Table S4. Identification of differentially expressed proteins in the antennae of sexually mature drone of *Apis mellifera ligusitca* and *Apis cerana cerana*

Spot Number	Experimental p*I* /*M*r(kDa)	Theoretical p*I* /*M*r(kDa)	Sequence Coverage	Matched/ Searched	Score	Protein Name	Accession Number	Mean± SD *Apis mellifera ligustica*	Mean± SD *Apis cerana cerana*	p-value
Carbohydrate and energy metabolism										
D11	79.98/6.80	73.27/6.75	37%	25/79	145	**Succinate dehydrogenase (scs-fp, EC 1.3.5.1)**	gil66505480	3002±41^{a}	1137±19^{b}	0.001116
D14	70.76/6.65	60.23/5.84	50%	34/71	217	**Malic enzyme(Men)**	gil110761561	2056±79^{a}	241±9^{b}	0.003162
D12	76.89/6.82	73.272/6.75	40%	26/76	121	**Succinate dehydrogenase (EC 1.3.5.1)**	gil66505480	416±18^{a}	264±6^{b}	0.00352
D15	72/6.84	60.57/6.35	35%	16/40	131	**Zwischenferment (Zw, EC 1.1.1.49)**	gil110750934	757±27^{a}	333±11^{b}	0.001193
D18	61.56/6.02	40.33/5.66	62%	24/62	222	**arginine kinase (Argk)**	gil58585146	1055±29^{a}	618±14^{b}	0.029249
D19	61.33/6.29	55.94/6.69	49%	22/57	193	**Aldehyde dehydrogenase (Aldh, EC 1.2.1.3)**	gil66530423	8672±176^{a}	742±30^{b}	1.04E-05
D20	60.38/7.47	55.94/6.69	49%	22/57	127			764±38^{a}	0	
D21	58.82/6.79	40.181/5.51	53%	25/76	159	**Enolase (Eno, EC 4.2.1.11)**	gil110761968	5734±99^{a}	1579±32^{b}	0.010647
D23	52.016/7.87	47.016/6.87	85%	35/124	271	**Isocitrate dehydrogenase (EC 1.1.1.42)**	gil110764717	1342±45^{a}	0	
D29	42.471/7.63	36.873/6.67	45%	15/33	146	**aldehyde reductase (ARY, EC 1.1.1.21)**	gil110763386	3502±63^{a}	1024±21^{b}	0.021907
D30	48.55/7.21	36.87/6.67	51%	21/76	195		gil110763386	2015±63^{a}	1054±27^{b}	0.035228
D34	38.843/7.17	40.873/7.17	35%	6/24	130		gil110763386	1851±50^{a}	1012±40^{b}	0.018753
D31	48.81/8.84	36146/8.11	38%	11/37	118	**Glyceraldehyde-3-phosphate dehydrogenase 2 (GAPDH II, EC 1.2.1.12)**	gil48142692	6272±98^{a}	0	
D35	42.15/6.45	36.19/6.25	40%	16/39	134	**Malate dehydrogenase (MDH1, EC 1.1.1.37)**	gil66506786	1245±42^{a}	573±14^{b}	0.027093

D37	41.78/6.64	29.93/6.35	479%	22/49	138	**Carbonic anhydrase 1 (CAH1, EC 4.2.1.1)**	gil48095863	1502±37^{a}	0	
D39	39.49/7.91	26.29/7.67	68%	15/37	163	**Vacuolar ATP synthase subunit E (vha26)**	gil66556287	919±45^{a}	397±51^{b}	0.027183
D42	36.17/7.60	35.4/9.36	57%	27/91	167	**Phosphoglyceromutase (Pglym78, EC 5.4.2.1)**	gil66550890	5645±76^{a}	0	
D44	36.47/6.12	28.86/7.01	34%	9/25	112	**CG9360 (EC 1.1.-.-)**	gil110749017	984±41^{a}	0	
D45	34.16/6.78		51%	11/36	128			6061±95^{a}	1322±25^{b}	3.34E-05
D46	35.91/7.25		29%	10/29	110			1815±92^{a}	0	
D47	35/7.12		29%	10/29	110			6920±76^{a}	4482±79^{b}	0.016126
D66	20.3/4.44	17607/5.09	39%	5/15	85	**lethal (1) G0230 (l(1)G0203, EC 3.6.3.14, EC 3.6.3.6)**	gil66517317	7536±30^{a}	1121±82^{b}	0.003263
D74	71.67/6.76	60231	19%	2/9	344	**Malic enzyme (Men)**	gil110761561	0	686±16^{a}	
D77	61.59/6.58	55936/ 6.69	31%	4/18	527	**Aldehyde dehydrogenase (Aldh, EC 1.2.1.3)**	gil66530423	0	1818±31^{a}	
D78	61.22/6.68		28%	2/13	431			0	1073±23^{a}	
D79	61.22/6.78		34%	6/19	777			0	3713±67^{a}	
D83	57.28/7.81	48649/ 8.11	46%	18/39	447	**lethal (1) G0255 (l(1)G0255)**	gil110767168	0	3825±41^{a}	
D103	18.68/4.59	17607/ 5.09	21%	2/4	213	**lethal (1) G0230 (l(1)G0203, EC 3.6.3.14, EC 3.6.3.6)**	gil66517317	0	10611±187^{a}	
D84	54.3/7.66	47016/ 6.87	47%	13/27	275	**Isocitrate dehydrogenase (Idh)**	gil110764717	0	656±30^{a}	
D86	49.37/7.85	39975/7.57	70%	21/40	676	**Aldolase (Ald)**	gil110748949	0	2174±55^{a}	
D88	49.57/6.89	39.68/7.52	50%	17/86	144	**lethal (1) G0156 (l(1)G0156 , EC 1.1.1.41)**	gil48102814	2118±79^{b}	4598±89^{a}	0.00044
D89	45.36/6.75	36873/ 6.67	45%	19/27	518	**aldehyde reductase (ARY, EC 1.1.1.21)**	gil110763386	234±24^{b}	3360±53^{a}	0.006824

D90	46.74/6.27	36193/6.25	47%	16/24	412	**mitochondrial malate dehydrogenase precursor (Mdh1, EC 1.1.1.37)**	gil66506786	0	5330±91^{a}	
Fatty acid metabolism										
D8	78.02/6.32	64.20/6.12	37%	22/42	147	**juvenile hormone esterase (Jhe, EC 3.1.1.59)**	gil58585076	1956±59^{a}	607±23^{b}	0.004123
D9	76.62/6.21		43%	26/51	172			1993±236^{a}	571±19^{b}	0.002618
D10	77.33/6.57		32%	18/49	122			3561±68^{a}	754±17^{b}	0.005011
D16	73.323/5.84	83.333/5.94	14%	12/17	352	**long-chain-fatty-acid-CoA ligase (LCFAC, EC 6.2.1.3)**	gil110762211	595±30^{a}	0	
D27	55.73/7.27	46.83/8.51	42%	19/51	129	**Probable medium-chain specific acyl-CoA dehydrogenase (MCAD, EC 1.3.99.3)**	gil66499429	1522±13^{a}	0	
D36	41.76/5.28	34.517/5.15	68%	21/73	169	**4-nitrophenylphosphatase (EC 3.1.3.41)**	gil48141571	2775±55^{a}	0	
D48	42.865/8.26	32996/8.16	31%	15/35	109	**acyltransferase (EC 2.3.1.-)**	gil110763897	1119±11^{a}	716±32^{b}	0.012024
D100	31.63/8.68	26.939/7.77	56%	15/67	164	**Triosephosphate isomerase 1 (Tpi, EC 5.3.1.1)**	gil148224276	3730±22^{b}	5651±31^{a}	0.020554
Amino acid and Nucleotide metabolism										
D3	90.35/6.75	76.63/6.09	27%	29/57	164	**Nucleotidyltransferase (EC 2.7.7.7)**	gil110755367	1855±65^{a}	968±51^{b}	0.002182
D40	53.53/6.77	46.444/5.36	28%	12/45	89	**serine-type endopeptidase (HtrA2,EC 3.4.21)**	gil110758534	812±39^{a}	0	
D75	66.65/7.58	62060/	43%	6/27	882	**Glutamate dehydrogenase (GDH, EC 1.4.1.3)**	gil66523390	570±45^{b}	964±61^{a}	0.001799
D76	66.65/7.68		55%	26/49	598			429±36^{b}	3204±61^{a}	0.007587
D85	53.34/5.95	41.808/6.42	30%	11/55	84	**glutamine synthetase (Gs1)**	gil283436154	1306±38^{b}	2195±32^{a}	0.000748
Development										
D24	53.67/5.95	48.98/6.97	33%	19/92	100	**skpA associated protein (skpA, EC 6.2.1.5)**	gil66548261	2636±43^{a}	1392±31^{b}	0.000474

D49	32.61/7.76	27.697/6.86	48%	11/67	100	**Windbeutel (Wbl)**	gil110751310	1456±43[a]	851±14[b]	0.000335
D82	60.06/8.50	59.76/9.00	33%	27/56	214	**Bellwether (Blw)**	gil48100966	7227±145[b]	26838±336[a]	0.001237
D96	36.36/4.79	28.17/4.79	33%	10/28	86	**14-3-3 protein zeta (14-3-3zeta)**	gil48097086	2102±38[b]	4552±68[a]	0.019766
Antioxidant system										
D50	32.71/8.18	26.608/6.45	49%	14/57	105	**short-chain dehydrogenases/reductases (SDR) family**	gil110749015	2306±42[a]	0	
D51	31.52/5.12	17.69/5.40	39%	10/38	126	**Glutathione S transferase S1 (GstS1, EC 2.5.1.18))**	gil66534655	2428±44[a]	733±28[b]	0.00012
D53	31.17/5.49		39%	7/29	103			12156±345[a]	7624±99[b]	0.000805
D52	30.19/5.25		35%	8/25	112			3140±71[a]	788±40[b]	0.003115
D58	31.30/9.30	20.34/5.60	39%	11/24	110	**Glutathione S-transferase 1-1 (GstD1 , EC 2.5.1.18)**	gil110763730	2673±32[a]	0	
D55	31.29/7.73	31.44/6.01	52%	17/73	104			1263±20[a]	0	
D54	30.18/7.19	21.94/5.65	68%	13/92	101	**thioredoxin peroxidase 1 (Jafrac1, EC 1.11.1.15)**	gil66548188	2691±59[a]	1309±55[b]	0.002069
D59	30.32/5.59		49%	10/22	129			3418±12[a]	481±10[b]	0.006273
D60	30.27/5.98		66%	16/84	141			11332±855[a]	1422±60[b]	0.009647
D56	31.48/8.98	31.44/6.01	45%	8/19	98	**Glutathione S-transferase 1 (GstD1, EC 2.5.1.18)**	gil76262439	6505±137[a]	0	
D57	31.48/8.98	31.44/6.01	45%	8/19	98			6505±137[a]	0	
D63	22.95/7.03	19.373/7.63	58%	13/90	104	**Glutathione peroxidase (PHGPx)**	gil66546646 gil66546646	1087±21[a]	0	
D65	22.08/6.99	16.714/6.58	52%.	8/59	90	**Peroxiredooxin 5**	gil110756016	1873±50[a]	160±21[b]	0.041248
D67	19.75/6.59	15.795/6.21	73%	10/57	125	**superoxide dismutase [Cu-Zn] (Sod, EC 1.15.1.1)**	gil66513527	6733±42[a]	4103±40[b]	0.022842
D101	29.28/6.4	21944/5.65	80%	21/39	510	**thioredoxin peroxidase 1 (Jafrac1, EC 1.11.1.15)**	gil66548188	0	9079±86[a]	
Protein folding										

D1	99.62/5.01	92.15/4.96	41%	40/68	245	**Glycoprotein 93 (Gp93)**	gil110758921	1610±22^{a}	534±12^{b}	0.011845
D2	93.59/5.69	83.79/4.98	33%	29/77	147	**heat shock protein 90 (hsp83)**	gil229892248	1107±57^{a}	191±31^{b}	0.001086
D7	80.30/5.27	60.55/5.64	43%	26/69	166	**Heat shock protein 60 (Hsp60)**	gil66547450	3020±88^{a}	753±52^{b}	0.000824
D13	70.84/5.27		31%	16/32	142			2833±88^{a}	1300±62^{b}	0.00137
D41	38.6/7.45	27.8/6.95	40%	8/28	94	**Protein Efl21 (l(2)efl, EC 1.1.-.-)**	gil110750764	1937±38^{a}	713±51^{b}	0.011455
D43	34.21/5.14	23102/ 5.40	24%	4/7	87	**Protein lethal(2)essential for life(l(2)efl, EC 1.1.-.-)**	gil110750766	1045±51^{a}	445±9^{b}	0.010105
D73	53.86/7.66	47.49/6.30	31%	18/41	143	**Calreticulin (Crc)**	gil66545506	21057±421^{b}	124107±980^{a}	0.000122
D80	59.79/4.83	42.68/4.84	26%	11/40	98	**Hsc70-interacting protein 2 (HIP-R)**	gil66511001	1386±67^{b}	2602±27^{a}	0.000474
D99	30.81/6.01	22661/5.88	56%	12/52	139	**Protein lethal(2)essential for life(l(2)efl, EC 1.1.-.-)**	gil110750754	1395±32^{b}	3305±84^{a}	0.022754
D106	12.56/8.61	11.396/8.01	50%	7/23	97	**CG11267**	gil66547447	3638±175^{b}	9385±184^{a}	0.000343
Cytoskeleton										
D17	64.1/4.97	50.6/4.75	45%	19/46	175	**Beta-1-tubulin (betaTub56D)**	gil48095525	19977±137^{a}	6005±52^{b}	0.005035
D32	46.25/4.74	32.25/4.73	52%	17/111	102	**Tropomyosin 2 (Tm2)**	gil66522386	3751±39^{a}	1464±26^{b}	0.018795
D64	22.14/6.15	17.05/6.17	57%	13/43	95	**Twinstar (Tsr)**	gil110751158	3367±65^{a}	2221±19^{b}	0.01199
D61	24.39/5.23		71%	15/35	134			1354±19^{a}	0	
D72	11.20/4.65	33.00/4.74	46%	18/61	140	**Tropomyosin 1 (Tm1)**	gil48094441	3232±79^{a}	0	
D93	36.98/4.97	23.53/4.78	52%	12/18	457	**Myosin regulatory light chain 2 (MLC-2)**	gil66555437	932±36^{b}	2210±26^{a}	8.78E-06
D95	37.93/4.45		61%	18/86	85			444±15^{b}	2620±88^{a}	0.002253
D94	37.23/4.73		65%	19/82	95			588±20^{b}	2765±27^{a}	1.17E-05
D102	22.54/6.27	17049/ 35%	33%	2/5	217	**Protein twinstar (tsr)**	gil110875115	0	1121±45^{a}	
Transporter										
D4	87.48/6.76	80.03/6.77	39%	25/99	166	**Transferring (tsf1)**	gil58585086	672±51^{a}	185±26^{b}	0.001984

D5	87.06/6.94		33%	21/57	164			1890 ± 51^{a}	503 ± 40^{b}	0.026263
D6	87.14/7.13		48%	31/79	234			2665 ± 18^{a}	782 ± 75^{b}	0.017511
D25	59.65/6.87	43.86/5.37	51%	28/107	126	**CG31974 (EC 1.1.1.37)**	gil110758754	3212 ± 69^{a}	0	
D26	52.47/6.85	46.72/7.57	43%	22/75	89	**CG10513 (EC 1.10.2.2, EC 3.4.24.-)**	gil66522463	3708 ± 112^{a}	773 ± 39^{b}	0.001221
D28	52.2/7.88		64%	43/102	221			18339 ± 285^{a}	6989 ± 59^{b}	0.002255
D33	45.95/5.8	38.14/5.76	23%	10/25	98	**Guanine nucleotide-binding protein subunit beta-1 (Gbeta13F)**	gil66523907	1789 ± 73^{a}	1184 ± 74^{b}	
D38	40.19/6.91	31757/6.20	51%	19/57	110	**Vibrator (vib)**	gil66557640	4001 ± 40^{a}	0	
D68	18.72/5.93	15.60/5.71	62%	12/37	139	**odorant binding protein 14 (obp14/Obp99a)**	gil94158822	5163 ± 57^{a}	91.7 ± 8^{b}	0.001442
D69	13.55/4.69	15.54/4.76	44%	6/15	100	**odorant binding protein 21 (0bp21/Obp56d)**	gil94158718	1661 ± 52^{a}	0	
D70	12.29/4.48	15.54/4.55	31%	6/16	87	**odorant-binding protein 16 (obp16, obp57c)**	gil94158709	2627 ± 39^{a}	0	
D71	13.97/5.58	16.95/6.30	61%	22/42	123	**odorant binding protein 5 (obp5/Obp56a)**	gil58585124	2733 ± 58^{a}	1545 ± 74^{b}	0.004612
D81	59.18/7.81	61.25/8.53	18%	11/37	83	**CG1640 (EC 2.6.1.2, EC 4.4.1.14)**	gil66563168	1087 ± 61^{b}	4976 ± 38^{a}	0.009975
D87	52.09/8.57	46719/ 7.57	43%	16/28	387	**CG10513 (EC 1.10.2.2, EC 3.4.24.-)**	gil66522463	0	45719 ± 842^{a}	
D97	34.93/8.18	30634/ 8.25	45%	6/11	604	**porin**	gil66521459	0	13452 ± 548^{a}	
D98	33.47/7.93	24.857/6.96	63%	13/67	128	**ran**	gil48097366	1965 ± 51^{b}	5184 ± 184^{a}	0.000683
D104	12.59/4.19	14.03/4.44	67%	18/62	99	**General Odorant Binding Protein Asp2 Chain A (obp2/Obp56h)**	gil78100778	2326 ± 99^{b}	5245 ± 21^{a}	0.001012
D105	11.53/4.49	13.88/4.21	50%	2/105	105	**chemosensory protein 1 (CSP1)**	gil94158718	0	13165 ± 722^{a}	
Protein biosynthesis										

D22	55.54/7.46	53.014/8.16	52%	26/76	150	**Elongation factor Tu mitochondrial (EfTuM)**	gi|66518848	5800±120[a]	0	
D62	23.74/5.16	17.92/5.19	72%	12/75	96	**eIF-5A**	gi|110767655	5138±239[a]	1808±80[b]	0.001158
Unknown function										
D91	39.25/6.63	34.89/6.52	33%	6/12	318	**CG11550 (EC 1.11.1.15)**	gi|66499360	891±85[b]	6850±205[a]	0.000374
D92	38.32/6.53		39%	9/19	102			1695±97[b]	3895±343[a]	0.003519

Notes: Spot Number corresponds to the number of protein spots in Figure 3. Theoretical molecular weight (*M*r) and isoelectric point (p*I*) of the identified proteins were retrieved from the protein database of NCBInr. Experimental *M*r and p*I* were calculated with PDQuest Software and internal standard molecular mass markers. Sequence coverage is the ratio of the number of amino acids in every peptide that matches with the mass spectrum divided by the total number of amino acids in the protein sequence. Matched peptide is the number of paring an experimental fragmentation spectrum to a theoretical segment of protein and searched is the total searched peptide. Mascot score is search against the database NCBInr. Protein name is given when proteins were identified by MALDI-TOF/MS. Accession number is the unique number given to mark the entry of a protein in the database NCBInr. Relative V±SE is the mean values of relative protein amount. p-value ≤ 0.05 were considered as differentially expressed proteins where a was significant higher than b.