

Vip-Sel: number of Tags in the Vip-Sel library

Vip-Unsel: number of Tags in the Vip-Unsel library

Norm. Vip-Sel: number of tags in Vip-Sel normalized to 268000 [See Materials & Methods for details]

Norm. Vip-Unsel: number of tags in Vip-Unsel normalized to 268000 [See Materials & Methods for details]

p-value: Statistical value associated with the different in tag copy number between libraries calculated according to Audic and Claverie (1997)

FC: fold.change (Norm. Vip-Sel vs. Norm. Vip-Unsel)

Heliothis virescens CONTIG match: Identifier of the Contig sequence of *Heliothis virescens* (from Perera et al., 2015) that perfectly matched (26bp) with the corresponding tag in Blastn search

List of over-expressed Unitaigs sequences, copy number, fold change and annotations to the *Heliothis virescens* sequence contigs database

General classification (Process/Molecular Function)	TAG	Vip-Sel	Vip-Unsel	Norm. Vip-Sel	Norm. Vip-Unsel	p-value	FC	Heliothis virescens CONTIG match	Contig also (nt)	Tag position in the contig (nt)	Protein annotation blastx	E-value
-	Tag_32 CATGTTGTGCTCTGGCTGGAAACGGCG	3631	2	921.434	1.959	0.00E+00	461.013	no hit	-	-	-	-
-	Tag_211 CATGCACCTGGCGGAGCGGTGGTGG	311	1	78.922	0.999	1.40E-29	78.973	no hit	-	-	-	-
Defense	Tag_61 CATGTTGCTGGCTGCTGCAGCACCG	1474	5	374.055	4.997	2.26E-135	74.859	Hv_Contig_8456	1247	88-113	AFH57159 REPAT39 <i>Spodoptera exigua</i>	7.00E-30
Unknown	Tag_35 CATGAGAATGCTAAACTGGGTGGTG	1857	7	471.248	6.996	5.57E-169	67.364	Hv_Contig_22902	646	221-246	ABH10141 HMG176 <i>Helicoverpa armigera</i>	7.00E-53
-	Tag_255 CATGGCAGCCTAGCCTGGCCCGCGT	245	1	62.173	0.999	3.39E-23	62.213	no hit	-	-	-	-
-	Tag_293 CATGTGAGCTAGCTTCGCCCCGCGT	215	1	54.560	0.999	2.65E-20	54.595	no hit	-	-	-	-
-	Tag_340 CATGGCAGCTAGCTTCGCCCCACGT	190	1	45.678	0.999	5.14E-17	45.708	no hit	-	-	-	-
-	Tag_362 CATGGCAGCCTAGCTTCGCCCCGCGT	173	1	43.902	0.999	2.88E-16	43.930	no hit	-	-	-	-
-	Tag_392 CATGGCACTAGCTTCGCCCCGCGT	154	1	39.080	0.999	1.90E-14	39.105	no hit	-	-	-	-
-	Tag_414 CATGGTGGTGACTCCGTGTGAGCC	144	1	36.543	0.999	1.71E-13	36.566	no hit	-	-	-	-
-	Tag_416 CATGGCAGCCTATCTTCGCCCCGCGT	143	1	36.289	0.999	2.13E-13	36.312	no hit	-	-	-	-
-	Tag_241 CATGGCAGCCAGCTTCGCCCCGCGT	272	2	69.025	1.999	2.36E-24	34.535	no hit	-	-	-	-
Nucleic acid binding	Tag_435 CATGCCGCGCGCGCGCGCGCAGG	132	1	33.497	0.999	2.38E-12	33.519	Hv_Contig_11935	1025	846-871	XP_01436776 zinc finger protein 586 <i>Papilio machaon</i>	0.00E+00
-	Tag_436 CATGGCAGCCTAGCTTCGCCCTGCGT	132	1	33.497	0.999	2.38E-12	33.519	no hit	-	-	-	-
-	Tag_444 CATGGCAGCCTAGTTTCGCCCCGCGT	127	1	32.229	0.999	7.10E-12	32.249	no hit	-	-	-	-
-	Tag_279 CATGGCAGCCTAGCTTCGCCCCGTGT	229	2	58.113	1.999	2.84E-20	29.075	no hit	-	-	-	-
-	Tag_498 CATGCACGTGGCGCGCAGGTGAGTG	107	1	27.153	0.999	5.57E-10	27.171	no hit	-	-	-	-
-	Tag_217 CATGAGGCGCGCAGACCCGCCCTCG	304	3	77.146	2.998	4.43E-26	25.732	no hit	-	-	-	-
-	Tag_68 CATGCGCACGGCAGCAGAAAGGGTGT	1291	13	327.615	12.992	5.18E-106	25.217	no hit	-	-	-	-
-	Tag_541 CATGTTGCGCTCTGGCTGSCCAACG	98	1	24.869	0.999	3.93E-09	24.885	no hit	-	-	-	-
Unknown	Tag_544 CATGGAGCGCGACGGCGGGGCGCG	97	1	24.616	0.999	4.88E-09	24.631	Hv_Contig_36272	406	293-318	XP_011559079 uncharacterized protein LOC105389633 <i>Plutella xylostella</i>	2.00E-30
Unknown	Tag_550 CATGGCCGCGCCCGCAGCTGCGCGG	95	1	24.108	0.999	7.52E-09	24.123	Hv_Contig_368	4062	459-434	XP_014362832 cytoplasmic dynein 1 intermediate chain isoform X6 <i>Papilio machaon</i>	0.00E+00
-	Tag_235 CATGAGAATGCTAAACTGGGTGGTA	284	3	72.070	2.998	3.35E-24	24.039	no hit	-	-	-	-
Protein folding/Recycling	Tag_326 CATGGCGGTGGACGCGCTGCCCGCGC	189	2	47.962	1.999	1.67E-16	23.997	Hv_Contig_7535	1329	1223-1248	XP_013135438 presenilin homolog <i>Papilio polytes</i>	8.00E-169
-	Tag_553 CATGCACTCGGCCGAGCAGCCGCTGG	94	1	23.854	0.999	9.34E-09	23.870	no hit	-	-	-	-
-	Tag_333 CATGACAGCTAGCTTCGCCCCGCGT	185	2	46.947	1.999	3.96E-16	23.489	no hit	-	-	-	-
mRNA processing/splicing	Tag_335 CATGTGCGCGCGCCCGCCACCGCT	183	2	46.440	1.999	6.08E-16	23.235	Hv_Contig_2277	2278	2217-2342	XP_013188918 protein virilizer <i>Amyelotus transilella</i>	0.00E+00
-	Tag_573 CATGCACTCGGCCGAGCGCCGATGG	89	1	22.585	0.999	2.75E-08	22.600	no hit	-	-	-	-
-	Tag_344 CATGAGAATGCTAAACTGGGTGGTC	176	2	44.663	1.999	2.75E-15	22.346	no hit	-	-	-	-
Unknown	Tag_87 CATGAGCCCTCTCTGCCGCACAGT	866	10	219.764	9.994	5.36E-70	21.990	Hv_Contig_16164	842	517-542	XP_013135392 eukocyte surface antigen CD53-like isoform X1 <i>Papilio polytes</i>	7.00E-73
Unknown	Tag_18 CATGCGCACGGCAGCAGAAAGGGTGA	8622	105	2187.993	104.933	0.00E+00	20.851	Hv_Contig_31364	498	360-385	CCF46246 hypothetical protein CH063_15059, partial <i>Colletesrichum hagenianum</i>	2.00E-14
-	Tag_12 CATGGCAGCCTAGCTTCGCCCCGCGC	11598	142	2943.209	141.909	0.00E+00	20.740	no hit	-	-	-	-
Unknown	Tag_125 CATGTGGCGGGCTCGCATCGAGTT	570	7	144.648	6.996	4.65E-46	20.677	Hv_Contig_5434	1575	808-834	XP_012546736 P3 protein-like <i>Bombyx mori</i>	1.00E-39
Cytoskeleton	Tag_606 CATGGAACGCGAGGCTGAGACGCGT	81	1	20.555	0.999	1.54E-07	20.568	Hv_Contig_9943	1142	579-604	XP_013141160 tetraspanin-15-like <i>Papilio polytes</i>	1.00E-39
-	Tag_378 CATGCACTCGGCCGAGCGCCAGTGG	161	2	40.857	1.999	6.91E-14	20.441	no hit	-	-	-	-
-	Tag_387 CATGCTCTCAAGTCGAATGGTTG	156	2	39.588	1.999	2.02E-13	19.807	no hit	-	-	-	-
-	Tag_110 CATGCGCACGGCAGCAGAAAGGGTGC	700	9	177.638	8.994	9.33E-56	19.750	no hit	-	-	-	-
Translation/Ribosome biogenesis	Tag_393 CATGGCAGCGCGCTCGTGCAGGCA	153	2	38.827	1.999	3.83E-13	19.426	Hv_Contig_28542	953	124-149	NP_01298510 40S ribosomal protein S20 <i>Papilio polytes</i>	9.00E-81
-	Tag_281 CATGGCAGCCTGGCTTCGCCCGCGT	228	3	57.859	2.998	5.62E-19	19.299	no hit	-	-	-	-
-	Tag_401 CATGCTCTACAGATGTCGCTAAG	150	2	38.065	1.999	7.27E-13	19.045	no hit	-	-	-	-
-	Tag_291 CATGGCTGTTGAGCAGCAAGAGCG	217	3	55.068	2.998	5.57E-18	18.368	no hit	-	-	-	-
Translation/Ribosome biogenesis	Tag_230 CATGTGTCGCTTCAGACGCCGCGTGA	289	4	73.339	3.997	1.72E-23	18.347	Hv_Contig_7237	1357	1195-1220	AAL62468 ribosomal protein L3 <i>Spodoptera frugiperda</i>	0.00E+00
-	Tag_651 CATGTACACGACAAATCGTATCC	72	1	18.271	0.999	1.06E-06	18.283	no hit	-	-	-	-
-	Tag_36 CATGCGCACGGCAGCAGAAAGGGTGG	3164	44	802.924	43.972	1.58E-242	18.260	no hit	-	-	-	-
-	Tag_295 CATGGCGCAGCTGCCGCTAGCGACG	215	3	54.560	2.998	8.98E-18	18.198	no hit	-	-	-	-
Primary metabolic process/oxidoreductase activity	Tag_653 CATGTGCGGCAGCTCGGAATGTCCT	71	1	18.018	0.999	1.31E-06	18.029	Hv_Contig_17230	806	340-365	ACY78421 disappea biotock protein-like protein <i>Helicoverpa armigera</i>	7.00E-128
Unknown	Tag_3 CATGGCAGCTAGCTTCGCCCCGCGT	103728	1501	26322.915	1500.037	0.00E+00	17.548	Hv_Contig_40219	299	64-89	ABH10141 HMG176 <i>Helicoverpa armigera</i>	2.00E-22
-	Tag_432 CATGCGCGCTACGTGCGGCACAGG	134	2	34.005	1.999	2.13E-11	17.013	no hit	-	-	-	-
-	Tag_174 CATGGCGGCTAGCTTCGCCCGCGT	402	6	102.015	5.996	1.14E-31	17.013	no hit	-	-	-	-
-	Tag_679 CATGTGCGCGGCTCGATCGAGTC	66	1	16.749	0.999	3.79E-06	16.759	no hit	-	-	-	-
Translation/Ribosome biogenesis	Tag_883 CATGTTGGCCCCGAGTCTCGAAGG	65	1	16.495	0.999	4.68E-06	16.506	Hv_Contig_20199	717	229-254	Q9638705 ribosomal protein L9 <i>Spodoptera frugiperda</i>	3.00E-130
-	Tag_140 CATGGCAGCGCAGCAGAGGGGTAA	516	8	130.945	7.995	6.36E-40	16.379	no hit	-	-	-	-
Transport/Trafficking	Tag_442 CATGATCGTGTGCGAGCTCGGCCGCA	128	2	32.482	1.999	7.80E-11	16.252	Hv_Contig_949	3061	2432-2457	XP_014363077 phosphatidylinositol transfer protein alpha isoform <i>Papilio machaon</i>	9.00E-166
-	Tag_884 CATGCGAGCTAGCTTTGCCCCGCGT	64	1	16.241	0.999	5.80E-06	16.252	no hit	-	-	-	-
Protein folding/Recycling	Tag_451 CATGGAGCGGCTCGGCTCTCCAAAG	124	2	31.467	1.999	1.82E-10	15.744	Hv_Contig_16650	823	611-636	ADK55517 heat shock protein 90 cognate <i>Spodoptera litura</i>	4.00E-130
-	Tag_452 CATGTGCTGACGAGTCTCTCGAAC	124	2	31.467	1.999	1.82E-10	15.744	no hit	-	-	-	-
-	Tag_716 CATGGCAGCTAGCTTCGCCCCGAC	60	1	15.226	0.999	1.35E-05	15.236	no hit	-	-	-	-
-	Tag_221 CATGCGCGGGCGCGCGGCCCGCCGA	296	5	75.116	4.997	4.79E-23	15.033	no hit	-	-	-	-
-	Tag_343 CATGAGAATGCTAAACTGGGTGGG	177	3	44.917	2.998	2.77E-14	14.982	no hit	-	-	-	-

-		Tag_472 CATGCATTGGCCGAGGCCGGTGG	118	2	29.945	1.999	6.42E-10	14.982	no hit	-	-	-	-
Unknown		Tag_268 CATGACGCGCGCTGTGCCCTTCC	234	4	59.382	3.997	1.93E-18	14.855	Hv_Contig_25956	593	65-90	EH71292 hypothetical protein KGM_01454 <i>Danaus plexippus</i>	8.00E-25
-		Tag_269 CATGCGACGCGACGCGAAGGGTAG	234	4	59.382	3.997	1.93E-18	14.855	no hit	-	-	-	-
-		Tag_347 CATGTTGTCTCTGGGTGAACGGCA	175	3	44.410	2.998	4.22E-14	14.813	no hit	-	-	-	-
-		Tag_732 CATGGCTGAAGGAAGGAACAGCTC	58	1	14.719	0.999	2.06E-05	14.728	no hit	-	-	-	-
-		Tag_476 CATGCCCGCTGGTGCGCTCCCT	116	2	29.437	1.999	9.78E-10	14.728	no hit	-	-	-	-
-		Tag_734 CATGACGAGGTGAGGGCCCTGGAACG	57	1	14.465	0.999	2.54E-05	14.474	no hit	-	-	-	-
-		Tag_741 CATGGCGCCTAGCTTGGCCCCGGG	56	1	14.211	0.999	3.14E-05	14.220	no hit	-	-	-	-
-		Tag_364 CATGGCAGTCTAGCTTGGCCCCGCT	167	3	42.379	2.998	2.26E-13	14.136	no hit	-	-	-	-
-		Tag_180 CATGCATCGGCCGAGCGACCGGTGG	387	7	98.208	6.996	3.14E-29	14.039	no hit	-	-	-	-
Primary metabolic process/hydrolase activity		Tag_492 CATGCAAGCTGCTGCCCATCTCTCT	110	2	27.915	1.999	3.44E-09	13.966	Hv_Contig_7038	1378	1149-1174	CAA06419 carboxypeptidase A <i>Helicoverpa armigera</i>	0.00E+00
-		Tag_9 CATGCAGCCTAGCTTGCCTCCCGG	14940	273	3791.304	272.825	0.00E+00	13.896	no hit	-	-	-	-
-		Tag_368 CATGCAGCCTAGCTTACCCCGCT	164	3	41.618	2.998	4.22E-13	13.882	no hit	-	-	-	-
-		Tag_761 CATGACTCGGCGTGGCGCGGTGG	54	1	13.704	0.999	4.78E-05	13.712	no hit	-	-	-	-
-		Tag_373 CATGCGACGCGACGAGAGGTC	162	3	41.111	2.998	6.41E-13	13.712	no hit	-	-	-	-
Chitin-binding		Tag_163 CATGCACACGGCGTGGGAGAGAT	427	8	108.359	7.995	8.04E-32	13.554	Hv_Contig_36527	400	289-314	002443 larval cuticle protein 1 <i>Helicoverpa armigera</i>	4.00E-25
-		Tag_165 CATGCATCGGCCGAGCGCCCGCGG	424	8	107.598	7.995	1.50E-31	13.458	no hit	-	-	-	-
-		Tag_518 CATGACGCGCGCTGCGGCATCTC	104	2	26.392	1.999	1.20E-08	13.204	no hit	-	-	-	-
Primary metabolic process/hydrolase activity		Tag_310 CATGACTGGATCACACACATCTGT	206	4	52.276	3.997	6.62E-16	13.077	Hv_Contig_42719	259	150-175	ACR15971.2 serine protease 37 <i>Manesira configurata</i>	1.00E-12
-		Tag_396 CATGCATCGGCCAAGCGCCCGTGG	152	3	38.573	2.998	5.13E-12	12.866	no hit	-	-	-	-
Transport/Trafficking		Tag_527 CATGAACCTTGAGGTGGATGGCG	101	2	25.631	1.999	2.24E-08	12.824	Hv_Contig_32968	462	383-408	ACB54948 laty acid-binding protein 1 <i>Helicoverpa armigera</i>	6.00E-70
-		Tag_529 CATGCCGCTGGCGACGGGCTCGGCG	101	2	25.631	1.999	2.24E-08	12.824	no hit	-	-	-	-
-		Tag_533 CATGGACCTAGCTTGTCCCGCT	100	2	25.377	1.999	2.76E-08	12.697	no hit	-	-	-	-
-		Tag_537 CATGAGCCCCCTCTGCCGACACGC	100	2	25.377	1.999	2.76E-08	12.697	no hit	-	-	-	-
-		Tag_790 CATGCACACGGCGGCGGCCCGTGG	50	1	12.688	0.999	1.10E-04	12.697	no hit	-	-	-	-
-		Tag_797 CATGATCTGTGGCGGTGGCCAGCG	49	1	12.435	0.999	1.36E-04	12.443	no hit	-	-	-	-
Translation/Ribosome biogenesis		Tag_799 CATGGAGGGTGTACAGATTCCTCT	49	1	12.435	0.999	1.36E-04	12.443	Hv_Contig_14723	898	769-794	XP_012552995 9S ribosomal protein L16, mitochondrial <i>Bombyx mori</i>	4.00E-132
Protein folding/Recycling		Tag_548 CATGGACACTGGCCCTCGTGCGGCC	96	2	24.362	1.999	6.32E-08	12.189	Hv_Contig_1209	2843	2010-2025	XP_013153028 ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial isoform X3 <i>Amyelais transiella</i>	0.00E+00
Extracellular matrix structural constituent		Tag_905 CATGGACGCGGGTGAACCGTGCGC	48	1	12.181	0.999	1.67E-04	12.189	Hv_Contig_11489	1050	903-878	K0B7008 suprative collagen alpha-2 IV chain protein <i>Opiophtera brunata</i>	1.00E-32
Translation/Ribosome biogenesis		Tag_812 CATGAGCATTTAAGAATGTCGTC	47	1	11.927	0.999	2.06E-04	11.935	Hv_Contig_34007	437	114-139	AAK59928 ribosomal protein S11 <i>Heliothis virescens</i>	1.00E-67
-		Tag_815 CATGATCTGTGCGGTTGTTCACGCT	47	1	11.927	0.999	2.06E-04	11.935	no hit	-	-	-	-
-		Tag_818 CATGAAGTCTCGTTGGTGTACCTT	47	1	11.927	0.999	2.06E-04	11.935	no hit	-	-	-	-
-		Tag_236 CATGCAGCTAACTTGCCTCCGCGC	277	6	70.294	5.996	2.49E-20	11.723	no hit	-	-	-	-
mRNA processing/splicing		Tag_561 CATGGCGGGCGGGCGGCCCGGGCG	92	2	23.347	1.999	1.44E-07	11.681	Hv_Contig_671	3422	733-758	XP_013190420 RNA-binding protein squid isoform X2 <i>Amyelais transiella</i>	3.00E-122
Primary metabolic process/hydrolase activity		Tag_119 CATGGAGTCTCGTTGGTGTACCTC	597	13	151.500	12.992	4.20E-42	11.661	Hv_Contig_21108	693	568-593	AF068320 trypsin <i>Heliothis virescens</i>	4.00E-119
-		Tag_427 CATGTTTTTATTCTCTCTGTACAC	137	3	34.766	2.998	1.14E-10	11.596	Hv_Contig_5986	1496	379-354	no hit	-
-		Tag_829 CATGGACCCGAGCTTGGCCCGCGG	45	1	11.420	0.999	3.11E-04	11.427	no hit	-	-	-	-
-		Tag_209 CATCGCTCGGCCGAGCGCCCGTGG	314	7	79.883	6.996	1.13E-22	11.391	no hit	-	-	-	-
-		Tag_571 CATGGTCAATAAATCTTTGGGTCA	89	2	22.585	1.999	2.68E-07	11.300	no hit	-	-	-	-
-		Tag_838 CATGGCGCCTAGCTTGGCCCGCGC	44	1	11.166	0.999	3.82E-04	11.173	no hit	-	-	-	-
-		Tag_579 CATGGACGCTAGCTTCCCTCGCT	88	2	22.332	1.999	3.29E-07	11.173	no hit	-	-	-	-
-		Tag_98 CATGCACTCGGCCGAGCGCCGCTGT	789	18	200.223	17.888	2.31E-54	11.131	no hit	-	-	-	-
-		Tag_851 CATGTTGTCTCTGGCGGCCGAGCG	42	1	10.658	0.999	5.77E-04	10.665	no hit	-	-	-	-
-		Tag_853 CATGCCCGCGGTGGCCCGCGCTG	42	1	10.658	0.999	5.77E-04	10.665	no hit	-	-	-	-
-		Tag_366 CATGCCCGCTGGTGCGCGCTCTCT	166	4	42.126	3.997	2.47E-12	10.538	no hit	-	-	-	-
-		Tag_866 CATGCTGACGCGCGCGCGCGGTGG	41	1	10.405	0.999	7.09E-04	10.411	no hit	-	-	-	-
-		Tag_158 CATGGACGCTAGCTTGGCCCGCAT	448	11	113.688	10.993	8.44E-31	10.342	no hit	-	-	-	-
-		Tag_256 CATGCACCGCGCGAGCGCCCGTGG	244	6	61.920	5.996	2.09E-17	10.327	no hit	-	-	-	-
-		Tag_807 CATGGCTCGGCAATCTTCTTGACTC	81	2	20.555	1.999	1.37E-06	10.284	no hit	-	-	-	-
Primary metabolic process/isomerase activity		Tag_188 CATGTGGCGAGACCGACCTCGCTA	361	9	91.610	8.994	5.61E-25	10.185	Hv_Contig_7598	1323	1097-1122	XP_012552008 UDP-glucose 4-epimerase-like <i>Bombyx mori</i>	0.00E+00
-		Tag_463 CATGCATCGGCCGAACGGCCGGTGG	120	3	30.452	2.998	3.65E-09	10.157	no hit	-	-	-	-
-		Tag_260 CATGCGGAGTCAACCCTGTGCGAGC	240	6	60.904	5.996	4.69E-17	10.157	no hit	-	-	-	-
-		Tag_815 CATGTTGTCTCTGGCTGGCCGAGCG	80	2	20.301	1.999	1.68E-06	10.157	no hit	-	-	-	-
-		Tag_883 CATGCGCTCGGCCGAGGTGAAGCAG	39	1	9.897	0.999	1.07E-03	9.903	no hit	-	-	-	-
Translation/Ribosome biogenesis		Tag_888 CATGAACAGGAGTCTTACACAA	38	1	9.643	0.999	1.31E-03	9.649	Hv_Contig_12709	870	242-267	Q95V32 40S ribosomal protein S6 <i>Spodoptera frugiperda</i>	7.00E-161
Translation/Ribosome biogenesis		Tag_195 CATGTGCAATAAATCTTTGGGTG	341	9	86.535	8.994	3.15E-23	9.621	Hv_Contig_14879	892	703-728	NP_001296530 60S ribosomal protein L19 <i>Papilio polytes</i>	9.00E-95
-		Tag_62 CATGCACTCGGCCGAGCGCCGGTGC	1446	39	366.949	38.975	9.51E-93	9.415	no hit	-	-	-	-
-		Tag_913 CATGCGACGCGACGAGAGGTTA	37	1	9.399	0.999	1.60E-03	9.395	no hit	-	-	-	-
-		Tag_646 CATGACGCGCGCGTGGCGCATCTA	73	2	18.525	1.999	6.93E-06	9.269	no hit	-	-	-	-
Protein folding/Recycling		Tag_80 CATGCCCGCGGTATGCCCGGGCA	1046	29	265.442	28.981	7.16E-67	9.159	Hv_Contig_4349	1752	1532-1557	AIZ00749 heat shock cognate 70 protein, partial <i>Sesamia inferens</i>	0.00E+00
-		Tag_917 CATGATCACTGTCTCGCGCGCGTG	36	1	9.136	0.999	1.98E-03	9.142	no hit	-	-	-	-
-		Tag_920 CATGTTGTCTCGGCTGGCCAGCG	36	1	9.136	0.999	1.98E-03	9.142	no hit	-	-	-	-
-		Tag_232 CATGCATCGGCCGAGTGGCCGGTGG	287	8	72.832	7.995	2.10E-19	9.110	no hit	-	-	-	-
-		Tag_855 CATGCCCGCGCGACGCGCGTGGCGG	71	2	18.018	1.999	1.04E-05	9.015	no hit	-	-	-	-
-		Tag_658 CATGCATCGCGGAGCGGCCCGTGG	71	2	18.018	1.999	1.04E-05	9.015	no hit	-	-	-	-
Nucleic acid binding		Tag_942 CATGTGCCGCGCCTGTGCGGCGAGC	35	1	8.882	0.999	2.40E-03	8.888	Hv_Contig_1945	2412	1901-1876	XP_013143932 NFX1-type zinc finger-containing protein 1-like <i>Papilio polytes</i>	4.00E-160
-		Tag_949 CATGGCTGCGGCCAGGAGAGCGCT	35	1	8.882	0.999	2.40E-03	8.888	no hit	-	-	-	-

-	Tag_659	CATGTTGCTGGCTCGAGCCACCA	70	2	17.764	1.999	1.27E-05	8.888	no hit	-	-	-	-
Translation/Ribosome biogenesis	Tag_50	CATGCCCGCTGTGGCGCGCTCCCG	2016	58	511.598	57.963	1.88E-125	8.826	Hv_Conlig_27905	563	285-310	KP11520605 acidic ribosomal protein P2 Papilio machaon	2.00E-33
-	Tag_422	CATGAGCCCTCTCTGCGCCACACGG	139	4	35.274	3.997	5.69E-10	8.824	no hit	-	-	-	-
Unknown	Tag_2	CATGCACTCGCGCGAGCGCGGTGG	123487	3575	31337.130	3572.707	0.00E+00	8.771	Hv_Conlig_47003	206	115-140	KP115203hypothetical protein RR48_09230 Papilio machaon	9.00E-24
-	Tag_668	CATGACACGGGCTGCGGAGGAGCAG	68	2	17.256	1.999	1.89E-05	8.634	no hit	-	-	-	-
-	Tag_381	CATGCACTCGGTGAGCGCGCGGTGG	3077	91	780.846	90.942	2.19E-188	8.586	Hv_Conlig_5683	1540	1460-1485	no hit	-
Primary metabolic process/hydrolase activity	Tag_270	CATGATCTCGCGAGGATGGCTCGATG	233	7	59.128	6.996	1.37E-15	8.452	Hv_Conlig_15523	867	627-652	XP_004931376trypsin, alkaline A-like Bombyx mori	1.00E-44
-	Tag_976	CATGACATTGGTTCAAGAAGCTTGG	33	1	8.374	0.999	3.59E-03	8.380	no hit	-	-	-	-
-	Tag_979	CATGCTGCAAGCGCGCTGGGCGTGG	33	1	8.374	0.999	3.59E-03	8.380	no hit	-	-	-	-
-	Tag_981	CATGCCGCTGGTGGCGCGCTCTCG	33	1	8.374	0.999	3.59E-03	8.380	no hit	-	-	-	-
-	Tag_985	CATGATCTGCGCGCGCTGGCCAGCG	33	1	8.374	0.999	3.59E-03	8.380	no hit	-	-	-	-
-	Tag_203	CATGCACTCGGCTGAGCGCGCGGTGG	326	10	82.729	9.994	4.38E-21	8.278	no hit	-	-	-	-
-	Tag_204	CATGCACTGAGCGGAGCGCGCGGTGG	326	10	82.475	9.994	5.33E-21	8.253	no hit	-	-	-	-
Primary metabolic process/hydrolase activity	Tag_996	CATGTTGTGCGCGGCTGTGCTCGATG	32	1	8.121	0.999	4.39E-03	8.126	Hv_Conlig_16622	824	601-626	AF068320trypsin Heliothis virescens	6.00E-97
-	Tag_1001	CATGCCAGCTAGCTTACCCCCGGG	32	1	8.121	0.999	4.39E-03	8.126	no hit	-	-	-	-
-	Tag_695	CATGCCGCGGCGCGCGCGCGCGCGG	63	2	15.987	1.999	5.10E-06	7.999	no hit	-	-	-	-
-	Tag_170	CATGCCGCGCTCACACACGCTGTGG	405	13	102.776	12.992	2.27E-25	7.911	no hit	-	-	-	-
-	Tag_1008	CATGCCGCGGTGACTCGGAGGCCCT	31	1	7.867	0.999	5.36E-03	7.872	no hit	-	-	-	-
-	Tag_1012	CATGCGCACGCGACGCGGAGGGTGA	31	1	7.867	0.999	5.36E-03	7.872	no hit	-	-	-	-
-	Tag_1014	CATGAGATGTAAACTGGGTGGAG	31	1	7.867	0.999	5.36E-03	7.872	no hit	-	-	-	-
-	Tag_701	CATGTTGTCTCTGGCTGACCCAACG	62	2	15.734	1.999	6.21E-05	7.872	no hit	-	-	-	-
-	Tag_89	CATGACGCGCGCGGTGCGCGCATCTT	859	28	217.987	27.982	1.02E-51	7.790	no hit	-	-	-	-
-	Tag_297	CATGCTGGCGGATCACGCTGCCAGCG	214	7	54.306	6.996	5.69E-14	7.763	no hit	-	-	-	-
-	Tag_710	CATGTTGTCTCTGTTGGCCCAACG	61	2	15.480	1.999	7.56E-05	7.745	no hit	-	-	-	-
-	Tag_712	CATGGCAGAGACGTTTCCACGAGC	61	2	15.480	1.999	7.56E-05	7.745	no hit	-	-	-	-
Unknown	Tag_177	CATGCTGGACGCGCTACGCTCATCGG	391	13	99.224	12.992	3.45E-24	7.637	Hv_Conlig_21487	682	580-605	XP_015035128[uncharacterized protein Dpse_GA32788] Drosophila pseudobscura pseudobscura	2.00E-48
-	Tag_1033	CATGACGCGCGCGGTGCGCGCATCTT	30	1	7.613	0.999	6.54E-03	7.618	no hit	-	-	-	-
-	Tag_1036	CATGCACTCGCGGAGCGACCGGTGA	30	1	7.613	0.999	6.54E-03	7.618	no hit	-	-	-	-
Primary metabolic process/hydrolase activity	Tag_468	CATGCCGCGCGCGGTGCGGCGCGG	119	4	30.198	3.997	2.91E-08	7.554	Hv_Conlig_8166	1270	1201-1226	EHJ1294JAA family ATPase Danaus plexippus	2.00E-178
Unknown	Tag_569	CATGAGAGGTGTAGCTAAGTGGAG	89	3	22.585	2.998	1.76E-06	7.533	Hv_Conlig_25755	595	33-58	XP_002426744[conserved hypothetical protein Pediculus humanus corporis]	3.00E-27
-	Tag_724	CATGGAGTCTCTGTGGTGCACCTA	59	2	14.972	1.999	1.12E-04	7.491	no hit	-	-	-	-
-	Tag_1051	CATGCACTCGCGGAGCGCGCGGTAT	29	1	7.359	0.999	7.97E-03	7.364	no hit	-	-	-	-
-	Tag_1053	CATGCACTCGCGGAGCGCGCGGTAT	29	1	7.359	0.999	7.97E-03	7.364	no hit	-	-	-	-
-	Tag_1055	CATGGGTGGCAATCCTCTCGGACCT	29	1	7.359	0.999	7.97E-03	7.364	no hit	-	-	-	-
-	Tag_733	CATGCTGGCAGTGTAGCTGCTAACG	58	2	14.719	1.999	1.36E-04	7.364	no hit	-	-	-	-
-	Tag_96	CATGCACTCGCGGAGCGCGCGGTAG	808	28	205.045	27.982	1.97E-47	7.328	no hit	-	-	-	-
-	Tag_349	CATGAGAATGCTAAACTGGGTGGGG	173	6	43.902	5.996	2.74E-11	7.322	no hit	-	-	-	-
-	Tag_249	CATGCACTCGCGGAGCGCGCGGTGG	257	9	65.219	8.994	4.85E-16	7.251	no hit	-	-	-	-
-	Tag_484	CATGTTGCCAGGTTGACGCTATCAG	113	4	28.676	3.997	9.31E-08	7.174	no hit	-	-	-	-
-	Tag_485	CATGTTGTGCTCCGCTGGCCCAACG	112	4	28.422	3.997	1.13E-07	7.110	no hit	-	-	-	-
-	Tag_1074	CATGCTGCGCACTGTAGCTGTAAAG	28	1	7.106	0.999	9.71E-03	7.110	no hit	-	-	-	-
-	Tag_1081	CATGCGCGCGGCTCGTGTGGGCA	28	1	7.106	0.999	9.71E-03	7.110	no hit	-	-	-	-
Translation/Ribosome biogenesis	Tag_290	CATGCCAAGCGTGTCTGAAGATTGG	218	8	55.322	7.995	1.53E-13	6.920	Hv_Conlig_18998	729	469-494	AB551457ribosomal protein L23a Heliconius melipomene	2.00E-32
Primary metabolic process/hydrolase activity	Tag_89	CATGTTGTGCTCTGGCTGGAACGGTG	1273	48	323.047	47.969	8.47E-71	6.734	Hv_Conlig_40932	287	33-58	ABW37098[putative chymotrypsin-like proteinase Heliothis virescens]	4.00E-29
-	Tag_765	CATGGCTGCTAGCTTCCGCCGCGGT	53	2	13.450	1.999	3.59E-04	6.729	no hit	-	-	-	-
Translation/Ribosome biogenesis	Tag_766	CATGACATTGGTTCAAGAAGCTTGA	53	2	13.450	1.999	3.59E-04	6.729	Hv_Conlig_33959	449	255-280	KP82256405 ribosomal protein S29 Papilio aulius	5.00E-32
-	Tag_771	CATGGAGTCTCGTGTGGTGCACCTG	53	2	13.450	1.999	3.59E-04	6.729	no hit	-	-	-	-
Unknown	Tag_515	CATGCTGACGAGAGCATCCGTCC	105	4	26.646	3.997	4.33E-07	6.666	Hv_Conlig_2018	2379	1953-1978	XP_013176241[uncharacterized protein LOC106124291] Papilio aulius	0.00E+00
-	Tag_775	CATGCCCGCACCGGGTGCCACCGCA	52	2	13.195	1.999	4.36E-04	6.602	no hit	-	-	-	-
-	Tag_1120	CATGTTGCTGTCAGGTCAGCGCTTACG	26	1	6.598	0.999	1.44E-02	6.602	no hit	-	-	-	-
-	Tag_1139	CATGACAATGTAACTCTTAAATTGC	26	1	6.598	0.999	1.44E-02	6.602	no hit	-	-	-	-
Translation/Ribosome biogenesis	Tag_783	CATGCCGCTGGAATCAAGATATCA	51	2	12.942	1.999	5.28E-04	6.475	Hv_Conlig_36338	380	105-130	EHJ67727605 ribosomal protein L38 Danaus plexippus	2.00E-39
-	Tag_1144	CATGACATTTTGTGTGAGAGGTGG	25	1	6.344	0.999	1.75E-02	6.348	no hit	-	-	-	-
-	Tag_1151	CATGCTGACGCGCGCGCTGAGCGTGG	25	1	6.344	0.999	1.75E-02	6.348	no hit	-	-	-	-
-	Tag_1168	CATGACCTTAACCTACCCGACACGCC	25	1	6.344	0.999	1.75E-02	6.348	no hit	-	-	-	-
Primary metabolic process/hydrolase activity	Tag_403	CATGACAGACTCTGCATGTTGCTTA	149	6	37.812	5.995	2.68E-09	6.306	Hv_Conlig_20720	703	619-644	AAK85539[aminopeptidase N Helicoverpa armigera]	3.00E-23
Primary metabolic process/hydrolase activity	Tag_219	CATGCTGCGCACTGTAGCTGCTAAC	298	12	75.623	11.992	3.21E-17	6.306	Hv_Conlig_11142	1070	940-965	ACL36827trypsin 2 Helicoverpa armigera	7.00E-151
-	Tag_540	CATGACGTGGCACGCGCGCGCGCG	98	4	24.869	3.997	1.63E-06	6.221	no hit	-	-	-	-
-	Tag_793	CATGCTGACGCGCGCGCTGGCGTAA	49	2	12.435	1.999	7.74E-04	6.221	no hit	-	-	-	-
-	Tag_796	CATGTTGTGCTCTGGCTGTTCACAG	49	2	12.435	1.999	7.74E-04	6.221	no hit	-	-	-	-
Transport/Trafficking	Tag_649	CATGGGCTCCGCTCTAGGGCTGCAG	72	3	18.271	2.998	4.60E-05	6.094	Hv_Conlig_10316	1117	736-761	KO871518[Protein transport protein sec13] Orygaster brumata	0.00E+00
-	Tag_850	CATGTGCACTGTAGGATCTGTGTT	72	3	18.271	2.998	4.60E-05	6.094	Hv_Conlig_13805	945	840-865	no hit	-
-	Tag_154	CATGCCGCGTGGTGGCGCGCTCCCA	456	19	115.719	18.988	4.16E-26	6.094	no hit	-	-	-	-
-	Tag_1187	CATGAGGACGCGCGCAGCGCCATGC	24	1	6.090	0.999	2.12E-02	6.094	no hit	-	-	-	-
-	Tag_1188	CATGAGCGCGCTGAGCAACAGCGGT	24	1	6.090	0.999	2.12E-02	6.094	no hit	-	-	-	-
Translation/Ribosome biogenesis	Tag_1195	CATGTCGCGCACCCCGCTCATCT	24	1	6.090	0.999	2.12E-02	6.094	Hv_Conlig_6836	1399	1105-1130	AEB26319seryl-tRNA synthetase Helicoverpa armigera	0.00E+00
-	Tag_1196	CATGGAGACGCGGACGCGCCACGC	24	1	6.090	0.999	2.12E-02	6.094	no hit	-	-	-	-

-	Tag_1198	CATGCTCGCTTAATTAACCAATACC	24	1	6.090	0.999	2.12E-02	6.094	no hit	-	-	-	-
-	Tag_24	CATGCACTCGGCGAGCGCCGGTGA	5396	226	1369.336	225.855	9.96E-278	6.063	no hit	-	-	-	-
-	Tag_811	CATGCAAGCCGGGGGGGCTGCTTG	47	2	11.927	1.999	1.13E-03	5.967	no hit	-	-	-	-
-	Tag_557	CATGCTGTCTCTGGCTGGCCCAACG	93	4	23.600	3.997	4.17E-06	5.904	no hit	-	-	-	-
-	Tag_186	CATGGCTGAGGACGCCGCCACC	370	16	93.894	15.990	2.95E-20	5.872	no hit	-	-	-	-
Primary metabolic process/transferase activity	Tag_37	CATGTCTCGCGCACGCTGGCGCCCC	3131	136	794.550	135.913	1.28E-158	5.846	Hv_Contig_24145	622	380-405	AMK97473 UCT40D2v2 <i>Helicoverpa armigera</i>	2.00E-110
-	Tag_1204	CATGACGGGGGACGGGTCTCCGCT	23	1	5.837	0.999	2.57E-02	5.840	no hit	-	-	-	-
-	Tag_1207	CATGGACGCCGCTGCTCAGCG	23	1	5.837	0.999	2.57E-02	5.840	no hit	-	-	-	-
-	Tag_1212	CATGTGGCGGTACTCGGTGGCCG	23	1	5.837	0.999	2.57E-02	5.840	no hit	-	-	-	-
-	Tag_1214	CATGCGCACACACGAGAAGGTGA	23	1	5.837	0.999	2.57E-02	5.840	no hit	-	-	-	-
Primary metabolic process/oxidoreductase activity	Tag_1218	CATGCAGCTAACGACAGTCCGAC	23	1	5.837	0.999	2.57E-02	5.840	Hv_Contig_21281	688	418-441	XP_013192952 inactive hydroxysteroid dehydrogenase-like protein 1 isoform X2 <i>Amyelotus transiella</i>	2.00E-76
-	Tag_1230	CATGACGGGCTCCCGTGGCGCGC	23	1	5.837	0.999	2.57E-02	5.840	no hit	-	-	-	-
-	Tag_1231	CATGACGCGCGGACGCGCGGTGG	23	1	5.837	0.999	2.57E-02	5.840	no hit	-	-	-	-
-	Tag_1235	CATGCGCGGTGACCCGGTGCCCC	23	1	5.837	0.999	2.57E-02	5.840	no hit	-	-	-	-
-	Tag_306	CATGGCGCGCAAMAGAAGCAATGG	162	8	46.195	7.995	1.33E-10	5.777	no hit	-	-	-	-
-	Tag_674	CATGCGCACGGACGAGAGGGTAT	67	3	17.002	2.998	1.17E-04	5.671	no hit	-	-	-	-
Translation/Ribosome biogenesis	Tag_386	CATCGCGCTGGAGATGCCGATCTC	156	7	39.588	6.996	3.48E-09	5.659	Hv_Contig_27404	571	425-450	XP_013195182 translation machinery-associated protein 16 homolog <i>Amyelotus transiella</i>	53-88
-	Tag_570	CATGTCTGGGGGAGAGCTGGAGT	89	4	22.585	3.997	8.78E-06	5.650	no hit	-	-	-	-
Protein folding/Recycling	Tag_1248	CATGATTGCCCTGCCGCCGCCGCC	22	1	5.583	0.999	3.11E-02	5.586	Hv_Contig_3821	1220	697-722	XP_011564371 ubiquitin-conjugating enzyme E2-34 kDa isoform X1 <i>Plutella xylostella</i>	3.00E-105
-	Tag_1249	CATGACGAGCTCGGTGCCGACG	22	1	5.583	0.999	3.11E-02	5.586	no hit	-	-	-	-
mRNA processing/splicing	Tag_1251	CATGAGTTCTGGTGACTCTCGGTGT	22	1	5.583	0.999	3.11E-02	5.586	Hv_Contig_16399	832	120-145	XP_013185327 RNA-binding protein Rsf1 <i>Amyelotus transiella</i>	8.00E-41
-	Tag_1253	CATGAGACACTTGAACGCTGAC	22	1	5.583	0.999	3.11E-02	5.586	no hit	-	-	-	-
Nucleic acid binding	Tag_1259	CATGTCTCAGCTCTGTGCCGTGCA	22	1	5.583	0.999	3.11E-02	5.586	Hv_Contig_12568	993	364-339	XP_004928597 Zyxin <i>Bombyx mori</i>	3.00E-64
-	Tag_1265	CATGCTGTCTCTGGTGGCCACGG	22	1	5.583	0.999	3.11E-02	5.586	no hit	-	-	-	-
-	Tag_56	CATGCGACCTAGCTCGCCCCGGA	1745	81	442.826	80.948	9.53E-86	5.471	no hit	-	-	-	-
-	Tag_499	CATGCTGTGGATCATCGGCCGCTAGC	107	5	27.153	4.997	1.41E-06	5.434	no hit	-	-	-	-
-	Tag_353	CATGTACTCGGCGAGGCGCGGTGG	171	8	43.994	7.995	1.00E-09	5.428	no hit	-	-	-	-
-	Tag_589	CATGCTGCTGGTGGTGCCCTCCCA	85	4	21.570	3.997	1.83E-05	5.396	no hit	-	-	-	-
-	Tag_1278	CATGACGAGGAGGGCTCGGCTGA	21	1	5.329	0.999	3.76E-02	5.333	no hit	-	-	-	-
Translation/Ribosome biogenesis	Tag_1282	CATGTGATCTGGCGACCTGCCTC	21	1	5.329	0.999	3.76E-02	5.333	Hv_Contig_12933	975	747-772	ABX5585 ribosomal protein L7A <i>Spodoptera exigua</i>	1.00E-136
-	Tag_1283	CATGCTGACGCGCGCTGGCATGG	21	1	5.329	0.999	3.76E-02	5.333	no hit	-	-	-	-
-	Tag_1293	CATGCGCGCGGTGGGCCCGGCTA	21	1	5.329	0.999	3.76E-02	5.333	no hit	-	-	-	-
-	Tag_1301	CATGAGGACGCTGCAGGCCACGC	21	1	5.329	0.999	3.76E-02	5.333	no hit	-	-	-	-
-	Tag_849	CATGCGCGGTAACTCGGTGGCCCT	42	2	10.658	1.999	2.88E-03	5.333	no hit	-	-	-	-
Unknown	Tag_273	CATGCTCCGTTAATTAACCAATATC	231	11	58.621	10.980	1.58E-12	5.333	Hv_Contig_5986	1496	448-423	no hit	-
Nucleic acid binding	Tag_118	CATGCGCGCGGCTCGCTGTGGCC	621	30	157.590	29.981	7.36E-31	5.256	Hv_Contig_3143	2001	1530-1555	EH74904 putative DNA repair protein xpc- <i>Danaus plexippus</i>	0.00E+00
-	Tag_899	CATGTTGTGCTCTGGCTGGCCAGCC	62	3	15.734	2.998	2.96E-04	5.248	no hit	-	-	-	-
-	Tag_904	CATGTGTGGTGGCATCGATGAGCT	82	4	20.809	3.997	3.17E-05	5.206	no hit	-	-	-	-
Translation/Ribosome biogenesis	Tag_216	CATGCCTCGTGGTGGCTGCCCTCCG	305	15	77.399	14.990	8.97E-16	5.163	Hv_Contig_27713	566	277-252	AAL62467 60S acidic ribosomal protein P2 <i>Spodoptera frugiperda</i>	5.00E-27
-	Tag_528	CATGTTGTGCCCTGGCTGGCCCAACG	101	5	25.631	4.997	4.19E-06	5.129	no hit	-	-	-	-
Primary metabolic process/hydrolase activity	Tag_166	CATGTTGTGCGCTGATCTTAGACG	420	21	106.583	20.987	6.19E-21	5.079	Hv_Contig_13773	938	634-659	AF068325 trypsin <i>Heliothis virescens</i>	2.00E-180
-	Tag_1311	CATGCTGCTGGGATGGCTACCTCTA	20	1	5.075	0.999	4.54E-02	5.079	no hit	-	-	-	-
-	Tag_1319	CATGGACGAGCCCCGGTGGCCGCG	20	1	5.075	0.999	4.54E-02	5.079	no hit	-	-	-	-
-	Tag_1321	CATGCGAAGGCTAAAGGTAAAGGT	20	1	5.075	0.999	4.54E-02	5.079	no hit	-	-	-	-
-	Tag_1325	CATGGCGGCCCAAMAGAAGCAATGA	20	1	5.075	0.999	4.54E-02	5.079	no hit	-	-	-	-
-	Tag_1326	CATGCGCGCGGTGGCCCGGCGCTC	20	1	5.075	0.999	4.54E-02	5.079	no hit	-	-	-	-
-	Tag_1329	CATGCGCACGGCACGAGAAGGTCT	20	1	5.075	0.999	4.54E-02	5.079	no hit	-	-	-	-
-	Tag_1332	CATGCGCGGCTGACTCCGGTGACCG	20	1	5.075	0.999	4.54E-02	5.079	no hit	-	-	-	-
-	Tag_1334	CATGGACGCCAGCTTGCCCCGGT	20	1	5.075	0.999	4.54E-02	5.079	no hit	-	-	-	-
-	Tag_1338	CATGAGCCCCCTCTGCCGACACGA	20	1	5.075	0.999	4.54E-02	5.079	no hit	-	-	-	-
-	Tag_1343	CATGCTGCAGCAGCTCACGCGCACAC	20	1	5.075	0.999	4.54E-02	5.079	no hit	-	-	-	-
-	Tag_1349	CATGGACGCTAGCTTGCCCCGCT	20	1	5.075	0.999	4.54E-02	5.079	no hit	-	-	-	-
-	Tag_612	CATGCGCTGGCGGACGGCTGGGCC	80	4	20.301	3.997	4.56E-05	5.079	no hit	-	-	-	-
-	Tag_617	CATGGGTGGGCAATCTCTTGACTA	80	4	20.301	3.997	4.56E-05	5.079	no hit	-	-	-	-
-	Tag_319	CATGCCCGCTGGTGGCGGCTGCC	199	10	50.500	9.994	1.17E-10	5.053	no hit	-	-	-	-
-	Tag_471	CATGGGCTGGACATCCGCCGCCCG	118	6	29.945	5.996	8.08E-07	4.994	no hit	-	-	-	-
-	Tag_629	CATGCGCGGATGACTCCGGTGCCCT	78	4	19.794	3.997	6.54E-05	4.952	no hit	-	-	-	-
-	Tag_877	CATGCTCGTTAATTAACCAATACG	39	2	9.897	1.999	5.01E-03	4.952	no hit	-	-	-	-
-	Tag_272	CATGCACTGGCCGGGCGCCGGTGG	231	12	58.621	11.992	6.65E-12	4.888	no hit	-	-	-	-
-	Tag_280	CATGAGCGGTGCAAGAGBACCGCA	229	12	58.113	11.992	9.47E-12	4.846	no hit	-	-	-	-
-	Tag_885	CATGCTGCACTGCGCGTGGCGGTGG	38	2	9.643	1.999	6.01E-03	4.825	no hit	-	-	-	-
-	Tag_896	CATGCTCGTGAAGCCCGCTTGCC	38	2	9.643	1.999	6.01E-03	4.825	no hit	-	-	-	-
-	Tag_997	CATGTTGTGCTCTGGCTGGAACGTC	38	2	9.643	1.999	6.01E-03	4.825	no hit	-	-	-	-
Translation/Ribosome biogenesis	Tag_57	CATGGGCTGAGGACGCCGCCACCA	1676	89	425.316	88.943	2.26E-75	4.782	Hv_Contig_11605	1043	833-858	XP_014367750 40S ribosomal protein SA <i>Papilio machaon</i>	3.00E-162
-	Tag_489	CATGTGCTGCTCTGGCTGGCCCAACG	111	6	28.168	5.996	2.80E-06	4.698	no hit	-	-	-	-
-	Tag_906	CATGTTGCCCTCTGGCTGGCCGACG	37	2	9.389	1.999	7.20E-03	4.698	no hit	-	-	-	-
-	Tag_563	CATGGACGCTAGCTTGCCCCGACG	92	5	23.347	4.997	2.10E-05	4.672	no hit	-	-	-	-

-	Tag_316	CATGTCCTGGCAGCGTGCGCCCT	202	11	51.261	10.993	2.77E-10	4.663	no hit	-	-	-	-
-	Tag_743	CATGCCCGCTGGTGGCGCGCTCCGG	55	3	13.957	2.998	1.05E-03	4.655	no hit	-	-	-	-
-	Tag_292	CATGCACTAGCCGAGCGCCGGTGG	217	12	55.068	11.992	7.76E-11	4.592	no hit	-	-	-	-
Translation/Ribosome biogenesis	Tag_758	CATGCTGTTGAGCAGCACAGTGTGA	54	3	13.704	2.998	1.25E-03	4.571	Hv_Contig_4980	1646	1477-1502	XP_013192117 eukaryotic initiation factor 4A-8 <i>Ameyelos transfella</i>	0.00E+00
-	Tag_763	CATGGCACGAACTTTGGGTGCGG	54	3	13.704	2.998	1.25E-03	4.571	no hit	-	-	-	-
-	Tag_824	CATGGCAGCTAGCATCGCCCGCGT	36	2	9.136	1.999	8.63E-03	4.571	no hit	-	-	-	-
Chitin-binding	Tag_92	CATGGGTGCGCAATCCTCTGGACTT	827	46	208.867	45.970	7.54E-37	4.565	Hv_Contig_35958	389	349-374	A0B43611 chitin deacetylase 5a <i>Helicoverpa armigera</i>	1.00E-67
-	Tag_769	CATGGCACGAACTTTGGGTGCGC	53	3	13.450	2.998	1.50E-03	4.486	no hit	-	-	-	-
Unknown	Tag_574	CATGTTATCGCAGGACGTGCGACGC	88	5	22.332	4.997	4.23E-05	4.469	Hv_Contig_5830	1398	1231-1256	XP_011565303 transmembrane emp24 domain-containing protein 2 <i>Plutella xylostella</i>	5.00E-121
-	Tag_580	CATGCGGAAGTACTACAGGCTCTGG	88	5	22.332	4.997	4.23E-05	4.469	no hit	-	-	-	-
Unknown	Tag_511	CATGTTCTCCCTCGCTAGAGGCCCG	105	6	26.646	5.996	8.01E-06	4.444	Hv_Contig_36632	373	285-290	XP_002425519 conserved hypothetical protein <i>Pedicularis humanus</i>	1.00E-20
-	Tag_945	CATGCTCTCGCTCGAGGTGCTCG	35	2	8.882	1.999	1.03E-02	4.444	no hit	-	-	-	-
-	Tag_948	CATGACTCCGCGAGGCGGAGGGCG	35	2	8.882	1.999	1.03E-02	4.444	no hit	-	-	-	-
-	Tag_517	CATGTGTGCTCTGCTGGACGCGTA	104	6	26.392	5.996	9.52E-06	4.401	no hit	-	-	-	-
Nucleic acid binding	Tag_95	CATGCCGCTGGCGGACGGCTCGGCT	813	47	206.314	46.970	3.13E-35	4.392	Hv_Contig_9535	1240	1158-1183	XP_011565761 replication factor C subunit 2-like <i>Plutella xylostella</i>	0.00E+00
-	Tag_661	CATGCCGAGCGCGCGCTGGGGTGG	69	4	17.510	3.997	3.23E-04	4.380	no hit	-	-	-	-
Primary metabolic process/hydrolase activity	Tag_106	CATGGGCTGGACATCCGCCGCCCA	735	43	186.520	42.972	1.00E-31	4.340	Hv_Contig_5369	1587	1236-1261	KP101021 lysosomal aspartic protease <i>Papilio machaon</i>	0.00E+00
-	Tag_312	CATGCCCGCTGGTGGCGCGCTCCAG	205	12	52.023	11.992	6.18E-10	4.338	no hit	-	-	-	-
-	Tag_103	CATGTGCAAGCGCGCTGGCGGTGC	750	44	190.326	43.972	2.87E-32	4.328	no hit	-	-	-	-
-	Tag_953	CATGAATTGATCCGTGCGGACCCACC	34	2	8.628	1.999	1.23E-02	4.317	no hit	-	-	-	-
-	Tag_955	CATGGACAAGTACCACCTGGCTACG	34	2	8.628	1.999	1.23E-02	4.317	no hit	-	-	-	-
-	Tag_962	CATGATCGGTGCGGTTGTCTCAGG	34	2	8.628	1.999	1.23E-02	4.317	no hit	-	-	-	-
-	Tag_242	CATGGGTATCTCGGCCACGCGCTG	269	16	68.264	15.990	1.89E-12	4.269	no hit	-	-	-	-
-	Tag_362	CATGCTCTGGCAGCGTGCGGCCCA	168	10	42.633	9.994	2.66E-08	4.266	no hit	-	-	-	-
-	Tag_677	CATGCTCGTGGGGAAGAGCTGGAGA	67	4	17.002	3.997	4.57E-04	4.253	no hit	-	-	-	-
-	Tag_317	CATGACGCGCGCGTGC GCGCATCTG	201	12	51.007	11.992	1.22E-09	4.253	no hit	-	-	-	-
Signal transduction	Tag_49	CATGTGAGCTCGCGGAGCGGAGGC	2040	123	517.688	122.921	7.08E-83	4.212	Hv_Contig_50	6564	5427-6452	XP_004926833 plexin A3 <i>Bombyx mori</i>	0.00E+00
-	Tag_406	CATGTGCGGTGACTCGTGGGCCCT	149	9	37.812	8.994	1.91E-07	4.204	no hit	-	-	-	-
-	Tag_972	CATGCTGCAAGCGCACTGGCGTGG	33	2	8.374	1.999	1.47E-02	4.190	no hit	-	-	-	-
Primary metabolic process/hydrolase activity	Tag_84	CATGTTGTGCTTGCTGGCCCAATG	938	57	238.035	56.963	7.75E-39	4.179	Hv_Contig_13904	932	626-651	ABR88248 trypsin T5 <i>Heliothis virescens</i>	3.00E-145
Primary metabolic process/hydrolase activity	Tag_5	CATGTTGTCTCTGGCTGGCCCAAG	29930	1821	7595.296	1819.832	0.00E+00	4.174	Hv_Contig_46294	214	44-69	CAA72957 trypsin-like protease <i>Helicoverpa armigera</i>	1.00E-16
-	Tag_481	CATGTGTCCTCAAGCGCCGGTACTCT	113	7	28.676	6.996	7.17E-06	4.099	no hit	-	-	-	-
-	Tag_483	CATGTTGTCTCTGGCGGCCCAAG	113	7	28.676	6.996	7.17E-06	4.099	no hit	-	-	-	-
-	Tag_991	CATGCTGCAAGCGCGCTGGCGTGG	32	2	8.121	1.999	1.75E-02	4.063	no hit	-	-	-	-
Primary metabolic process/hydrolase activity	Tag_77	CATGGGTGTGCAACTCCGCGTGTCT	1116	70	283.206	69.955	1.08E-44	4.048	Hv_Contig_10548	1075	114-138	ABR88240 serine protease SP1 <i>Heliothis virescens</i>	5.00E-136
-	Tag_621	CATGAGGAGCGCGCAGCGCCACAC	79	5	20.048	4.997	1.99E-04	4.012	no hit	-	-	-	-
-	Tag_822	CATGCTGCAAGCGCGCTGGCGCGG	79	5	20.048	4.997	1.99E-04	4.012	no hit	-	-	-	-
-	Tag_813	CATGTTGTCTCTGGCTGGCTCAAG	47	3	11.927	2.998	4.25E-03	3.978	no hit	-	-	-	-
Protein folding/Recycling	Tag_7	CATGCTGACGCGCGCTGGCGGTGG	18875	1219	4789.883	1218.218	0.00E+00	3.932	Hv_Contig_1372	2724	2406-2431	ADK55517.2 heat shock protein 90 cognate <i>Spodoptera litura</i>	0.00E+00
-	Tag_497	CATGCCCGCGCGTATCCCGCGCGG	108	7	27.407	6.996	1.68E-05	3.918	no hit	-	-	-	-
Primary metabolic process/hydrolase activity	Tag_294	CATGTTGTCTCTCGGTGTGCTCATG	215	14	54.560	13.991	1.37E-09	3.900	Hv_Contig_46774	209	53-78	AF068320 trypsin <i>Heliothis virescens</i>	2.00E-32
-	Tag_825	CATGTTGTACTCTGCTGGCCCAAG	46	3	11.673	2.998	5.05E-03	3.894	no hit	-	-	-	-
Nucleic acid binding	Tag_704	CATGTGCTGGCGTGCCCGCCCGAGT	61	4	15.480	3.997	1.27E-03	3.872	Hv_Contig_46599	210	124-149	XP_012548675 PR domain zinc finger protein 10-like isoform X4 <i>Bombyx mori</i>	4.00E-24
Primary metabolic process/hydrolase activity	Tag_15	CATGTTGTCTCTGGCTGGCCCAAG	9867	649	2503.935	648.584	0.00E+00	3.861	Hv_Contig_20694	704	6_31	ABW37093 putative trypsin-like proteinase <i>Heliothis virescens</i>	3.00E-31
-	Tag_400	CATGCGGTGGTGAATCGGTGCCCT	151	10	38.319	9.994	4.61E-07	3.834	no hit	-	-	-	-
-	Tag_514	CATGCACTCGGTGAGCGCGCGGTGA	105	7	26.646	6.996	2.74E-05	3.809	no hit	-	-	-	-
-	Tag_1016	CATGTAGCTAGCTTCGCCCCGGG	30	2	7.613	1.999	2.48E-02	3.809	no hit	-	-	-	-
-	Tag_1019	CATGAAGATGTGCTTGATGGAGG	30	2	7.613	1.999	2.48E-02	3.809	no hit	-	-	-	-
-	Tag_1021	CATGGGGAGCGCGCAGCCCAAGC	30	2	7.613	1.999	2.48E-02	3.809	no hit	-	-	-	-
-	Tag_1024	CATGACCCCAAGTCTCTGAGAAC	30	2	7.613	1.999	2.48E-02	3.809	no hit	-	-	-	-
-	Tag_193	CATGCGCGGTGGCTCCGGTGCCCT	344	23	87.296	22.985	3.72E-14	3.798	no hit	-	-	-	-
-	Tag_370	CATGCACTCGCGGAGCGGCCGTGCG	164	11	41.618	10.993	1.75E-07	3.786	no hit	-	-	-	-
-	Tag_723	CATGTGCGTGACGCGCTGTGTGC	59	4	14.972	3.997	1.78E-03	3.745	no hit	-	-	-	-
-	Tag_725	CATGCACTCGCGGAGCGGCCGGTAA	59	4	14.972	3.997	1.78E-03	3.745	no hit	-	-	-	-
-	Tag_469	CATGGGCTAACGACCGTGTGTGA	118	8	29.945	7.995	1.02E-05	3.745	no hit	-	-	-	-
Primary metabolic process/hydrolase activity	Tag_146	CATGTTGCTCAGGGTCAAGCGCTACC	494	34	125.362	33.978	3.67E-19	3.689	Hv_Contig_12402	1001	837-862	ABR88231 chymotrypsin-like protease C1 <i>Heliothis virescens</i>	0.00E+00
-	Tag_247	CATGCGCGGTGACTCCGCGGCCCT	261	18	66.234	17.988	7.97E-11	3.682	no hit	-	-	-	-
-	Tag_1037	CATGTGTGCTCTGGCTGGCCCAATC	29	2	7.359	1.999	2.95E-02	3.682	no hit	-	-	-	-
-	Tag_1041	CATGATCTGTCCGGTGGTCCGCGG	29	2	7.359	1.999	2.95E-02	3.682	no hit	-	-	-	-
Cytoskeleton	Tag_1047	CATGACTGCTGCAATAGAGGTCTTC	29	2	7.359	1.999	2.95E-02	3.682	Hv_Contig_3757	1868	149-124	KP163269 Myosin-Vb <i>Papilio machaon</i>	0.00E+00
-	Tag_1057	CATGAATCAATGCTGAAGTAGCGC	29	2	7.359	1.999	2.95E-02	3.682	no hit	-	-	-	-
-	Tag_1059	CATGCTCTCGGCTCCAGGCTGTGCG	29	2	7.359	1.999	2.95E-02	3.682	no hit	-	-	-	-
-	Tag_437	CATGCGGCAAGTACTCCGGTGCCCT	130	9	32.990	8.994	4.52E-06	3.668	no hit	-	-	-	-
Protein folding/Recycling	Tag_238	CATGACGACGAGGAGGCTCGGCTGG	272	19	69.025	18.988	4.23E-11	3.635	Hv_Contig_1727	2507	381-356	XP_012553124 protein sel-1 homolog 1 isoform X2 <i>Bombyx mori</i>	0.00E+00
Cytoskeleton	Tag_52	CATGACTCCCGCAGGCGAGGGTG	1996	140	506.522	139.910	6.48E-71	3.620	Hv_Contig_29832	530	407-432	XP_008294349 ubulin alpha chain-like <i>Stigeoceras parvius</i>	1.00E-34
-	Tag_262	CATGGTGGGCAATCTCTCGGACTA	239	17	66.651	16.989	8.80E-10	3.570	no hit	-	-	-	-
-	Tag_736	CATGCACTCGGCTAGCGCCGGTGG	56	4	14.211	3.997	2.93E-03	3.555	no hit	-	-	-	-

-		Tag_1063	CATGCTGCAGCGCGCTGGGTGTGG	28	2	7.106	1.999	3.49E-02	3.555	no hit	-	-	-	-
Cytoskeleton		Tag_1064	CATGTGCAGCCTTTGGGCACAGAT	28	2	7.106	1.999	3.49E-02	3.555	Hv_Conlig_153	5015	3805-3778	XP_012547232 pericentriolar material 1 protein isoform X5 Bombyx mori	0.00E+00
-		Tag_1067	CATGCTGCTGGTGGTCCGCTCCAG	28	2	7.106	1.999	3.49E-02	3.555	no hit	-	-	-	-
-		Tag_1069	CATGCGGTGTGACTCCGGTGGCCCG	28	2	7.106	1.999	3.49E-02	3.555	no hit	-	-	-	-
-		Tag_1077	CATGGCGCGCTACACACCGCTGTGA	28	2	7.106	1.999	3.49E-02	3.555	no hit	-	-	-	-
-		Tag_1662	CATGAGGCTGCAGCTCATCTTCTCCT	69	5	17.510	4.997	1.05E-03	3.504	no hit	-	-	-	-
-		Tag_1666	CATGCGCTGGACCCGCTCCGCCGA	69	5	17.510	4.997	1.05E-03	3.504	no hit	-	-	-	-
-		Tag_1860	CATGAAGCGGTTCCCCAGGGCGAG	41	3	10.405	2.998	1.17E-02	3.470	no hit	-	-	-	-
mRNA processing splicing		Tag_10	CATGGAGACGCCGACGCCCCACGC	12548	922	3184.289	921.409	0.00E+00	3.456	Hv_Conlig_22	7324	7183-7208	XP_013154675 pre-mRNA-processing-splicing factor 8 Amyelotus transilella	0.00E+00
-		Tag_313	CATGCCTCTCGTCTCAGGGTGCCTGT	203	15	51.515	14.990	2.94E-08	3.437	no hit	-	-	-	-
Unknown		Tag_754	CATGGGGAGGAAGATACGCCCCCG	54	4	13.704	3.997	4.06E-03	3.428	Hv_Conlig_30533	516	416-441	EHJ72631 hypothetical protein KGM_18901 Danaus plexippus	2.00E-24
Primary metabolic process hydrolase activity		Tag_759	CATGCACGCCAGCTGGATCTTAGTCT	54	4	13.704	3.997	4.06E-03	3.428	Hv_Conlig_31422	496	121-146	AFM28262 chymotrypsin, partial Heliothis virescens	1.00E-102
-		Tag_1084	CATGCACCTCGCCGAGCGCGCGGAGG	27	2	6.852	1.999	4.13E-02	3.428	no hit	-	-	-	-
-		Tag_1087	CATGATCTGTGGGAGTGGCGCGG	27	2	6.852	1.999	4.13E-02	3.428	no hit	-	-	-	-
-		Tag_1094	CATGTCTGTGCTGGCTGCCCAAGG	27	2	6.852	1.999	4.13E-02	3.428	no hit	-	-	-	-
-		Tag_1099	CATGTGTGTGCTCAGGCTGCCCAAG	27	2	6.852	1.999	4.13E-02	3.428	no hit	-	-	-	-
-		Tag_1101	CATGCGCGGTGACTCCGGTGGTCCG	27	2	6.852	1.999	4.13E-02	3.428	no hit	-	-	-	-
-		Tag_1556	CATGCCGCTATTCTCATCAGCAAG	94	7	23.854	6.996	1.63E-04	3.410	no hit	-	-	-	-
Translation Ribosome biogenesis		Tag_170	CATGACGCCGAGCTGGCGGAGGACC	67	5	17.002	4.997	1.45E-03	3.403	Hv_Conlig_1119	2911	1269-1294	XP_013164109 agile X mental retardation syndrome-related protein 1 isoform X1 Papilio xuthus	0.00E+00
-		Tag_1676	CATGCTGCTTCCAGACGCCGCTGG	67	5	17.002	4.997	1.45E-03	3.403	no hit	-	-	-	-
Translation Ribosome biogenesis		Tag_244	CATGACCCCAAGTCTTGAGAACCC	267	20	67.756	19.987	2.80E-10	3.390	Hv_Conlig_13599	945	763-788	NP_001037518 ribosomal protein L29 Bombyx mori	5.00E-18
-		Tag_360	CATGGCTGGCAATCTCTTGACTGT	173	13	43.902	12.992	3.83E-07	3.379	no hit	-	-	-	-
-		Tag_559	CATGCGCGGTGACTCCGGTGGCTCT	93	7	23.600	6.996	1.92E-04	3.374	no hit	-	-	-	-
Protein folding Recycling		Tag_30	CATGGCAGCCCGCTGGTGGCGGAGG	4404	333	1117.597	332.786	1.19E-142	3.358	Hv_Conlig_33321	456	222-247	XP_004933282 proteasome subunit beta type-4 Bombyx mori	1.00E-41
-		Tag_135	CATGGGTGGCAATCTCTCGGACTG	528	40	133.990	39.974	1.27E-18	3.352	no hit	-	-	-	-
-		Tag_1624	CATGTGTGCTCTGGCTGGCCCAACT	79	6	20.048	5.996	6.14E-04	3.343	no hit	-	-	-	-
-		Tag_1119	CATGCGCGCGCACGAGAGGGTGA	26	2	6.598	1.999	4.88E-02	3.301	no hit	-	-	-	-
-		Tag_1124	CATGAGTGTTCGCGTTAACGGTCC	26	2	6.598	1.999	4.88E-02	3.301	no hit	-	-	-	-
-		Tag_1127	CATGCTGCAGCGGTCTCGGGCGTGG	26	2	6.598	1.999	4.88E-02	3.301	no hit	-	-	-	-
Primary metabolic process hydrolase activity		Tag_17	CATGATCTGTCGGTGTGGTCAGCG	9184	714	2330.611	713.542	2.75E-286	3.266	Hv_Conlig_14824	894	647-672	CAA72955 trypsin-like protease Helicoverpa armigera	1.00E-130
-		Tag_778	CATCGCGCTGCGCGCGACCTCTAG	51	4	12.942	3.997	6.58E-03	3.238	no hit	-	-	-	-
-		Tag_1689	CATGCTCGCGCGCGCTGGCGCTGG	63	5	15.987	4.997	2.73E-03	3.200	no hit	-	-	-	-
-		Tag_202	CATGGGTGGCGCGGTGCTTCAACC	327	26	82.982	25.983	1.42E-11	3.194	no hit	-	-	-	-
-		Tag_787	CATGTCACGCGCTCGACCGCTACA	50	4	12.688	3.997	7.71E-03	3.174	no hit	-	-	-	-
-		Tag_425	CATGATCTGTGCGGTTGGTCCAGCC	137	11	34.766	10.993	1.27E-06	3.163	no hit	-	-	-	-
Unknown		Tag_899	CATGCCTGCTGCTGCTTCAGACCCAC	37	3	9.389	2.998	2.23E-02	3.132	Hv_Conlig_1330	2751	2429-2454	KP188384 hypothetical protein RR46_09500 Papilio xuthus	2.00E-169
-		Tag_905	CATGACCTGTCGGCGTGGCCAGCG	37	3	9.389	2.998	2.23E-02	3.132	no hit	-	-	-	-
-		Tag_908	CATGTGAGCTCGCGCGCGAGAGGT	37	3	9.389	2.998	2.23E-02	3.132	no hit	-	-	-	-
-		Tag_1644	CATGGGAGGTTCTGCTCAGGACTGT	74	6	18.779	5.996	1.34E-03	3.132	no hit	-	-	-	-
-		Tag_41	CATGCAGCGCGCGCGGCGACGCGC	2702	220	685.683	219.859	2.52E-81	3.119	no hit	-	-	-	-
-		Tag_271	CATGCGCGGCGGACTCCGGTGCGDCT	233	19	59.128	18.988	1.82E-08	3.114	no hit	-	-	-	-
-		Tag_19	CATGCGCGGTGACTCCGGTGGCCCC	8505	700	2158.302	699.551	2.41E-248	3.085	no hit	-	-	-	-
mRNA processing splicing		Tag_588	CATGCTGGATGCTACCTCGGGGCTG	85	7	21.570	6.996	6.66E-04	3.083	Hv_Conlig_20288	715	464-489	KP302294 Putative U5 small nuclear ribonucleoprotein 200 kDa helicase Papilio xuthus	6.00E-108
-		Tag_257	CATGGGTGTGACTCGCTCGGCTGG	242	20	61.412	19.987	1.27E-08	3.073	no hit	-	-	-	-
Translation Ribosome biogenesis		Tag_150	CATGGAGTTGGCGGTTAACGGTCTG	481	40	122.063	39.974	1.54E-15	3.054	Hv_Conlig_22213	663	209-234	Q95V13 40S ribosomal protein S16 Spodoptera frugiperda	3.00E-95
-		Tag_714	CATGCTCCGCTAATCTACCAACTCT	60	5	15.226	4.997	4.38E-03	3.047	no hit	-	-	-	-
Translation Ribosome biogenesis		Tag_1803	CATGAAGTGGTTCACAGAAATACG	48	4	12.181	3.997	1.05E-02	3.047	Hv_Conlig_5248	1605	732-757	NP_001298894 60S ribosomal protein L11 Papilio xuthus	4.00E-119
Translation Ribosome biogenesis		Tag_124	CATGATCGCACACCGCGCGCGTGG	571	48	144.902	47.989	6.28E-18	3.021	Hv_Conlig_10163	1127	940-965	XP_013152781 probable tRNA N6-adenosine (tricyclo)carboxyltransferase Amyelotus transilella	0.00E+00
-		Tag_166	CATGGAGTTGGCGGTTAACGGTCA	71	6	18.018	5.996	2.13E-03	3.005	no hit	-	-	-	-
-		Tag_507	CATGCGCGGCTGACTCCAGTGCCCT	106	9	26.899	8.994	1.94E-04	2.991	no hit	-	-	-	-
-		Tag_1816	CATGGCTCGGCAATCTCTCGGACGT	47	4	11.927	3.997	1.23E-02	2.984	no hit	-	-	-	-
Nucleic acid binding		Tag_1602	CATGGTTCCAAACGCTCGCGGAAG	82	7	20.809	6.996	1.05E-03	2.975	Hv_Conlig_13411	953	712-737	XP_013186282 homodimer protein Hox A7-like Amyelotus transilella	1.00E-88
-		Tag_44	CATGGGTGGCAATCTCTCGGACTT	2325	200	590.012	199.872	9.06E-66	2.952	no hit	-	-	-	-
-		Tag_1824	CATGTTGTGCTCTGACTGGCCDAAG	46	4	11.673	3.997	1.44E-02	2.920	no hit	-	-	-	-
-		Tag_1827	CATGCTCGCGACGCTGGCGCCCCG	46	4	11.673	3.997	1.44E-02	2.920	no hit	-	-	-	-
-		Tag_447	CATGCTCGAGTCGTAAGTCTTAACA	126	11	31.975	10.993	6.60E-05	2.909	no hit	-	-	-	-
Primary metabolic process oxidoreductase activity		Tag_199	CATGGCAACGCAAACTTTGGATGCGT	332	29	84.251	26.981	1.34E-10	2.907	Hv_Conlig_1262	1263	1171-1196	XP_013200704 retinol dehydrogenase 11-like Amyelotus transilella	6.00E-121
-		Tag_1616	CATGCGAAGTACTACAGGCTGTGT	80	7	20.301	6.996	1.42E-03	2.902	no hit	-	-	-	-
Primary metabolic process hydrolase activity		Tag_4	CATGCGCGGTGACTCCGGTGGCCCT	79387	6961	20145.932	6956.535	0.00E+00	2.896	Hv_Conlig_14443	909	655-680	AFM28249 chymotrypsin Heliothis virescens	7.00E-150
-		Tag_966	CATGCTGCTGGTGGTGGCGCTCCCC	34	3	8.628	2.998	3.58E-02	2.878	no hit	-	-	-	-
-		Tag_227	CATGTGTGTGCTGCTGGCGCCAAAC	292	26	74.100	25.983	2.47E-09	2.852	no hit	-	-	-	-
-		Tag_491	CATGCGCGGTGACTCCGGTACCCCT	110	10	27.915	9.994	2.72E-04	2.793	no hit	-	-	-	-
-		Tag_1680	CATGCGCGGTGTCTCCGTTGGCCCT	66	6	16.749	5.996	4.50E-03	2.793	no hit	-	-	-	-
-		Tag_1631	CATGCAAGTGTGACTCCGGTGGCCCT	77	7	19.540	6.996	2.21E-03	2.793	no hit	-	-	-	-
mRNA processing splicing		Tag_577	CATGCGGCTGCCACTCTCCCGGGG	88	8	22.332	7.995	1.08E-03	2.793	Hv_Conlig_13952	968	832-857	XP_013185622 splicing factor 3A subunit 2 isoform X1 Amyelotus transilella	3.00E-139
-		Tag_225	CATGCGCGCGGTGGGCGCGGCTT	293	27	74.354	26.983	5.25E-09	2.756	no hit	-	-	-	-
-		Tag_751	CATGGAATCCGCGAGGCGAGGGTCT	54	5	13.704	4.997	1.08E-02	2.742	no hit	-	-	-	-

Primary metabolic process/hydrolase activity	Tag_586 CATGGCTGCACTGCAAAATTGGTGAT	86	8	21.824	7.995	1.46E-03	2.730	Hv_Contig_5238	1606	36-11	XP_004823722[putative serine protease K1244.7 <i>Bombyx mori</i>]	0.00E+00
Translation/Ribosome biogenesis	Tag_223 CATGGTCTTCAAGGACGACGATAGAC	295	28	74.862	27.982	9.48E-09	2.675	Hv_Contig_13427	952	506-531	XP_013138403[ubiquitin-40S ribosomal protein S27a isoform X2 <i>Papilio polytes</i>]	1.00E-84
-	Tag_696 CATGCGCGGTGGCTCCGGTGGCCCG	63	6	15.987	5.996	6.98E-03	2.666	no hit	-	-	-	-
Cytoskeleton	Tag_101 CATGCGCAGTGCCGCGTCGCGTGCG	755	72	191.595	71.954	7.95E-20	2.663	Hv_Contig_42	6714	6601-6626	XP_013169164[myosin heavy chain, non-muscle <i>Papilio xuthus</i>]	0.00E+00
unknown	Tag_160 CATGTTGGCGTGAACGGGCTGTGTGT	437	42	110.897	41.973	4.90E-12	2.642	Hv_Contig_3059	2024	1967-1992	XP_014361499[protein yellow-like <i>Papilio machaon</i>]	0.00E+00
-	Tag_700 CATGCGCGGTGATTCCGGTGCCCT	62	6	15.734	5.996	8.05E-03	2.624	no hit	-	-	-	-
-	Tag_521 CATGCGCGGTGACTCTGGTGCCCT	103	10	26.138	9.994	7.38E-04	2.615	no hit	-	-	-	-
-	Tag_859 CATGCGCTGACACAGGTGAAGCAG	41	4	10.405	3.997	3.04E-02	2.603	no hit	-	-	-	-
Translation/Ribosome biogenesis	Tag_961 CATGCGCCAGTCTCTGGTCTTCC	41	4	10.405	3.997	3.04E-02	2.603	Hv_Contig_36982	389	264-239	NP_001298498[60S ribosomal protein L37 <i>Papilio polytes</i>]	6.00E-50
-	Tag_967 CATGTCTTGGCAGCGGTGGGCGCTC	41	4	10.405	3.997	3.04E-02	2.603	no hit	-	-	-	-
Unknown	Tag_100 CATGCGCGCGGTGTGACGTACAGG	757	74	192.103	73.953	3.23E-19	2.598	Hv_Contig_2569	2167	1840-1865	XP_004829441[WEF family protein Aaag27595, chloroplastic-like isoform X1 <i>Bombyx mori</i>]	1.00E-180
-	Tag_780 CATGTTGTGCTCGGCTGGCCAAAG	51	5	12.942	4.997	1.67E-02	2.590	no hit	-	-	-	-
Nucleic acid binding	Tag_183 CATGTCCACGGCTCGCACCGCTACG	382	38	96.940	37.976	2.97E-10	2.553	Hv_Contig_11722	1036	776-801	XP_004822819[pnc finger protein 330 homolog <i>Bombyx mori</i>]	1.00E-143
Signal transduction	Tag_969 CATGCGGCGCTGCGGTGCTGCCGC	40	4	10.151	3.997	3.51E-02	2.539	Hv_Contig_3666	1889	507-482	XP_013200279[protein LMBRL1 <i>Amyelois transitella</i>]	0.00E+00
-	Tag_871 CATGTTGTGTTCTGCTGGCCAMCG	40	4	10.151	3.997	3.51E-02	2.539	no hit	-	-	-	-
Unknown	Tag_660 CATGCCAGCTCCGCCGCGAGGCATC	70	7	17.764	6.996	6.02E-03	2.539	Hv_Contig_9034	1206	624-649	EH172715[hypothetical protein KGM_16094 <i>Danaus plexippus</i>]	6.00E-132
-	Tag_263 CATGGTCCGCAATCTCTCGGACTC	239	24	60.651	23.985	6.84E-07	2.529	no hit	-	-	-	-
-	Tag_9 CATGCGGCGGTGACTCCGGTGCCCG	12982	1305	3294.425	1304.163	5.17E-287	2.526	no hit	-	-	-	-