

Table 1: Data mass spectroscopy (GC/MS-MS)

Sample	Protein name	Accession number	Protein molecular weight	Protein identification probability	Exclusive unique peptide count	Total spectrum count	Percentage sequence coverage	Mascot score
1	Uncharacterized protein OS= <i>Apis mellifera</i>	A0A088AS56_API ME	367,625.3	100	135	218	47.4	3503
2	Protein families 1 Vitellogenin OS= <i>Apis mellifera</i>	A0A088ADL8_API ME	200,959.8	100	5	104	45.5	1419
2	Protein families 1 Vitellogenin OS= <i>Apis mellifera</i>	VIT_API ME	201,051.9	100	2	99	41.4	1269
3	Protein families 1 Vitellogenin OS= <i>Apis mellifera</i>	A0A088ADL8_API ME	200,959.8	100	4	56	31.9	768
3	Protein families 1 Vitellogenin OS= <i>Apis mellifera</i>	VIT_API ME	201,051.9	100	2	54	29.3	707
4	Pyruvate carboxylase OS= <i>Apis mellifera</i>	A0A087ZNH6_API ME	131,882.5	100	8	8	9.7	98
4	Protein families 1 Vitellogenin OS= <i>Apis mellifera</i>	A0A088ADL8_API ME	200,959.8	100	4	45	25.9	644
4	Protein families 1 Vitellogenin OS= <i>Apis mellifera</i>	VIT_API ME	201,051.9	100	2	43	23.3	587
Triple	Uncharacterized protein OS= <i>Apis mellifera</i>	A0A088A3B7_API ME	87,207.6	100	3	3	6.49	92
Triple	6-phosphofructokinase OS= <i>Apis mellifera</i>	A0A088AHG6_API ME	98,518.8	100	2	2	2.93	69
Triple	Uncharacterized	A0A087Z	71,772.3	100	4	4	7.75	50

	protein OS= <i>Apis mellifera</i>	Q27_API ME						
Triple	Alpha-glucosidase OS= <i>Apis mellifera</i>	A0A0B4J2P5_API ME	66,596.7	100	7	7	13.1	105
Triple	Uncharacterized protein OS= <i>Apis mellifera</i>	A0A087ZTY7_API ME	75,404.6	100	3	3	6.11	42
Triple	Alpha-glucosidase; Uncharacterized protein OS= <i>Apis mellifera</i>	Q25BT8_API ME	67,359.4	100	4	4	7.99	80
Triple	Aconitate hydratase, mitochondrial OS= <i>Apis mellifera</i>	A0A087ZXXK3_API ME	85,998.7	100	20	22	28.8	234
Triple	Transferrin OS= <i>Apis mellifera</i>	A0A088AFH7_API ME	78,630.7	100	30	43	49.9	760
Triple	Uncharacterized protein OS= <i>Apis mellifera</i>	A0A088AJI5_API ME	76,681.3	100	19	29	34.1	612
Triple	Uncharacterized protein OS= <i>Apis mellifera</i>	A0A088AQB0_API ME	75,709.1	100	9	10	21.8	230