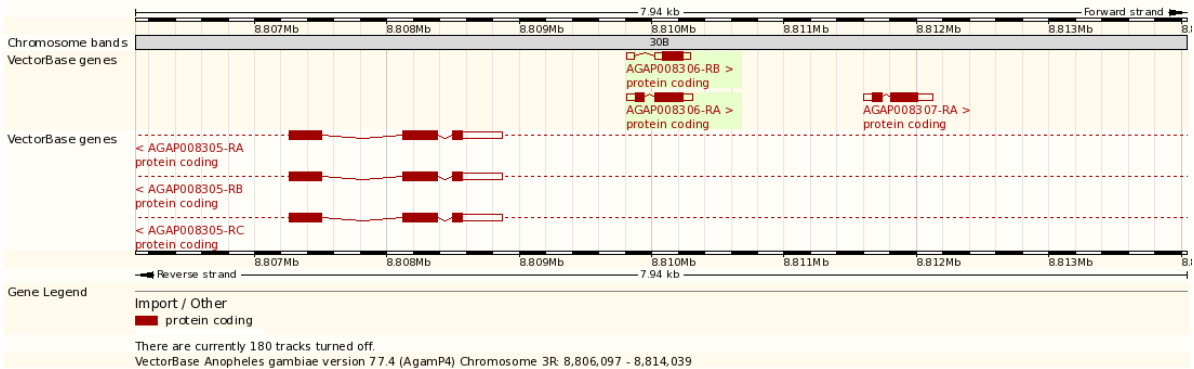


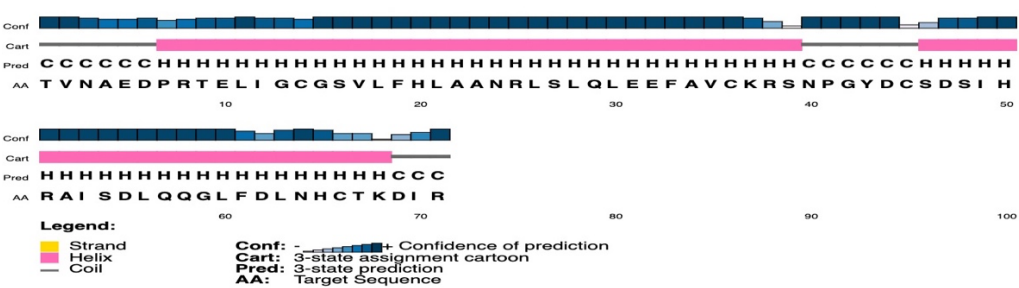
Figure S2: hyp10 and hyp12

(a)

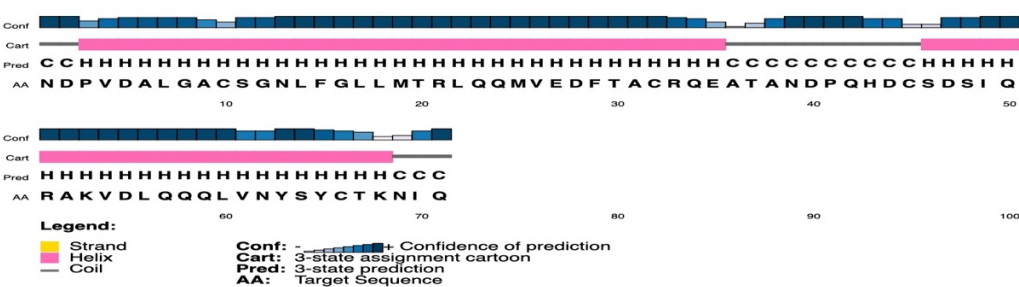


(b)

hyp10



hyp12



(c)

Sequence alignment

hyp12	1	MRFCVALIGLLC--SVQSVTANDPVDALGACSGNLFGLLMTRLQQMVE	48
hyp10	1	MRFLTVLTVGLLVWGVFATVNAEDPRTTELIGCGSVLFHLAANRLSLQLE	50
hyp12	49	DFTACRQEATANDPQHDCSDSIQRAKVDLQQQLVNYSYCTKNIQ	92
hyp10	51	EFAVCKR---SNPGYDCSDSIHRAISDLQQGLFDLNHCTKDIR	90

(d)

	Most frequent aminoacids		
hyp10	14.4% Leu	8.9% Val	
hyp12	12% Leu	10.9% Gln	8.7 Ala

Figure S2: hyp10 (AGAP008306)/hyp12 (AGAP008307) gene cluster. (a): scheme of the genomic region (chromosome 3R) where hyp10 and hyp12 are placed and separated by a short region of 1.2 kbp. (b): PSIPRED secondary structure prediction: the cartoons summarize the predictions of secondary structures of mature peptides (without SP) as calculated by PSIPRED on-line tool for hyp10 and hyp12. Structures with two helices (and 4 cysteines) are predicted. (c): sequence alignment of hyp10 and hyp12: cysteines are conserved. (d): table summarizing the most frequent aminoacids in the two candidates: both candidates present a high content of leucine.