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Title: Infection of honey bees with Acute bee paralysis virus does not trigger humoral or cellular immune responses

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Table S1 Proteins up-regulated in fourth instar bee larvae 24 h post-injection of 10^3 ABPV particles (illustrated in Fig. 3A and Fig. 4A)

No.	Protein	Accession (NCBI)	Calc. masses [Da][a]	SP[b]	Mowse score[d]	Sequence coverage [%][e]
1	Glycogen phosphorylase	66557932	97.329	-	490	14
	Elongation factor-2 like	66508439	94.582	-	510	15
	TER 94	66534286	88.895	-	190	13
2	Heat shock protein 90	229892248	83.383	-	415	31
	Heat shock protein 1α	110749824	82.753	-	375	22
3	Heat shock protein cognate 5	229892203	75.403	-	509	18
4	Protein disulfide-isomerase A3 (ERp60)	66546657	55.856	18	406	19
	Hexamerin 70a (238-684)[c]	148357839	53.497	21	593	41
	Hexamerin 70b (255-683)[c]	58585148	49.359	21	805	46
5	Major Royal Jelly Protein 1	58585098	48.886	19	810	45
6	3-Ketoacyl-CoA thiolase (=Yippee interacting protein 2)	48097100	42.503	-	1258	68
7	Aldose reductase like	66525576	36.082	-	360	33
	Lambda crystallin-like protein	209180477	35.860	-	392	29
	Glyceraldehyde-3-phosphate dehydrogenase 2	48142692	35.883	-	333	30
8	N-acetylneuraminate pyruvate lyase	110755974	34.019	-	243	24
9	Trypsin-like serine protease	110762229	28.596	18	340	25
	15-Hydroxyprostaglandin dehydrogenase	66518230	28.776	-	310	23
	3-Hydroxyacyl-CoA dehydrogenase	110760701	27.099	-	189	18
	Short-chain dehydrogenase/reductase (SDR)	58585184	27.191	-	175	27
	Proteasome subunit alpha	66541426	26.718	-	144	19
10	Heat shock protein beta-1-like	110757651	25.565	-	160	14
	Peroxiredoxin-like protein	283436152	25.133	-	143	13
	Glutathione S-transferase S1	237681308	23.761	-	173	27
11	Thioredoxin-2	48104680	12.016	-	185	16
	Heat shock protein 10kD	66547447	11.403	-	390	41

[a] Molecular weights were deduced from the Expasy/ProtParam program

[b] Predictions for signal peptides (SP) and cleavage sites were obtained with the TargetP program

[c] Putative lengths of degradation products

[d] Protein scores are derived from ion scores. Individual ion scores >60 indicate identity or extensive homology ($p<0.05$)

[e] The sequence coverage represents the percentage of coverage by tryptic peptides