSv1_gmap (XP_001121625.1 LG15:4578466..4580519)
<i>Ca. floridanus</i>	CFLO15242	250	scaffold309	1	49954	48426	3	OGSv1.0 (EFN64644/GL441542.1)
<i>T. castaneum</i>	TC011662	250	ChLG9	1	20564637	20562939	3	TCOGS2, XP_001808361.1
<i>Ac. pisum</i>	ACYPI004638	264	GL349857	-	502336	498348	2	
<i>P. humanus</i>	PHUM026280	258	DS235004.1	1	457230	458434	3	

Osiris 10								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG15593-PB	741	3R	1	2089581	2093117	4	possibly 10a+10b
	CG15593-PA	576	3R	1	2089698	2093117	5	possibly 10a+10b
<i>D. pseudoobscura</i>	GA13835-PC	634	2	1	15738413	15735593	5	possibly 10a+10b
	GA13835-PB	767	2	1	15738488	15735593	4	possibly 10a+10b
<i>D. virilis</i>	GJ14257	592	scaffold_12822	1	1775378	1771016	5	possibly 10a+10b
<i>D. grimshawi</i>	GH14026	509	scaffold_14624	1	2787800	2784545	5	possibly 10a+10b missing 5' end
<i>An. gambiae</i>	AGAP004132	610	2R	1	50579082	50585938	5	possibly 10a+10b
<i>Ae. aegypti</i>	AAEL004303	565	supercont1.113	-	205352	160117	5	possibly 10a+10b
<i>Cu. quinquefasciatus</i>	CPIJ008138	564	supercont3.179	1	260063	230396	5	possibly 10a+10b
<i>B. mori</i>	BGIBMGA000046	314	nscaf1071	1	839498	846172	4	10a or 10b only
<i>Ap. mellifera</i>	XP_003249790.1	314	Group15.14	1	602439	603849	2	10a, NCBI_RefSeq
<i>Ca. floridanus</i>	GB13856	223	Group15.14	1	606624	607462	3	10b, Amel_2.0_OGSv1_gmap
	CFL015243	283	scaffold309	1	46630	44997	2	10a, OGSv1.0 (EFN64643/GL441542.1)
<i>T. castaneum</i>	CFL015244	219	scaffold309	1	40662	39172	3	10b, OGSv1.0 (EFN64644/GL441542.1)
	XP_967021.2	533	ChLG9	1	20561128	20557379	8	LOC655388, TC011663+TC011664 possibly 10a+10b
<i>Ac. pisum</i>	ACYPI37205	360	GL349857	-	494658	484212	4	10a
	ACYPI37204	240	GL349857	+	477903	479043	2	10b
<i>P. humanus</i>	PHUM026300	307	DS235004.1	1	470753	471897	4	10a
	PHUM026310	165	DS235004.1	1	476,424	477503	4	10b

Osiris 11								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG15596	302	3R	-1	2094410	2093502	1	
<i>D. pseudoobscura</i>	GA13838	317	2	-1	15734475	15735428	1	
<i>D. virilis</i>	GJ14489	321	scaffold_12822	-1	1769902	1770867	1	
<i>D. grimshawi</i>	GH14282	326	scaffold_14624	-1	2783391	2784371	1	
<i>An. gambiae</i>	AGAP004134	263	2R	1	50594209	50595000	1	
<i>Ae. aegypti</i>	AAEL004298	263	supercont1.113	+	85610	86401	1	
<i>Cu. quinquefasciatus</i>	CPIJ008136	262	supercont3.179	1	198762	197867	1	
<i>B. mori</i>	BGIBMGA00000	253	nscaf1071	-1	851744	850983	1	
<i>Ap. mellifera</i>	XP_003249794.	202	Group15.14	-1	609315	608097	3	NCBI-RefSeq model corresponding to GB14757, but without extra 12 aa at 5' end
<i>Ca. floridanus</i>	CFLO15250	193	scaffold309	-1	35342	37142	3	OGSv1.0, missing 5' region (EFN64641/GL441542.1)
<i>T. castaneum</i>	TC012810	279	ChLG9	-1	20555016	20556390	2	TCOGS2 (XP_996928.2 missing 5' and 3')
<i>Ac. pisum</i>	ACYPI003143	316	GL349857	-	465923	448880	5	
<i>P. humanus</i>	PHUM026320	346	DS235004.1	-1	482961	481380	3	

Osiris 12								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG1154	295	3R	1	2104429	2107526	2	
<i>D. pseudoobscura</i>	GA11059	310	2	1	15724932	15722318	2	
<i>D. virilis</i>	GJ14258	296	scaffold_12822	1	1759247	1755541	2	
<i>D. grimshawi</i>	GH14027	306	scaffold_14624	1	2773783	2770028	2	
<i>An. gambiae</i>	AGAP013195	245	2R	1	50611644	50612588	2	
<i>Ae. aegypti</i>	AAEL002957a	232	supercont1.73	+	533897	545601	2	based on AAEL002957 ex4-ex5:
<i>Cu. quinquefasciatus</i>	CPIJ008135	342	supercont3.179	1	128851	120079	5	
<i>B. mori</i>	BGIBMGA000047	234	nscaf1071	1	860527	877819	3	BGIBMGA00004 missing 3' end; Augustus model nscaf1071:860527..860929,866403..866530,877646..877819
<i>Ap. mellifera</i>	XP_001121769.1	263	Group15.14	1	614359	615150	1	NCBI_RefSeq model corresponding to GB18845, but with extra 41 aa at N-term (LG15:4593479..4594270)
<i>Ca. floridanus</i>	CFLO15245	257	scaffold309	1	31139	30366	1	OGSv1.0 (EFN64640/GL441542.1)
<i>T. castaneum</i>	TC011665	237	ChLG9	1	20552342	20551573	2	TCOGS2, XP_966834.1
<i>Ac. pisum</i>	ACYPI000603	255	GL349857	+	445712	449651	2	
<i>P. humanus</i>	None							

Osiris 13								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG15595	210	3R	1	2117624	2118491	2	
<i>D. pseudoobscura</i>	GA13837	219	2	1	15713662	15712936	2	
<i>D. virilis</i>	GJ14260	207	scaffold_12822	1	1745092	1744398	2	
<i>D. grimshawi</i>	GH14029	208	scaffold_14624	1	2759717	2758601	2	
<i>An. gambiae</i>	None							
<i>Ae. aegypti</i>	None							
<i>Cu. quinquefasciatus</i>	None							
<i>B. mori</i>	BGIBMGA00004	222	nscaf1071	1	889090	891513	3	Weak similarity
<i>Ap. mellifera</i>								
<i>Ca. floridanus</i>	CFLO15246	225	scaffold309	1	23657	21613	3	OGSv1.0 (EFN64638/GL441542.1) weak similarity
<i>T. castaneum</i>	None							
<i>Ac. pisum</i>	None							
<i>P. humanus</i>	None							



Osiris 14								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG1155	268	3R	1	2124973	2126299	3	
<i>D. pseudoobscura</i>	GA11061	269	2	1	15707310	15706315	3	
<i>D. virilis</i>	GJ14261	277	scaffold_12822	1	1737239	1736231	3	
<i>D. grimshawi</i>	GH14030	270	scaffold_14624	1	2750767	2749290	3	
<i>An. gambiae</i>	AGAP003465	280	2R	1	38016606	38018316	3	
<i>Ae. aegypti</i>	AAEL002962	290	supercont1.73	+	921829	928099	3	
<i>Cu. quinquefasciatus</i>	CPIJ009837	273	supercont3.253	-	539625	536876	3	
<i>B. mori</i>	BGIBMGA00005	189	nscaf1071	1	899025	905630	4	
<i>Ap. mellifera</i>	GB19255	267	Group15.14	1	625746	627315	3	Amel_2.0_OGSv1_gmap (XP_392084.1 LG15:4604768..4606632)
<i>Ca. floridanus</i>	CFLO15247	262	scaffold309	1	18470	16528	3	OGSv1.0 (EFN64637/GL441542.1)
<i>T. castaneum</i>	TC011827	245	ChLG9	1	17784120	17783271	3	TCOGS2, XP_972144.1
<i>Ac. pisum</i>	ACYPI010031	258	GL349857	-	367021	365776	3	
<i>P. humanus</i>	PHUM026630	271	DS235004.1	1	514933	515929	3	

Osiris 15								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG1157	214	3R	1	2127635	2128897	3	
<i>D. pseudoobscura</i>	GA11070	214	2	1	15704652	15703720	3	
<i>D. virilis</i>	GJ14262	215	scaffold_12822	1	1734711	1733651	3	
<i>D. grimshawi</i>	GH14031	214	scaffold_14624	1	2747671	2746647	3	
<i>An. gambiae</i>	AGAP003466	206	2R	1	38023425	38027635	3	
<i>Ae. aegypti</i>	AAEL002949	206	supercont1.73	+	947347	977880	3	
<i>Cu. quinquefasciatus</i>	CPIJ009835	208	supercont3.253	-	520208	503607	3	
<i>B. mori</i>	None							
<i>Ap. mellifera</i>	GB14511	233	Group15.14	1	629349	631777	2	Amel_2.0_OGSv1_gmap (XP_001121861.1 LG15:4608426..4611097)
<i>Ca. floridanus</i>	CFLO15248	234	scaffold309	1	14885	12348	2	OGSv1.0 (EFN64636/GL441542.1)
<i>T. castaneum</i>	TC011828	188	ChLG9	1	17771168	17770175	2	TCOGS2, XP_971987.1
<i>Ac. pisum</i>	None							
<i>P. humanus</i>	None							

Osiris 16								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG31561	278	3R	1	2130992	2131887	2	
<i>D. pseudoobscura</i>	GA16326	277	2	1	15701265	15700368	2	
<i>D. virilis</i>	GJ14264	278	scaffold_12822	1	1731967	1730888	2	
<i>D. grimshawi</i>	GH14033	276	scaffold_14624	1	2745403	2744257	2	
<i>An. gambiae</i>	AGAP003467	238	2R	1	38030429	38031217	2	16a
	AGAP003472	238	2R	1	38077169	38077957	2	16b
<i>Ae. aegypti</i>	AAEL002961	254	supercont1.73	+	1025518	1038012	2	
<i>Cu. quinquefasciatus</i>	CPIJ009834	243	supercont3.253	-	495771	494975	2	
<i>B. mori</i>	BGIBMGA00005	248	nscaf1071	1	916070	920540	2	16a
	BGIBMGA00005	222	nscaf1071	1	924686	927766	2	16b
	See Osiris-like located here							
<i>Ap. mellifera</i>	GB16524	303	Group15.14	1	636935	638007	2	Amel_2.0_OGSv1_gmap (XP_001121887.1 includes extra 3')
<i>Ca. floridanus</i>	CFLO15249	294	scaffold309	1	6971	5865	2	OGSv1.0 (EFN64635/GL441542.1)
<i>T. castaneum</i>	TC012679	257	ChLG9	-1	17774547	17775320	1	16b, TCOGS2, XP_972042.1
	TC012680	260	ChLG9	-1	17778206	17781508	2	16a, TCOGS2, XP_972093.1
<i>Ac. pisum</i>	ACYPI37215	395	GL349857	-	264785	258197	3	16c
	ACYPI37213	335	GL349857	-	335265	325498	3	16b
	ACYPI37212	206	GL349857	-	347582	342664	3	16a
	ACYPI37197	271	GL349857	+	386913	389207	2	16f, located before Osi14
	ACYPI37210	284	GL349857	-	398236	395754	2	16e, located before Osi14
	ACYPI007501	287	GL349857	-	402294	399369	2	16d, located before Osi14
<i>P. humanus</i>	None							

Osiris 17								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG15598	648	3R	1	2141609	2152519	8	
<i>D. pseudoobscura</i>	GA26496-PA	740	2	1	15692057	15683149	9	Isoforms
	GA26496-PC	654	2	1	15692183	15683149	9	Isoforms
<i>D. virilis</i>	GJ14266	705	scaffold_12822	1	1717024	1703545	9	
<i>D. grimshawi</i>	GH14034a	761	scaffold_14624	1	2735733	2723660	9	last exon removed. Revised model: (2723660..2723801,2726507..2726685,2726749..2726859,2728780..2728978,2729765..2730073,2730663..2730850,2733027..2733280,2733378..2733611,2735064..2735
<i>An. gambiae</i>	AGAP003468	661	2R	1	38042427	38056441	8	
<i>Ae. aegypti</i>	AAEL002966a	598	supercont1.73	+	1118311	1246764	8	AAEL002966 + AAEL002952 genewise model: CDS(1118311..1118617,1155934..1156176,1166316..1166569,1182188..1182342,1183777..1184010,1193705..1193876,1215056..1215336,1246614..1246764), start codon not found
<i>Cu. quinquefasciatus</i>	CPIJ009830a	669	supercont3.253	-	449432	366128	8	CPIJ009830+CPIJ009831+CPIJ009832+CPIJ009833; genewise model: CDS(449432..449153,417630..417388,413069..412816,406802..406639,403596..403396,393345..393201,379175..378895,366278..366128); Need to check
<i>B. mori</i>	BGIBMGA000054	588	nscaf1071	1	968425	985551	10	
<i>Ap. mellifera</i>	XP_001121915.2	586	Group15.14	1	655434	658194	4	NCBI-RefSeq model corresponding to GB16817, but with extra 91 aa at N-term (LG15:4634123..4638274)
<i>Ca. floridanus</i>	CFLO14498	560	scaffold767	-	348549	345974	5	OGSv1.0 (EFN71496/GL436778.1)
<i>T. castaneum</i>	None							
<i>Ac. pisum</i>	ACYPI006202	525	GL349975	+	190119	206662	7	
<i>P. humanus</i>	PHUM497620a	645	DS235830.1	-	141828	133937	8	PHUM497620+PHUM497610; GeneWise model: 141828..141297, 138866..138492, 135455..135226, 135153..134991, 134907..134726, 134649..134541, 134461..134257, 134078..133937

Osiris 18								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG1169	306	3R	1	2156073	2157285	2	
<i>D. pseudoobscura</i>	GA11143	313	2	1	15676247	15675240	2	
<i>D. virilis</i>	GJ14267	309	scaffold_12822	1	1700037	1699044	2	
<i>D. grimshawi</i>	GH14035	318	scaffold_14624	1	2720195	2719171	2	
<i>An. gambiae</i>	AGAP003469	265	2R	-1	38058328	38057430	2	
	AGAP012548	106	UNKN	-1	14659597	14654022	2	Almost identical copy in unknown location; possible assembly mistake; see
<i>Ae. aegypti</i>	AAEL002965	266	supercont1.73	-	1259787	1258929	2	
<i>Cu. quinquefasciatus</i>	CPIJ009829	267	supercont3.253	+	356854	357720	2	
<i>B. mori</i>	BGIBMGA00000	270	nscaf1071	-1	993294	992334	3	
<i>Ap. mellifera</i>	GB16900	249	Group15.14	1	659884	660816	3	Amel_2.0_OGSv1_gmap (XP_001121942.2 LG15:4638990..4640092)
<i>Ca. floridanus</i>	CFLO14499	246	scaffold767	-	342467	341404	3	OGSv1.0 (EFN71495/GL436778.1)
<i>T. castaneum</i>	TC012820	246	ChLG9	-1	20684703	20685544	3	TCOGS2, XP_968992.1
<i>Ac. pisum</i>	ACYPI009026	242	GL349975	+	217232	219193	4	
<i>P. humanus</i>	PHUM497600	285	DS235830.1	+	123337	124403	3	

Osiris 19								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG15189-PA	266	3R	1	2161165	2162662	4	isoform
	CG15189-PB	257	3R	1	2161165	2162659	4	isoform
<i>D. pseudoobscura</i>	GA13557	273	2	1	15672361	15670940	4	
<i>D. virilis</i>	GJ14268	266	scaffold_12822	1	1695141	1693812	4	
<i>D. grimshawi</i>	GH14036	262	scaffold_14624	1	2716195	2714924	4	
<i>An. gambiae</i>	AGAP003470	232	2R	1	38061429	38062320	3	
	AGAP012549	247	UNKN	+	14662691	14663580	3	Almost identical copy in unknown location; possible assembly mistake; see
<i>Ae. aegypti</i>	AAEL002960	250	supercont1.73	+	1285435	1286307	3	
<i>Cu. quinquefasciatus</i>	CPIJ009828	251	supercont3.253	-	344600	343725	3	
<i>B. mori</i>	BGIBMGA01071	258	nscaf3003	-	3992132	3991021	3	
<i>Ap. mellifera</i>	GB16804	247	Group15.14	1	663088	663932	2	Amel_2.0_OGSv1_gmap (XP_001121961.1 LG15:4642085..4643841)
<i>Ca. floridanus</i>	CFLO14500	247	scaffold767	-	339201	338256	2	OGSv1.0 (EFN71494/GL436778.1)
<i>T. castaneum</i>	TC012821	243	ChLG9	-1	20686916	20687749	3	19a, TCOGS2, XP_969068.1
	TC012822	196	ChLG9	-1	20689368	20690009	2	19b, TCOGS2, XP_969215.1
<i>Ac. pisum</i>	ACYPI000796	190	GL349975	+	226304	227943	4	
<i>P. humanus</i>	PHUM497590	255	DS235830.1	-	122029	121084	3	

Genome	Osiris 20							Note
	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	
<i>D. melanogaster</i>	CG15188	280	3R	1	2165910	2166818	2	
<i>D. pseudoobscura</i>	GA13556	276	2	1	15666849	15665952	2	
<i>D. virilis</i>	GJ14269	277	scaffold_12822	1	1689890	1688986	2	
<i>D. grimshawi</i>	GH14037	280	scaffold_14624	1	2711690	2710778	2	
<i>An. gambiae</i>	AGAP003471	320	2R	1	38065791	38066897	2	
<i>Ae. aegypti</i>	AAEL002955	292	supercont1.73	+	1305642	1313330	2	
	AAEL014727	292	supercont1.1240	-	188349	182326	2	20b, Unlinked Osi20 copy; almost identical
<i>Cu. quinquefasciatus</i>	CPIJ009827	297	supercont3.253	-	330657	327540	2	
<i>B. mori</i>	BGIBMGA010717	293	nscaf3003	-	3982740	3981708	3	
<i>Ap. mellifera</i>	XP_001121985.1	270	Group15.14	1	665962	666847	2	NCBI_RefSeq model corresponding to GB15865, but with extra 120 aa at 5' end (LG15:4644922..4646726)
<i>Ca. floridanus</i>	CFLO14501	267	scaffold767	-	335705	334509	2	OGSv1.0 (EFN71493/GL436778.1)
<i>T. castaneum</i>	TC012823	248	ChLG9	-1	20691474	20692314	3	TCOGS2, XP_969284.1
<i>Ac. pisum</i>	ACYPI007146	281	GL349975	+	238670	239799	2	
<i>P. humanus</i>	PHUM497570	290	DS235830.1	-	117238	116133	4	

Osiris 22								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG8644	332	3R	1	9116438	9117497	2	
<i>D. pseudoobscura</i>	GA21234	342	2	1	9987757	9986666	2	
<i>D. virilis</i>	GJ10414	363	scaffold_12855	-	3036310	3035156	2	
<i>D. grimshawi</i>	GH18427	339	scaffold_14906	-	5747016	5745936	2	
<i>An. gambiae</i>	AGAP003420	366	2R	1	37510453	37511640	2	
<i>Ae. aegypti</i>	AAEL007198	359	supercont1.243	+	914044	915223	2	
<i>Cu. quinquefasciatus</i>	CPIJ011100	345	supercont3.316	+	372903	374003	2	
<i>B. mori</i>	BGIBMGA010678	163	nscaf2998	+	1317487	1322074	2	Middle region missing
<i>Ap. mellifera</i>	None							
<i>Ca. floridanus</i>	None							
<i>T. castaneum</i>	TC002385	151	unknown	+	15336400	15336898	2	Middle region missing
<i>Ac. pisum</i>	ACYPI002813	196	GL350227	-	167081	164772	3	Middle region
<i>P. humanus</i>	None							



Osiris 23								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>	CG15538	250	3R	-1	26270756	26269871	3	
<i>D. pseudoobscura</i>	GA13796	270	2	-1	1254748	1255676	3	
<i>D. virilis</i>	GJ22762	265	scaffold_13047	-	15824251	15823319	3	
<i>D. grimshawi</i>	GH17432	264	scaffold_14830	+	4185984	4186905	3	
<i>An. gambiae</i>	AGAP000957	293	X	-	18368810	18367147	4	
<i>Ae. aegypti</i>	None							Short similarity against AGAP000957 and CG15538 found in supercont1.202:13944741394301
<i>Cu. quinquefasciatus</i>	Cqui_Osi23	189	supercont3.42	+	474599	480673	3	GeneWise+Augustus model: 474599..474855,474955..475082,480489..480673; still missing 3'
<i>B. mori</i>	None							
<i>Ap. mellifera</i>	XP_001120227.2	254	Group8.6	-	87657	86288	3	NCBI_RefSeq model corresponding to GB14285, but with extra 14 aa at N-term (LG8:2309823..2307814)
<i>Ca. floridanus</i>	CFLO22710	249	scaffold799		210020	211808	3	OGSv1.0 (EFN70025/GL437711.1)
<i>T. castaneum</i>	TC030703a	226	ChLG2	+	11496092	11497260	3	TC030703:TCOGS2 with extra N/C-term. XP_970499.1 (non-Osi protein) includes this as part of its exons. AUGUSTUS model: 11496092..11496258,11496701..11496798,11496845..11497260
<i>Ac. pisum</i>	ACYPI50421	217	GL350440	-	80703	67062	3	
<i>P. humanus</i>	None							

Osiris 21								
Genome	ID	Length (AA)	Chromosome (linkage group)	Strand	Start	End	# exons	Note
<i>D. melanogaster</i>	CG14925	282	2L	-	11285603	11284586	2	
<i>D. pseudoobscura</i>	GA13356	280	4_group3	-	6710686	6709780	2	
<i>D. virilis</i>	GJ14913	277	scaffold_12963	+	2228486	2229378	2	
<i>D. grimshawi</i>	GH13529	291	scaffold_15126	+	1313369	1314317	2	
<i>An. gambiae</i>	AGAP005899	256	2L	-	23383765	23382399	3	21a
	AGAP010354	242	3L	-	2060900	2060107	2	21b
<i>Ae. aegypti</i>	AAEL004788	264	supercont1.130	+	1236881	1240903	3	21a
	AAEL014873	242	supercont1.1318	-	61163	25952	2	21b
<i>Cu. quinquefasciatus</i>	CPIJ006501	255	supercont3.125	-	457478	456268	2	21c
	CPIJ016349	255	supercont3.798	+	131376	132525	2	21b
	CPIJ004911	270	supercont3.80	+	580797	581778	3	21a
<i>B. mori</i>	BGIBMGA013568a	216	nscaf3078	+	404693	405837	4	BGIBMGA013568+BGIBMGA013569 GeneWise model: 404693..404875,404959..405151, 405257..405437,405754..405837; need to check
<i>Ap. mellifera</i>	None							
<i>Ca. floridanus</i>	None							
<i>T. castaneum</i>	TC013496	250	ChLG5	-	10767500	10766748	1	TCOGS2, XP_976416.1
<i>Ac. pisum</i>	ACYPI008994	252	GL350028	-	167549	164571	2	21c
	ACYPI43145	245	GL350028	-	154956	151423	2	21b
	ACYPI005783	258	GL350028	-	135395	126447	2	21a
	ACYPI064603	141	GL356106	+	0	3876	2	21a2, missing 5' and 3'-ends
<i>P. humanus</i>	None							

Osiris like								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>								
<i>D. pseudoobscura</i>								
<i>D. virilis</i>								
<i>D. grimshawi</i>								
<i>An. gambiae</i>								
<i>Ae. aegypti</i>								
<i>Cu. quinquefasciatus</i>								
<i>B. mori</i>	BGIBMGA000053	493	nscaf1071	1	931016	939783	7	located after Osi16b
<i>Ap. mellifera</i>								
<i>Ca. floridanus</i>								
<i>T. castaneum</i>								
<i>Ac. pisum</i>	ACYPI000560	419	GL349857	+	296605	308820	5	Located between 16b and c
	ACYPI37193	286	GL349857	+	266124	275397	3	Located between 16b and c
	ACYPI33621	262	GL350199	+	284013	299232	2	
<i>P. humanus</i>	PHUM025350	285	DS235004.1	-1	94973	93537	3	
	PHUM025360	360	DS235004.1	-1	110230	108271	4	
	PHUM465410	327	DS235812.1	-1	294251	290973	3	

CG15594 like								
Genome	ID	Length (AA)	Chromosome (linkage group)	Direct	Start	End	# exons	Note
<i>D. melanogaster</i>								
<i>D. pseudoobscura</i>								
<i>D. virilis</i>								
<i>D. grimshawi</i>								
<i>An. gambiae</i>								
<i>Ae. aegypti</i>								
<i>Cu. quinquefasciatus</i>								
<i>B. mori</i>	BGIBMGA000048272		nscaf1071	1	883002	886205	2	
<i>Ap. mellifera</i>	XP_003249795.1	169	Group15.14	-1	617796	616879	2	LG15:4597217..459575
<i>Ca. floridanus</i>	CFLO10930	225	scaffold309	-1	27850	28890	2	EFN64639/GL441542
<i>T. castaneum</i>								
<i>Ac. pisum</i>	ACYPI007103	364	GL349679	-1	542850	539522	6	
<i>P. humanus</i>								